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OM protein - protein search, using sw model

Run on: July 15, 2003, 11:03:04 ; Search time 14.3335 Seconds
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2493.521 Million cell updates/sec

Title: US-09-917-265-53
Perfect score: 1653
Sequence: 1 IWELEKDVYVVELDWHPDAP.....QARDRYYSSSWSDWASVSCS 307

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1653	100.0	307	10	US-09-917-265-53	Sequence 53, Appl
2	1653	100.0	329	10	US-09-917-265-59	Sequence 59, Appl
3	1653	100.0	329	10	US-09-917-265-108	Sequence 108, App
4	1653	100.0	511	10	US-09-917-265-67	Sequence 67, Appl
5	1653	100.0	533	10	US-09-917-265-62	Sequence 62, Appl
6	1554	94.0	307	12	US-10-079-616-2	Sequence 2, Appli
7	1554	94.0	329	10	US-09-917-265-30	Sequence 30, Appl
8	1554	94.0	329	12	US-10-079-616-1	Sequence 1, Appli
9	1550	93.8	328	10	US-09-917-265-56	Sequence 56, Appl
10	1546	93.5	307	10	US-09-917-265-27	Sequence 27, Appl
11	1546	93.5	511	10	US-09-917-265-44	Sequence 44, Appl
12	1546	93.5	533	10	US-09-917-265-39	Sequence 39, Appl
13	1419.5	85.9	328	9	US-10-172-399-8	Sequence 8, Appli
14	1419.5	85.9	526	10	US-09-828-825-4	Sequence 4, Appli
15	1419.5	85.9	527	10	US-09-828-825-2	Sequence 2, Appli
16	1419.5	85.9	537	10	US-09-828-825-8	Sequence 8, Appli
17	1419.5	85.9	537	10	US-09-828-825-16	Sequence 16, Appl
18	1419.5	85.9	542	10	US-09-828-825-6	Sequence 6, Appli
19	1419.5	85.9	542	10	US-09-828-825-14	Sequence 14, Appl
20	1419.5	85.9	547	10	US-09-828-825-10	Sequence 10, Appl
21	1419.5	85.9	547	10	US-09-828-825-12	Sequence 12, Appl
22	1418.5	85.8	328	9	US-10-247-463-6	Sequence 6, Appli
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25	1418.5	85.8	328	10	US-09-924-703-4	Sequence 4, Appli
26	1418.5	85.8	503	9	US-09-920-262A-9	Sequence 9, Appli
27	1058.5	64.0	335	9	US-10-172-399-4	Sequence 4, Appli
28	1058.5	64.0	335	9	US-10-247-463-7	Sequence 7, Appli
29	193	11.7	315	9	US-09-935-868-16	Sequence 16, Appl
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31	193	11.7	360	9	US-09-935-868-15	Sequence 15, Appl
32	193	11.7	360	9	US-10-287-035-15	Sequence 15, Appl
33	193	11.7	468	9	US-10-247-463-12	Sequence 12, Appl
34	193	11.7	592	9	US-09-935-868-8	Sequence 8, Appli
35	193	11.7	592	9	US-10-287-035-8	Sequence 8, Appli
36	193	11.7	1158	9	US-09-935-868-26	Sequence 26, Appl
37	193	11.7	1158	9	US-10-287-035-26	Sequence 26, Appl
38	193	11.7	1168	9	US-09-935-868-24	Sequence 24, Appl
39	193	11.7	1168	9	US-10-287-035-24	Sequence 24, Appl
40	176.5	10.7	460	9	US-10-247-463-13	Sequence 13, Appl
41	149.5	9.0	422	9	US-10-247-463-11	Sequence 11, Appl
42	149.5	9.0	422	10	US-09-924-338-2	Sequence 2, Appli
43	148.5	9.0	432	9	US-10-247-463-10	Sequence 10, Appl
44	146.5	8.9	441	10	US-09-924-338-4	Sequence 4, Appli
45	129	7.8	229	9	US-10-000-776-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-917-265-53
; Sequence 53, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-917-265-53

Query Match 100.0%; Score 1653; DB 10; Length 307;
Best Local Similarity 100.0%; Pred. No. 1e-131;
Matches 307; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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Db          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
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Db        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
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Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
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Db        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300

Qy        301 WASVSCS 307
              |||||||
Db        301 WASVSCS 307


RESULT 2
US-09-917-265-59
; Sequence 59, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-59

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  Best Local Similarity   100.0%;  Pred. No. 1.1e-131;
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Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
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Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
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Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
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Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 3
US-09-917-265-108
; Sequence 108, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-108

  Query Match             100.0%;  Score 1653;  DB 10;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-131;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
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Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
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Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
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Db        323 WASVSCS 329


RESULT 4
US-09-917-265-67
; Sequence 67, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-67

  Query Match             100.0%;  Score 1653;  DB 10;  Length 511;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-131;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
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Db         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120

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Db        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
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Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
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Db        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300

Qy        301 WASVSCS 307
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Db        301 WASVSCS 307


RESULT 5
US-09-917-265-62
; Sequence 62, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-62

  Query Match            100.0%;  Score 1653;  DB 10;  Length 533;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-131;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
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Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
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Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
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Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
                |||||||
Db        323 WASVSCS 329


RESULT 6
US-10-079-616-2
; Sequence 2, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 307 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-079-616-2

  Query Match            94.0%;  Score 1554;  DB 12;  Length 307;
  Best Local Similarity   93.8%;  Pred. No. 2.4e-123;
  Matches  288;  Conservative    9;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
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Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
                ||||||||||||:|||||| |||||||||| |||||:|||||||||||||||||||:
Db        121 WWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 180

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 240

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
                |||||||||||| :| |||||||||||| ||||||||||||||||||||||||||||:
Db        241 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 300

Qy        301 WASVSCS 307
                |||||||
Db        301 WASVSCS 307


RESULT 7
US-09-917-265-30
; Sequence 30, Application US/09917265
```

```
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-30

  Query Match            94.0%;  Score 1554;  DB 10;  Length 329;
  Best Local Similarity   93.8%;  Pred. No. 2.6e-123;
  Matches  288;  Conservative    9;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:|||||||||||||||||||||:|||||||||| |||||||||||||||||||
Db         23 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               ||||||||||:||| | |||||||||||||||:||||||||||||||||||||||||
Db         83 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||:|||||| |||||||||| |||||:|||||||||||||||||||||:
Db        143 WWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||.
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| :| |||||||||||| |||||||||||||||||||||||||||:
Db        263 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 8
US-10-079-616-1
; Sequence 1, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 329 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-079-616-1

  Query Match            94.0%;  Score 1554;  DB 12;  Length 329;
  Best Local Similarity   93.8%;  Pred. No. 2.6e-123;
  Matches  288;  Conservative    9;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:|||||||||||||||||||||:|||||||||| |||||||||||||||||||
Db         23 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               ||||||||||:||| | |||||||||||||||:||||||||||||||||||||||||
Db         83 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||:|||||| |||||||||| |||||:|||||||||||||||||||||:
Db        143 WWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||.
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| :| |||||||||||| |||||||||||||||||||||||||||:
Db        263 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 9
US-09-917-265-56
; Sequence 56, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
;   LENGTH: 328
;   TYPE: PRT
```

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;   ORGANISM: Felis catus
US-09-917-265-56

  Query Match             93.8%;  Score 1550;  DB 10;  Length 328;
  Best Local Similarity   93.8%;  Pred. No. 5.7e-123;
  Matches  287;  Conservative    9;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              |||||||:|||||||||||||||||||||:|||||||||| |||||||||||||||||||
Db         23 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||:||| | |||||||||||||||:|||||||||||||||||||||||||
Db         83 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||:|||||| |||||||||| ||||:||||||||||||||||||||||||:
Db        143 WWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| :| |||||||||||| ||||||||||||||||||||||||||||||:
Db        263 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 322

Qy        301 WASVSC 306
              ||||||
Db        323 WASVSC 328


RESULT 10
US-09-917-265-27
; Sequence 27, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 307
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-27

  Query Match             93.5%;  Score 1546;  DB 10;  Length 307;
  Best Local Similarity   93.5%;  Pred. No. 1.1e-122;
  Matches  287;  Conservative    9;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:|||||||||||||||||||||:|||||||||| |||||||||||||||||||
Db          1 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 60

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||:||| | |||||||||||||||:|||||||||||||||||||||||||
Db         61 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 120

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||:|||||| |||| ||||| ||||:||||||||||||||||||||||||:
Db        121 WWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 180

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 240

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| :| |||||||||||| ||||||||||||||||||||||||||||||:
Db        241 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 300

Qy        301 WASVSCS 307
              |||||||
Db        301 WASVSCS 307


RESULT 11
US-09-917-265-44
; Sequence 44, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-44

  Query Match             93.5%;  Score 1546;  DB 10;  Length 511;
  Best Local Similarity   93.5%;  Pred. No. 2.2e-122;
  Matches  287;  Conservative    9;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:|||||||||||||||||||||:|||||||||| |||||||||||||||||||
Db          1 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 60

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||:||| | |||||||||||||||:|||||||||||||||||||||||||
Db         61 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 120

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||:|||||| |||| ||||| ||||:||||||||||||||||||||||||:
Db        121 WWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 180

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 240

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| :| |||||||||||| ||||||||||||||||||||||||||||||:
Db        241 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 300

Qy        301 WASVSCS 307
              |||||||
Db        301 WASVSCS 307


RESULT 12
US-09-917-265-39
; Sequence 39, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
```

```
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-39

  Query Match             93.5%;  Score 1546;  DB 10;  Length 533;
  Best Local Similarity   93.5%;  Pred. No. 2.4e-122;
  Matches  287;  Conservative    9;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:||||||||||||||||||:|||||||||| ||||||||||||||||||||
Db         23 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               ||||||||||:||| | ||||||||||||||:||||||||||||||||||||||||
Db         83 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||:|||||| |||| ||||| |||||:||||||||||||||||||||:
Db        143 WWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| :| |||||||||||| ||||||||||||||||||||||||||:
Db        263 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 13
US-10-172-399-8
; Sequence 8, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 328
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-172-399-8

  Query Match             85.9%;  Score 1419.5;  DB 9;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 6e-112;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||||:||| |||||:|||||||||||||||:||| ||| ||:||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 14
US-09-828-825-4
; Sequence 4, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 526
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-4

  Query Match             85.9%;  Score 1419.5;  DB 10;  Length 526;
  Best Local Similarity   85.0%;  Pred. No. 1.1e-111;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||||:||| ||||:|||||||||||||||:||| ||| ||:||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

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Qy        301 WASVSCS 307
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RESULT 15
US-09-828-825-2
; Sequence 2, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
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;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 527
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-09-828-825-2

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  Best Local Similarity   85.0%;  Pred. No. 1.1e-111;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

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Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
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Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
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Search completed: July 15, 2003, 11:11:44
Job time : 15.3335 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:27:32 ; Search time 2795.89 Seconds
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Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	983.8	99.7	990	6	AR151071	AR151071 Sequence
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3	977.4	99.0	1015	4	CFU49100	U49100 Canis famil
4	969.4	98.2	990	6	AR151061	AR151061 Sequence
5	879.8	89.1	990	6	AX076200	AX076200 Sequence
6	879.8	89.1	990	6	AX076482	AX076482 Sequence
7	879.8	89.1	1006	4	FCIL12P40	Y07762 F.catus mRN
8	879.8	89.1	4522	6	AX076209	AX076209 Sequence
9	879.8	89.1	4522	6	AX076476	AX076476 Sequence
10	878.2	89.0	990	4	FCU83184	U83184 Felis catus
11	827	83.8	990	6	AX154603	AX154603 Sequence
12	811	82.2	1058	4	ECIL12P40	Y11129 Equus cabal
13	809.4	82.0	1626	12	AF401989	AF401989 Synthetic
14	790.6	80.1	984	6	AX154600	AX154600 Sequence
15	785.8	79.6	984	6	AX154599	AX154599 Sequence
16	772.6	78.3	987	6	AR008950	AR008950 Sequence
17	772.6	78.3	987	6	AX154633	AX154633 Sequence
18	772.6	78.3	987	6	BD007070	BD007070 IL-12 gen
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20	772.6	78.3	987	6	I28591	I28591 Sequence 1
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23	772.6	78.3	1389	6	AX084106	AX084106 Sequence
24	772.6	78.3	1399	6	AR091391	AR091391 Sequence
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32	771	78.1	1080	9	MMU19841	U19841 Macaca mula
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35	769.8	78.0	1012	4	AF007576	AF007576 Capra hir
36	766.6	77.7	984	4	AF209435	AF209435 Ovis arie
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39	761.8	77.2	1012	4	BTU11815	U11815 Bos taurus
40	761.8	77.2	1019	6	E35794	E35794 Process for
41	760.2	77.0	993	4	CEU57752	U57752 Cervus elap
42	756.6	76.7	975	6	AX154597	AX154597 Sequence
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ALIGNMENTS

RESULT 1
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LOCUS AR151071 990 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 11 from patent US 6231850.
ACCESSION AR151071
VERSION AR151071.1 GI:15117121
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 990)
AUTHORS Okano,F., Satoh,M. and Yamada,K.
TITLE Canine interleukin 12
JOURNAL Patent: US 6231850-A 11 15-MAY-2001;
FEATURES Location/Qualifiers

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BASE COUNT      279 a    244 c    249 g    218 t
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  Best Local Similarity   99.8%;  Pred. No. 3.1e-274;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db        961 AGCGACTGGGCATCTGTGTCCTGCAGT 987


RESULT 2
E15017
LOCUS       E15017                   990 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 40kDa subunit,complete cds.
ACCESSION   E15017
VERSION     E15017.1  GI:5709700
KEYWORDS    JP 1998036397-A/1.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 1 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/1
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
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            FT                   /organism='Canis sp.'
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FEATURES             Location/Qualifiers
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BASE COUNT      279 a    244 c    249 g    218 t
ORIGIN

  Query Match           99.7%;  Score 983.8;  DB 6;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 3.1e-274;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

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Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
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Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db        961 AGCGACTGGGCATCTGTGTCCTGCAGT 987


RESULT 3
CFU49100
LOCUS       CFU49100                1015 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p40 subunit mRNA, complete cds.
ACCESSION   U49100
VERSION     U49100.1  GI:1223907
KEYWORDS    .
SOURCE      Canis familiaris.
  ORGANISM  Canis familiaris
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            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1015)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
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                     /db_xref="GI:1223908"
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                     LKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCV
                     QAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCS"
BASE COUNT      285 a    251 c    254 g    225 t
ORIGIN

  Query Match           99.0%;  Score 977.4;  DB 4;  Length 1015;
  Best Local Similarity   99.4%;  Pred. No. 2.3e-272;
  Matches  981;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTTCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGACCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAAGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCGTACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||||| ||||||
Db        961 AGCGACTGGGCATCTGTGTCCTGCAGT 987


RESULT 4
AR151061
LOCUS       AR151061                990 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6231850.
ACCESSION   AR151061
VERSION     AR151061.1  GI:15117111
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 1 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="unknown"
BASE COUNT      278 a    243 c    251 g    218 t
ORIGIN

  Query Match           98.2%;  Score 969.4;  DB 6;  Length 990;
  Best Local Similarity   98.9%;  Pred. No. 4.7e-270;
  Matches  976;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  ||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||||| | ||||||
Db        961 AGCGACTGGGCATCTGTGCCCTGCAGT 987


RESULT 5
AX076200
LOCUS       AX076200                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 1 from Patent WO0104155.
ACCESSION   AX076200
VERSION     AX076200.1  GI:12710825
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 1 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p40"
BASE COUNT      283 a    249 c    248 g    210 t
ORIGIN

  Query Match           89.1%;  Score 879.8;  DB 6;  Length 990;
  Best Local Similarity   93.2%;  Pred. No. 4.9e-244;
  Matches  920;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||||  |||||||||||||||||  ||||||||||||  ||||||||||  ||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              |||||||||||||||||||||| |||||| |||| ||||||||||||||||||| |||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180
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Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  ||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||  ||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
               ||||  |||| ||||||||| ||||||||||||||||||||||||||||||| |||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||||||||||| |||||||||| |||||| |||||||||| ||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              || ||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||| |||||||||| |||||||||||||| |||| || ||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||||| | |||||||||||||| |||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||| |||||||||| ||||| ||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
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RESULT 6
AX076482
LOCUS       AX076482                990 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 8 from Patent WO0104280.
ACCESSION   AX076482
VERSION     AX076482.1  GI:12711034
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 8 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 2, IL-12 p40"
BASE COUNT      283 a    249 c    248 g    210 t
ORIGIN
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Query Match 89.1%; Score 879.8; DB 6; Length 990;
Best Local Similarity 93.2%; Pred. No. 4.9e-244;
Matches 920; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

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Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||||||||||| |||||||||||| ||||||||||  ||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              |||||||||||||||||||||||||| |||| |||| |||||||||||||||||||| |||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  ||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||  ||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
               ||||  |||| ||||||||| ||||||||||||||||||||||||||||||| |||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||||||||||| |||||||||| |||||| |||||||||| ||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              || ||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||| |||||||||| |||||||||||||| |||| || ||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||||| | ||||||||||||||| |||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||| |||||||||| ||||| ||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 7
FCIL12P40
LOCUS       FCIL12P40                1006 bp    mRNA    linear   MAM 13-MAY-1997
DEFINITION  F.catus mRNA for interleukin-12 p40 chain.
ACCESSION   Y07762
VERSION     Y07762.1  GI:2102664
KEYWORDS    interleukin-12 p40.
SOURCE      cat.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 1006)
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
  MEDLINE   97246745
   PUBMED   9089110
REFERENCE   2  (bases 1 to 1006)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
FEATURES             Location/Qualifiers
     source          1. .1006
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .990
                     /gene="IL-12.p40"
     CDS             1. .990
                     /gene="IL-12.p40"
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                     /codon_start=1
                     /product="interleukin-12 p40 chain"
                     /protein_id="CAA69068.1"
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                     GSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHK
                     LKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGV
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BASE COUNT      288 a    258 c    249 g    211 t
ORIGIN

  Query Match             89.1%;  Score 879.8;  DB 4;  Length 1006;
  Best Local Similarity   93.2%;  Pred. No. 4.9e-244;
  Matches  920;  Conservative    0;  Mismatches   67;  Indels   0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
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Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
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Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
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Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
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Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
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Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
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Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
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Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
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Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 8
AX076209
LOCUS       AX076209                 4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 10 from Patent WO0104155.
ACCESSION   AX076209
VERSION     AX076209.1  GI:12710834
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 4522)
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 10 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
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           CALIFORNIA (US)
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     source          1. .4522
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Plasmid pMol-fil12p40"
BASE COUNT     1180 a    1126 c    1106 g    1110 t
ORIGIN

  Query Match            89.1%;  Score 879.8;  DB 6;  Length 4522;
  Best Local Similarity   93.2%;  Pred. No. 6e-244;
  Matches  920;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
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Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
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Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
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Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
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Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
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Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
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Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
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Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
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Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
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Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
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Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033


RESULT 9
AX076476
LOCUS       AX076476               4522 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104280.
ACCESSION   AX076476
VERSION     AX076476.1  GI:12711028
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 4522)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4522
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BASE COUNT     1180 a    1126 c    1106 g    1110 t
ORIGIN

  Query Match            89.1%;  Score 879.8;  DB 6;  Length 4522;
  Best Local Similarity   93.2%;  Pred. No. 6e-244;
  Matches  920;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
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Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
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Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
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Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
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Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
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Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
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Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
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Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
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Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033
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RESULT 10
FCU83184
LOCUS       FCU83184                990 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p40 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83184
VERSION     U83184.1  GI:2735050
KEYWORDS    .
SOURCE      Felis catus.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
  MEDLINE   98182592
   PUBMED   9522125
REFERENCE   2  (bases 1 to 990)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
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BASE COUNT      283 a    251 c    249 g    207 t
ORIGIN
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  Best Local Similarity  93.1%;  Pred. No. 1.4e-243;
  Matches  919;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
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Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
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Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
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Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
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Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
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Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
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Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  ||||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              || |||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| ||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960
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Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||| |||||||||| ||||| ||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 11
AX154603
LOCUS       AX154603                990 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 7 from Patent WO0140257.
ACCESSION   AX154603
VERSION     AX154603.1  GI:14536186
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 990)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 7 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .990
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      270 a    250 c    254 g    216 t
ORIGIN

  Query Match             83.8%;  Score 827;  DB 6;  Length 990;
  Best Local Similarity   89.9%;  Pred. No. 1e-228;
  Matches  887;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   | ||||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               |||||||||||||||||||||| | |||||||||||||| ||||||||| |||| |||
Db         61 GTGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAATTGGACTGGTACCCGGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||| ||||  | || |||||||||||||| |||||| |||
Db        121 GCCCCTGGAGAAATGGTGGTCCTCGCCTGTGACACTCCTGAAGAAGATGGCATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              |||||||  |||||||||| ||| | ||  |||| ||||| ||||||||||| ||||||
Db        181 ACCTCAGACCAGAGCAGTGAGGTCTTGGGCACTGGCAAAACCCTGACCATCCACGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || ||||||||||||||||||| ||||| |  |||||||||   |||||||||| |||
Db        241 GAGTTTGGAGATGCTGGCCAGTACACCTGTCGCAAAGGAGGCGCAGTTCTGAGCCAGTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| |||||||||||||||||||||||||| ||||| || |||
Db        301 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAAGACCAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||  ||||||| |||||||||||||||||||||||||||||||| || ||||||||||
Db        361 AAAGAGCCCAAAAACAAGATCTTTCTGAAATGTGAGGCAAAGAATTACTCCGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||| |||||||||||| ||||||||| ||||||
Db        421 ACCTGCTGGTGGCTGACAGCAATCAGTACAGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||||||||||| ||||||| || ||||| || ||||||||||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCCGTTACACTCTCTGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGCATGGACCACAGGGAGTATAACAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCTGACCCACCCAAG 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || |||||||| |||||||| |||||||||| |||||
Db        721 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGACACGTGGAGATCAGCTGGGAGTACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||| |||||||||||||| |||||||  ||| |  | || |  |||||||
Db        781 GACACCTGGAGCATCCCACATTCCTACTTTTCCCTGATGTTTGGTGTTCAAGTTCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAAGAGAGAAAAGAAAGATAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||||| |||||||||||| || |||| |||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTACAGCTCATCTTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        961 AGCGAATGGGCATCTGTGCCCTGCAGT 987


RESULT 12
ECIL12P40
LOCUS       ECIL12P40               1058 bp    mRNA    linear   MAM 17-NOV-1999
DEFINITION  Equus caballus mRNA for interleukin 12 p40 subunit.
ACCESSION   Y11129
VERSION     Y11129.1  GI:5441622
KEYWORDS    interleukin-12 p40.
SOURCE      Equus caballus.
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 1058)
  AUTHORS   Nicolson,L., Penha-Goncalves,M.N., Keanie,J.L., Logan,N.A.,
            Argyle,D.J. and Onions,D.E.
  TITLE     Cloning and sequencing of horse interleukin-12 and interleukin-18
            cDNAs
  JOURNAL   Immunogenetics 50 (1-2), 94-97 (1999)
  MEDLINE   20009534
   PUBMED   10541814
REFERENCE   2  (bases 1 to 1058)
  AUTHORS   Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-FEB-1997) L. Nicolson, Dept. of Vet. Pathology,
            University of Glasgow Vet. School, Bearsden Rd., Glasgow G61 1QH,
            UK
FEATURES             Location/Qualifiers
     source          1. .1058
                     /organism="Equus caballus"
                     /db_xref="taxon:9796"
                     /cell_line="LPS-stimulated alveolar macrophages"
                     /cell_type="alveolar macrophages"
     gene            1. .990
                     /gene="IL-12 p40"
     CDS             1. .990
                     /gene="IL-12 p40"
                     /codon_start=1
                     /product="interleukin 12 p40 subunit"
                     /protein_id="CAA72011.1"
                     /db_xref="GI:5441623"
                     /translation="MCHQWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGE
                     MVVLTCNTPEEEGITWTSAQSNEVLGSGKTLTIQVKEFGDAGWYTCHKGGEVLSHSHL
                     LLHKKEDGIWSTDILKDQKESKNKTFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPAAEESLPIEIVVDAVHK
                     LKYENYTSGFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPETWSTPHSYFSLTFSI
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     misc_feature 1. .12
                 /gene="IL-12 p40"
                 /note="primer-derived sequence"
     variation   714
                 /gene="IL-12 p40"
                 /note="allelic difference, no change in amino acid
                 sequence"
                 /replace="g"
     misc_feature 1041. .1058
                 /note="primer-derived sequence"
BASE COUNT      284 a    269 c    282 g    223 t
ORIGIN

  Query Match             82.2%;  Score 811;  DB 4;  Length 1058;
  Best Local Similarity   88.9%;  Pred. No. 4.6e-224;
  Matches  877;  Conservative    0;  Mismatches  110;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||  ||||||| |||||||||||||||| ||||||||||||||||||||
Db          1 ATGTGTCACCAGTGGTTGGTCCTCTCCTGGTTTTCCCTGGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||||||| |||||||||| ||||| ||| ||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTGTATGTTGTAGAATTGGATTGGTACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||| |||||||||||||| | |||||| |||
Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGCAATACCCCTGAAGAAGAAGGCATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| || ||||||| ||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        181 ACCTCGGCCCAGAGCAATGAGGTCTTAGGCTCTGGCAAAACCTTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||  ||| ||||| || ||||||||| ||||||||||||  ||
Db        241 GAGTTTGGAGATGCTGGCTGGTACACCTGTCACAAAGGAGGCGAGGTTCTGAGCCATTCT 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              | |||| || ||||||| || |||||||||||||||||||||| || ||||| || |||
Db        301 CACCTGCTGCTTCACAAGAAGGAAGATGGAATTTGGTCCACTGACATTTTAAAAGACCAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        361 AAAGAATCCAAAAATAAGACCTTTCTAAAATGTGAGGCAAAGAATTATTCCGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
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Db        421 ACATGCTGGTGGCTGACAGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              || | |||||||||| ||||||| |||||||||| ||||| || ||||||||||||
Db        481 GGTTCCTCTGACCCCCGAGGGGTGACGTGTGGAGCAGCGACACTCTCCGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              || |||||| ||||||| |||||||||||||| ||||||||||||||||||||||||||
Db        541 AGCGTGGACGACAGGGAGTATAAGAAGTACACGGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  | |||||||||||||| ||||| ||| |||||||||||||| ||||||||||||||
Db        601 CCGGCCGCCGAGGAGAGCCTGCCCATTGAGATCGTGGTGGATGCTGTTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||| |||||||||||| ||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCGGCTTCTTCATCAGGGACATCATCAAACCAGACCCACCCAAG 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||||||||||||| || |||||||||| ||||||||||||||||| ||||||
Db        721 AACCTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              || |||||||||||||||||||||||||||||||||||||||| |  || |||| |||||||
Db        781 GAGACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTCTCTATTCAGGTCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |  |||| |||||| ||||||| | ||||  |||| |||||||  |||
Db        841 AAGAACAAGAAGGAAAGGAAAGACAGACTCTTCATGGATGAGACTTCAGCCACAGTCACA 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Db        901 TGCCACAAGGATGGCCAGATCCGTGTCCAAGCCAGGGACCGCTACTACAGCTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| ||||||||| || || ||||||
Db        961 AGCGAATGGGCATCCGTATCCTGCAGT 987


RESULT 13
AF401989
LOCUS       AF401989               1626 bp    mRNA    linear   SYN 14-FEB-2002
DEFINITION  Synthetic construct single chain interleukin-12 mRNA, complete cds.
ACCESSION   AF401989
VERSION     AF401989.1  GI:18656516
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 1626)
  AUTHORS   McMonagle,E.L.J., Taylor,S., van Zuilekom,H., Sanders,L.,
            Scholtes,N., Keanie,L.J., Hopkins,C.A., Logan,N.A., Bain,D.,
            Argyle,D.J., Onions,D.E., Schijns,V.E. and Nicolson,L.
  TITLE     Production of biologically active equine interleukin 12 through
            expression of p35, p40 and single chain IL-12 in mammalian and
            baculovirus expression systems
  JOURNAL   Equine Vet. J. 33 (7), 693-698 (2001)
  MEDLINE   21626920
   PUBMED   11770992
REFERENCE   2  (bases 1 to 1626)
  AUTHORS   McMonagle,L.J., Taylor,S., Keanie,L.J., Hopkins,C.A., Logan,N.A.,
            Argyle,D.J., Onions,D.E. and Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
            School, Bearsden Rd, Glasgow G61 1QH, UK
FEATURES             Location/Qualifiers
     source          1. .1626
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
     CDS             1. .1626
                     /note="derived from Equus caballus; N-terminal p40 subunit
                     linked by (Gly4Ser)3 linker to signal-peptide deleted p35
                     subunit"
                     /codon_start=1
                     /transl_table=11
                     /product="single chain interleukin-12"
                     /protein_id="AAL77817.1"
                     /db_xref="GI:18656517"
                     /translation="MGHQWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGE
                     MVVLTCNTPEEEGITWTSAQSNEVLGSGKTLTIQVKEFGDAGWYTCHKGGEVLSHSHL
                     LLHKKEDGIWSTDILKDQKESKNKTFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
                     GSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPAAEESLPIEIVVDAVHK
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                     QVQGKNKKERKDRLFMDETSATVTCHKDGQIRVQARDRYYSSSWSEWASVSCSGGGGS
                     GGGGSGGGGSRNLPTATPGPGMFQCLNHSQNLLRTVSNTLQKARQTLEFYSCTSEEID
                     HEDITKDKSSTVAACLPLELAPNESCLASREISFITNGSCLTPGKASSMMTLCLSSIY
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                     DFYKTKVKLCILLHAFRIRAVTINRMMGYLNAS"
     primer_bind     1. .14
     misc_feature    15. .987
                     /note="interleukin-12 p40 sequence"
     misc_feature    988. .1032
                     /note="linker"
     misc_feature    1033. .1611
                     /note="interleukin-12 p35 sequence"
     primer_bind     complement(1612. .1626)
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BASE COUNT      429 a    425 c    427 g    345 t
ORIGIN

  Query Match            82.0%;  Score 809.4;  DB 12;  Length 1626;
  Best Local Similarity  88.8%;  Pred. No. 1.4e-223;
  Matches  876;  Conservative    0;  Mismatches  111;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||  ||||||| |||||||||||||||| ||||||||||||||||||||
Db          1 ATGGGTCACCAGTGGTTGGTCCTCTCCTGGTTTTCCCTGGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||||||| |||||||||||  |||| ||| ||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTGTATGTTGTAGAATTGGATTGGTACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||| ||||||||||||||| | ||||| |||
Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGCAATACCCCTGAAGAAGAAGGCATCACCTGG 180

Qy        181 ACCTCAGCCCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| || ||||||| ||| ||| |||| |||| |||||  ||||||||||||||||
Db        181 ACCTCGGCCCAGAGCAATGAGGTCTTAGGCTCTGGCAAAACCTTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || ||||||||||||||  ||| ||||| || |||||||| ||||||||||  ||
Db        241 GAGTTTGGAGATGCTGGCTGGTACACCTGTCACAAAGGAGGCGAGGTTCTGAGCCATTCT 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              | |||| || ||||||| || |||||||||||||||||||||||| || ||||| || |||
Db        301 CACCTGCTGCTTCACAAGAAGGAAGATGGAATTTGGTCCACTGACATTTTAAAAGACCAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||| |||||| |||||||||||||||||||||||| |||||||||
Db        361 AAAGAATCCAAAAATAAGACCTTTCTAAAATGTGAGGCAAAGAATTATTCCGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              |||||||||||||||| |||||||||||||||||||||||||||||||| ||||||
Db        421 ACATGCTGGTGGCTGACAGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              || | |||||||||||| |||||||| |||||||| |||||| || |||||||||||||
Db        481 GGTTCCTCTGACCCCCGAGGGGTGACGTGTGGAGCAGCGACACTCTCCGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              || |||||| ||||||| |||||||||||||| ||||||||||||||||||||||||||
Db        541 AGCGTGGACGACAGGGAGTATAAGAAGTACACGGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  | |||||||||||||| ||||| ||| |||||||||||||| ||||||||||||||
Db        601 CCGGCCGCCGAGGAGAGCCTGCCCATTGAGATCGTGGTGGATGCTGTTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||| |||||||||||||| |||||||||||||||||||| ||||
Db        661 TATGAAAACTACACCAGCGGCTTCTTCATCAGGGACATCATCAAACCAGACCCGCCCAAG 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||||||||||||||| || |||||||||| |||||||||||||||| ||||||
Db        721 AACCTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              || |||||||||||||||||||||||||||||||||||| |  || |||| |||||||
Db        781 GAGACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTCTCTATTCAGGTCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |  |||| |||||| ||||||| | ||||  |||| |||||||  |||
Db        841 AAGAACAAGAAGGAAAGGAAAGACAGACTCTTCATGGATGAGACTTCAGCCACAGTCACA 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Db        961 AGCGAATGGGCATCCGTATCCTGCAGT 987


RESULT 14
AX154600
LOCUS       AX154600                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 4 from Patent WO0140257.
ACCESSION   AX154600
VERSION     AX154600.1  GI:14536183
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 4 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      272 a    254 c    247 g    211 t
ORIGIN

  Query Match            80.1%;  Score 790.6;  DB 6;  Length 984;
  Best Local Similarity  88.3%;  Pred. No. 3.9e-218;
  Matches  872;  Conservative    0;  Mismatches  109;  Indels    6;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
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Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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              || |||||||||||||||||||| ||||| |  |||||||||  |||||||||  |||
Db        241 GAGTTTGGAGATGCTGGCCAGTACACCTGTCGCAAAGGAGGCGCAGTTCTGAGCCAGTCA 300

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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||| |  |||||||  |||||||||||||||||||||||||||||||| || |||||||||
Db        361 AAAAAGCCCAAAAACAAGATCTTTCTGAAATGTGAGGCAAAGAATTACTCCGGACGTTTC 420

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Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
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Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
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Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
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Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
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Db        721 AACTTGCAACTGAGACCACTAAAGAATTCTCGACACGTGGAGATCAGCTGGGAGTACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
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Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Db        895 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACCACAGCTCATCTTGG 954

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db        955 AGCGAATGGGCATCTGTGCCCTGCAGT 981


RESULT 15
AX154599
LOCUS       AX154599                984 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 3 from Patent WO0140257.
ACCESSION   AX154599
VERSION     AX154599.1  GI:14536182
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 984)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 3 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .984
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BASE COUNT      267 a    246 c    254 g    217 t
ORIGIN

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  Best Local Similarity   88.0%;  Pred. No. 9.5e-217;
  Matches  869;  Conservative    0;  Mismatches  112;  Indels    6;  Gaps    1;

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Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
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Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
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Db        361 AAAGAACCCAAAGCTAAGAGTTTTTTAAAATGTGAGGCAAAGGATTATTCTGGACACTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
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Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
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Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCCGTTACACTCTCTGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||  |||||||||||||||||||| |||||||| |||||  | |||| ||||||
Db        781 GACACGTGGAGCACCCCACATTCCTACTTTTCCCTGACGTTTTGTGTTCAGGTCCAGGGA 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||      ||||| | ||||| | |||||||||||| |||
Db        841 AAGAACAAGAGAGAAAAGAA------ACTCTTCATGGACCAAACCTCAGCCAAAGTCACA 894

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||||||||| |||||||||||| || ||||| |||
Db        895 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTACAGCTCATCTTGG 954

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Job time : 2797.89 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 04:18:07 ; Search time 265.369 Seconds
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Perfect score: 987
Sequence: 1 atgcaccctcagcagttggt.....gggcatctgtgtcatgcagt 987

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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SUMMARIES

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1	983.8	99.7	990	19	AAV13817	Canine IL-12 P40 s
2	983.8	99.7	990	20	AAX35625	Nucleic acid encod
3	983.8	99.7	990	20	AAX03162	Nucleic acid encod
4	983.8	99.7	990	22	AAI64388	Canine coding sequ
5	972.6	98.5	990	19	AAV13816	Canine IL-12 P40 s
6	972.6	98.5	990	20	AAX35615	Nucleic acid encod
7	972.6	98.5	990	20	AAX03152	Nucleic acid encod
8	972.6	98.5	990	22	AAI64378	Canine coding sequ
9	959.6	97.2	2154	20	AAX18176	Canine full length
10	895.2	90.7	924	20	AAX18177	Canine mature CLAF
11	879.8	89.1	990	22	AAF26082	Feline IL-12p40 en
12	879.8	89.1	990	22	AAF26085	Feline IL-12p40 en
13	879.8	89.1	4522	22	AAF26076	Feline IL-12p40 en
14	879.8	89.1	4522	22	AAF26094	Plasmid pMol-fil12
15	878.2	89.0	2193	19	AAV56625	Feline FLAFp40 cDN
16	827	83.8	990	22	AAD15209	Modified human cyt
17	825	83.6	921	19	AAV56626	Feline FLAFp40 cDN
18	823.4	83.4	921	19	AAV56627	Feline FLAFp40 cDN
19	790.6	80.1	984	22	AAD15206	Modified human cyt
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21	772.6	78.3	987	16	AAQ97484	Human interleukin-
22	772.6	78.3	987	19	AAV07273	Human Interleukin-
23	772.6	78.3	987	19	AAV07217	DNA encoding human
24	772.6	78.3	987	20	AAZ40404	Human interleukin
25	772.6	78.3	987	22	AAD15210	Human cytokine p40
26	772.6	78.3	1007	22	AAD18585	Human interleukin-
27	772.6	78.3	1018	15	AAQ67879	EPV 42 kD promoter
28	772.6	78.3	1018	20	AAZ08510	EPV 42 kDa/human I
29	772.6	78.3	1389	22	AAF76880	Human p40-IL-2 cod
30	772.6	78.3	1397	18	AAV00401	40 kDa subunit of
31	772.6	78.3	1397	18	AAT77849	40 kDa subunit of
32	772.6	78.3	1397	18	AAT97969	40 kDa subunit of
33	772.6	78.3	1397	19	AAV37767	Cytotoxic lymphocy
34	772.6	78.3	1399	21	AAZ40021	Human p40 coding s
35	772.6	78.3	2362	13	AAQ23586	Natural killer cel
36	772.6	78.3	2362	17	AAT48098	Human interleukin-
37	772.6	78.3	2362	19	AAV42535	Human interleukin-
38	772.6	78.3	2362	19	AAV15227	Heterodimeric huma
39	772.6	78.3	2362	21	AAZ28862	Human interleukin-
40	772.6	78.3	2362	22	AAF56280	IL-12 vaccine adju
41	772.6	78.3	5686	20	AAZ40415	Plasmid pIN1143 co
42	772.6	78.3	6139	21	AAZ40023	Interleukin-12 fus
43	771	78.1	987	20	AAV83199	Interleukin (IL)-1
44	771	78.1	2300	21	AAA92406	Human interleukin
45	771	78.1	8578	24	AAD31545	pIRES-hB7-1-IL12.1

ALIGNMENTS

RESULT 1
AAV13817
ID AAV13817 standard; cDNA to mRNA; 990 BP.
XX
AC AAV13817;
XX
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P40 subunit cDNA.
XX
KW Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW antiviral; vaccine adjuvant; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1..990
FT /*tag= a
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XX
PN JP10036397-A.
XX
PD 10-FEB-1998.
XX
PF 08-NOV-1996; 96JP-0296789.
XX
PR 23-MAY-1996; 96JP-0128104.
PR 08-NOV-1995; 95JP-0289729.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1998-174914/16.

```
DR   P-PSDB; AAW41791.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 10; Pages 10-11; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

  Query Match             99.7%;  Score 983.8;  DB 19;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 3.9e-297;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
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Db          1 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
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Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
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Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
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Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||||||||||||||||| ||||||
Db        961 AGCGACTGGGCATCTGTGTCCTGCAGT 987


RESULT 2
AAX35625
ID   AAX35625 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX35625;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02342.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 14-15; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

  Query Match             99.7%;  Score 983.8;  DB 20;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 3.9e-297;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          1 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||||| ||||||
Db        961 AGCGACTGGGCATCTGTGTCCTGCAGT 987


RESULT 3
AAX03162
ID   AAX03162 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03162;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag= a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84373.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 30-32; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

  Query Match             99.7%;  Score 983.8;  DB 20;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 3.9e-297;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
                |||||||||||||||||||| ||||||
Db        961 AGCGACTGGGCATCTGTGTCCTGCAGT 987


RESULT 4
AAI64388
ID   AAI64388 standard; DNA; 990 BP.
XX
AC   AAI64388;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #3.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag=  a
FT                   /product= "Canine protein #1"
FT   sig_peptide     1..66
FT                   /*tag=  b
FT   mat_peptide     67..987
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66482.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Claim 6; Page 16-17; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 990 BP; 279 A; 244 C; 249 G; 218 T; 0 other;

  Query Match             99.7%;  Score 983.8;  DB 22;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 3.9e-297;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||||||| ||||||
Db        961 AGCGACTGGGCATCTGTGTCCTGCAGT 987
```

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RESULT 5
AAV13816
ID   AAV13816 standard; cDNA to mRNA; 990 BP.
XX
AC   AAV13816;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit cDNA.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag=  a
FT                   /product= interleukin-12_P40_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41790.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 8; Page 8; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P40
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;
```

```
  Query Match             98.5%;  Score 972.6;  DB 19;  Length 990;
  Best Local Similarity   99.1%;  Pred. No. 1.3e-293;
  Matches  978;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   | ||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
                |||||||||||||||||| | ||||||
Db        961 AGCGACTGGGCATCTGTGCCCTGCAGT 987


RESULT 6
AAX35615
ID   AAX35615 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX35615;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02339.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 12; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

  Query Match             98.5%;  Score 972.6;  DB 20;  Length 990;
  Best Local Similarity   99.1%;  Pred. No. 1.3e-293;
  Matches  978;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||||||||||||||||||||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
                |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
                |||||||||||||||||| | ||||||
Db        961 AGCGACTGGGCATCTGTGCCCTGCAGT 987


RESULT 7
AAX03152
ID   AAX03152 standard; cDNA to mRNA; 990 BP.
XX
AC   AAX03152;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
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KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag= a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;    98WO-JP02031.
XX
PR   16-MAY-1997;    97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F, Satoh M, Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84371.
XX
PT   New therapeutic and prophylactic agents - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 23-25; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

  Query Match             98.5%;  Score 972.6;  DB 20;  Length 990;
  Best Local Similarity   99.1%;  Pred. No. 1.3e-293;
  Matches  978;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||.|||||||||| ||||||||||||||||||||||||||||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||||||||||||||| | ||||||
Db        961 AGCGACTGGGCATCTGTGCCCTGCAGT 987


RESULT 8
AAI64378
ID   AAI64378 standard; DNA; 990 BP.
XX
AC   AAI64378;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #1.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..990
FT                   /*tag= a
FT                   /product= "Canine protein #1"
FT   sig_peptide     1..66
FT                   /*tag= b
FT   mat_peptide     67..987
FT                   /*tag= c
XX
PN   JP2001161378-A.
```

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XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66480.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian -
XX
PS   Claim 6; Page 14; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 990 BP; 278 A; 243 C; 251 G; 218 T; 0 other;

  Query Match            98.5%;  Score 972.6;  DB 22;  Length 990;
  Best Local Similarity  99.1%;  Pred. No. 1.3e-293;
  Matches  978;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||||||||||||||||||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||||| | ||||||
Db        961 AGCGACTGGGCATCTGTGCCCTGCAGT 987


RESULT 9
AAX18176
ID   AAX18176 standard; cDNA; 2154 BP.
XX
AC   AAX18176;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74322.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 30-31; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
```

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XX
SQ   Sequence 2154 BP; 663 A; 448 C; 477 G; 566 T; 0 other;

  Query Match            97.2%;  Score 959.6;  DB 20;  Length 2154;
  Best Local Similarity  98.8%;  Pred. No. 2.3e-289;
  Matches  978;  Conservative    0;  Mismatches    9;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         52 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 111

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 171

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 231

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 291

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 351

Qy        301 CTCCTGTTGATTCAC---AAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAA 357
              ||||||||   | |    |||||  ||||||||||||||||||||||||||||||||||
Db        352 CTCCTGTTTGATTCCACAAAAAAGAAAGATGGAATTTGGTCCACTGATATCTTAAAGGAA 411

Qy        358 CAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 CAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGT 471

Qy        418 TTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGC 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 TTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGC 531

Qy        478 AGAGGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGG 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 AGAGGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGG 591

Qy        538 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 597
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 GTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCC 651

Qy        598 TGCCCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTC 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 TGCCCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTC 711

Qy        658 AAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 717
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 AAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCC 771

Qy        718 ACAAACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATAC 777
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        772 ACAAACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATAC 831

Qy        778 CCCGACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAG 837
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        832 CCCGACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAG 891

Qy        838 GGCAAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTC 897
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        892 GGCAAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTC 951

Qy        898 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCC 957
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        952 GTGTGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCC 1011

Qy        958 TGGAGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||||||||||||||||||||||||| ||||||
Db       1012 TGGAGCGACTGGGCATCTGTGTCCTGCAGT 1041


RESULT 10
AAX18177
ID   AAX18177 standard; cDNA; 924 BP.
XX
AC   AAX18177;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p40 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74323.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 32; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 924 BP; 273 A; 222 C; 234 G; 195 T; 0 other;

  Query Match            90.7%;  Score 895.2;  DB 20;  Length 924;
  Best Local Similarity  98.8%;  Pred. No. 2e-269;
  Matches  913;  Conservative    0;  Mismatches    8;  Indels    3;  Gaps    1;

Qy         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        307 TTGATTCAC---AAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAA 363
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Db        241 TTTGATTCCACAAAAAAGAAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAA 300

Qy        364 GAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACA 423
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACA 360

Qy        424 TGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGC 483
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGC 420

Qy        484 TTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGA 543
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGA 480

Qy        544 GTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCC 603
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCC 540

Qy        604 TCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTAT 663
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 TCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTAT 600

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAAC 723
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAAC 660

Qy        724 CTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGAC 783
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGAC 720

Qy        784 ACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAG 843
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 ACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAG 780

Qy        844 AACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGC 903
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGC 840

Qy        904 CACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGC 963
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGC 900

Qy        964 GACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||| ||||||
Db        901 GACTGGGCATCTGTGTCCTGCAGT 924


RESULT 11
AAF26082
ID   AAF26082 standard; DNA; 990 BP.
XX
AC   AAF26082;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 8.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02262.
XX
PR   08-JUL-1999;   99CH-0001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats,
PT   contains nucleic acid sequence encoding viral protein under control of
PT   eukaryotic promoter -
XX
PS   Claim 14; Page 36; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response.
XX
SQ   Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 other;

  Query Match             89.1%;  Score 879.8;  DB 22;  Length 990;
  Best Local Similarity   93.2%;  Pred. No. 1.4e-264;
  Matches  920;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||||||||| |||||||||||| |||||||||| ||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              |||||||||||||||||||||| |||||| |||| |||||||||||||||||| |||
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  ||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||  |||| |||||||| |||||||||||||||||||||||||||||||||| |||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||||||||| |||||||||| ||||| |||||||||| ||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
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Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987
```

RESULT 12
AAF26085
ID AAF26085 standard; DNA; 990 BP.
XX
AC AAF26085;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p40 encoding DNA.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Felis sp.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE02263.
XX
PR 08-JUL-1999; 99CH-0001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs -
XX
PS Claim 3; Page 30; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ Sequence 990 BP; 283 A; 249 C; 248 G; 210 T; 0 other;

Query Match 89.1%; Score 879.8; DB 22; Length 990;
Best Local Similarity 93.2%; Pred. No. 1.4e-264;
Matches 920; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

```
Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
Db         61 ATGGCCATATGGGAACTGGAGAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
Db        121 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720
```

```
Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||| ||||||| |||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||||| | |||||||||||||| |||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||| |||||||||| ||||| ||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 13
AAF26076
ID   AAF26076 standard; DNA; 4522 BP.
XX
AC   AAF26076;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p40 encoding DNA SEQ ID 2.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02262.
XX
PR   08-JUL-1999;   99CH-0001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats,
PT   contains nucleic acid sequence encoding viral protein under control of
PT   eukaryotic promoter
XX
PS   Disclosure; Page 29-31; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response.
XX
SQ   Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 other;

  Query Match             89.1%;  Score 879.8;  DB 22;  Length 4522;
  Best Local Similarity   93.2%;  Pred. No. 3.4e-264;
  Matches  920;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||||||||| |||||||||||| |||||||||| ||||||||
Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              |||||||||||||||||||||| |||||| |||| |||||||||||||||||| |||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| | |||||||||||||||||| ||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||| |||||||||||||||||||| |||||||||||| |||||||||||  ||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||  |||| |||||||| ||||||||||||||||||||||||||||||| |||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||||| |||||||||||| |||||||| ||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||||||||| |||||||||| |||||| |||||||||| ||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              || |||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||| ||||||| |||||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||||| | |||||||||||||| |||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006
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Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||| |||||||||| ||||| ||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033


RESULT 14
AAF26094
ID   AAF26094 standard; DNA; 4522 BP.
XX
AC   AAF26094;
XX
DT   24-APR-2001  (first entry)
XX
DE   Plasmid pMol-fil12p40 DNA SEQ ID 10.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Synthetic.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02263.
XX
PR   08-JUL-1999;   99CH-0001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs  -
XX
PS   Example 1c; Page 33-35; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ   Sequence 4522 BP; 1180 A; 1126 C; 1106 G; 1110 T; 0 other;

  Query Match             89.1%;  Score 879.8;  DB 22;  Length 4522;
  Best Local Similarity   93.2%;  Pred. No. 3.4e-264;
  Matches  920;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||||||||||| |||||||||||| |||||||||||  ||||||||

Db       3047 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 3106

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db       3107 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 3166

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              |||||||||||||||||||||| |||||| |||| |||||||||||||||||||| |||
Db       3167 GCCCCCGGAGAAATGGTGGTCCTTACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 3226

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| | ||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       3227 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 3286

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||| |||||||||||||||||||| |||||||||||| |||||||||||  ||
Db       3287 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 3346

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||  |||| |||||||| |||||||||||||||||||||||||||||| |||||||
Db       3347 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 3406

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       3407 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 3466

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||||| |||||||||||| |||||||| ||||||
Db       3467 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 3526

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||||||||||| |||||||||| |||||| |||||||||| ||||
Db       3527 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 3586

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 3646

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| |||||||||||||||||||
Db       3647 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 3706

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              || |||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db       3707 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 3766

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||| |||||||||| |||||||||||||| |||| || ||||||||||||||
Db       3767 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 3826

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db       3827 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 3886

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||
Db       3887 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 3946

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||||| | |||||||||||||| |||||||||
Db       3947 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGGGACCGCTACTATAGCTCATCCTGG 4006

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||| |||||||||| ||||| ||||||
Db       4007 AGCAACTGGGCATCCGTGTCCTGCAGT 4033


RESULT 15
AAV56625
ID   AAV56625 standard; cDNA; 2193 BP.
XX
AC   AAV56625;
XX
```

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DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             64..1053
FT                   /*tag= a
FT   sig_peptide     64..129
FT                   /*tag= b
FT   mat_peptide     130..1050
FT                   /*tag= c
FT                   /product= "FLAFp40"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST..
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76173.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 19; Page 52-54; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp40. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence 2193 BP; 680 A; 451 C; 493 G; 569 T; 0 other;

  Query Match          89.0%;  Score 878.2;  DB 19;  Length 2193;
  Best Local Similarity   93.1%;  Pred. No. 7.1e-264;
  Matches  919;  Conservative    0;  Mismatches   68;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||  ||||||||  |||||||||  |||  ||||||||||   |||| |||
Db         64 ATGCATCCTCAGCAGCTGGTCATCGCCTGGTTTTACCTGGTTTTGCTGGCACCTCCTCTC 123

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db        124 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 183

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              |||||||||||||||||||||||||||| |||| ||||||||||||||||||| |||
Db        184 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 243

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  ||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        244 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 303

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||  ||
Db        304 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 363

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||  |||| ||||||||  ||||||||||||||||||||||||||||||||||| |||||||
Db        364 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 423

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        424 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 483

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db        484 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 543

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||||||||| ||||||||| |||||| |||||||||| ||||
Db        544 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 603

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 663

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        664 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 723

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              || |||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        724 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 783

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        784 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 843

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        844 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 903

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||||
Db        904 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 963

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Db        964 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 1023

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||| |||||||||| ||||| ||||||
Db       1024 AGCAACTGGGCATCCGTGTCCTGCAGT 1050

Search completed: July 16, 2003, 06:46:43
Job time : 266.369 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:30:08 ; Search time 1788.63 Seconds
(without alignments)
8936.974 Million cell updates/sec

Title: US-09-917-265-58
Perfect score: 987
Sequence: 1 atgcaccctcaqcaqttqqt.... .....qqqcatctqtqtcatqcaqt 987

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8297743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: qb_est1:*
10: qb_est2:*
11: qb_htc:*
12: qb_est3:*
13: qb_est4:*
14: qb_est5:*
15: em_estfun:*
16: em_estom:*
17: qb_qss:*
18: em_qss_hum:*
19: em_qss_inv:*
20: em_qss_pln:*
21: em_qss_vrt:*
22: em_qss_fun:*
23: em_qss_mam:*
24: em_qss_mus:*
25: em_qss_other:*
26: em_qss_pro:*
27: em_qss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	271.4	27.5	475	12	BF704417	BF704417 MI-P-E6-a
2	178.2	18.1	545	17	AZ441303	AZ441303 1M0232M24
c 3	166.6	16.9	564	17	AZ853726	AZ853726 2M0157M01
c 4	94.6	9.5	668	17	AG079702	AG079702 Pan trogl
c 5	64	6.5	424	17	AQ981401	AQ981401 RPCI-23-3
6	44.6	4.5	796	13	BI688400	BI688400 603316319
7	41.6	4.2	540	9	AA004891	AA004891 zh87q02.r
8	41.4	4.2	595	13	BI983925	BI983925 fu06c08.y
9	41	4.2	490	9	AA002214	AA002214 zh85a03.r
c 10	41	4.2	774	9	AI021962	AI021962 ox05d04.x
11	40.8	4.1	590	10	AW077736	AW077736 fj36h09.y
12	40.8	4.1	635	13	BI563149	BI563149 fr89b05.y
13	40.2	4.1	531	13	BM184881	BM184881 ft83f07.y
14	40	4.1	339	9	AA321223	AA321223 EST23725
15	39.6	4.0	332	12	BE764332	BE764332 IL5-NT007
c 16	39.6	4.0	581	17	AQ394113	AQ394113 CITBI-E1-
c 17	39.4	4.0	291	10	BB336883	BB336883 BB336883
18	39.4	4.0	580	9	AA210777	AA210777 zr90d07.r
19	39.4	4.0	584	10	AW950266	AW950266 EST362336
20	39.4	4.0	589	14	BM796252	BM796252 K-EST0078
c 21	39.4	4.0	619	9	AI568598	AI568598 tn41c07.x
c 22	39.4	4.0	664	9	AI942458	AI942458 wp80b11.x
23	39.4	4.0	673	9	AU134439	AU134439 AU134439
24	39.4	4.0	728	12	BF242884	BF242884 601877916
25	39	4.0	559	10	BE017035	BE017035 fk74f06.y
c 26	38.4	3.9	621	17	AQ199862	AQ199862 RPCI11-46
c 27	38.4	3.9	801	13	BI661062	BI661062 603304362
c 28	38.4	3.9	919	17	CNS006S5	AL065856 Drosophil
29	37.8	3.8	310	13	BI043015	BI043015 RC5-OT010
30	37.8	3.8	310	13	BI043109	BI043109 RC5-OT010
c 31	37.8	3.8	558	14	H36198	H36198 14720 Lambd
32	37.6	3.8	617	12	BG766768	BG766768 602740065
c 33	37.6	3.8	634	17	AQ480305	AQ480305 RPCI-11-2
c 34	37.6	3.8	660	10	BB626805	BB626805 BB626805
c 35	37.4	3.8	401	9	AL842443	AL842443 AL842443
36	37	3.7	1038	17	BH131637	BH131637 ENTOD13TR
c 37	37	3.7	1101	17	CNS00LT2	AL078714 Drosophil
38	36.8	3.7	562	17	AZ272397	AZ272397 RPCI-23-4
39	36.6	3.7	858	17	AQ743291	AQ743291 HS_5388_B
40	36.6	3.7	907	12	BG399465	BG399465 602441670
41	36.4	3.7	527	13	BM601517	BM601517 170006870
42	36.4	3.7	641	13	BM584527	BM584527 170006872
c 43	36.4	3.7	827	17	CNS04ELI	AL287199 Tetraodon
c 44	36.4	3.7	840	17	AZ528829	AZ528829 ENTCS53TR
c 45	36.4	3.7	1101	17	CNS00YW5	AL096911 Drosophil

ALIGNMENTS

RESULT 1
BF704417
LOCUS BF704417 475 bp mRNA linear EST 22-DEC-2000
DEFINITION MI-P-E6-acc-g-09-1-UM.sl MI-P-E6 Sus scrofa cDNA clone MI-P-E6-acc-g-09-1-UM 3', mRNA sequence.
ACCESSION BF704417
VERSION BF704417.1 GI:11989825
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 475)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Tuggle CK
Molecular Genetics Laboratory, Department of Animal Science
Iowa State University
201 Kildee Hall, Ames, IA 50011-3150, USA
Tel: 5152944252
Fax: 5152942401
Email: cktuggle@iastate.edu
Oligo-dT track not found, Not I site shown in beginning of sequence is likely internal to the message. cDNA Library Preparation: RJ Woods, JA Green, RS Prather S142 Animal Science Research Center, Department of Animal Science, University of Missouri-Columbia,

```
          65211 Clone distribution: clones will be available through Research
          Genetics (www.resgen.com)
          Seq primer: M13 Forward
          POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .475
                     /organism="Sus scrofa"
                     /strain="crossbreed"
                     /db_xref="taxon:9823"
                     /clone="MI-P-E6-acc-g-09-1-UM"
                     /clone_lib="MI-P-E6"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: EcoRI; The MI-P-E6
                     library is derived from fetus at gestational.day 20.  For
                     a detailed description of the  library from which this
                     clone was derived, please visit our web site at
                     http://pigest.genome.iastate.edu/.
                     TAG_SEQ=None found"
BASE COUNT      129 a    120 c    121 g    104 t      1 others
ORIGIN

  Query Match             27.5%;  Score 271.4;  DB 12;  Length 475;
  Best Local Similarity   78.8%;  Pred. No. 2.2e-63;
  Matches  339;  Conservative    0;  Mismatches   82;  Indels    9;  Gaps    1;

Qy          6 CCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTCATGGC 65
              ||   || || |   |||||||||||| || |||||||||||| |||||| ||||||||
Db         51 CCTCNAGAAGCTAACCATCTCCTGGTTTGCCATCGTTTTGCTGGTGTCTCCACTCATGGC 110

Qy         66 CATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCC 125
              ||| ||||| |||||||||||| |||||||||||||||| ||||||||   || ||||||||
Db        111 CATGTGGGAGCTGGAGAAAGACGTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCC 170

Qy        126 CGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTC 185
              |||||||  |||  |||||||||  | || ||||||||||||||||||| ||||||||
Db        171 TGGAGAAACAGTGAACCTCACCTGTGACACGCCTGAAGAAGATGACATCACCTGGACCTC 230

Qy        186 AGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATT 245
              ||  |||||   || |||| |||| ||||| || || |||||||||   |||||||| ||
Db        231 AGACCAGAGACATGGAGTCATAGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTT 290

Qy        246 TGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCT 305
              |  |||||||||||||| |||||||| ||||||||| ||  |||||||| |||||  ||
Db        291 TCTAGATGCTGGCCAGTACACCTGCCACAAAGGAGGCGAGACTCTGAGCCACTCACATCT 350

Qy        306 GTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGA 365
              | || | ||||| || ||| |||||||||||||||||| || |||         ||| |
Db        351 GCTGCTCCACAAGAAGGAAAATGGAATTTGGTCCACTGAAATTTTA---------AAAAA 401

Qy        366 ATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATG 425
              | |||||| |||| || ||||| ||||| |||   ||||| || ||||| ||||| ||
Db        402 TTTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTG 461

Qy        426 CTGGTGGCTG 435
              ||  ||| ||
Db        462 CTCATGGGTG 471


RESULT 2
AZ441303
LOCUS       AZ441303                 535 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0232M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0232M24 R, DNA sequence.
ACCESSION   AZ441303
VERSION     AZ441303.1  GI:10565316
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 535)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0232  row: M  column: 24
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 535.
FEATURES             Location/Qualifiers
     source          1. .535
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0232M24"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT      132 a    135 c    130 g    137 t      1 others
ORIGIN

  Query Match             18.1%;  Score 178.2;  DB 17;  Length 535;
  Best Local Similarity   81.6%;  Pred. No. 7.9e-38;
  Matches  218;  Conservative    0;  Mismatches   48;  Indels    1;  Gaps    1;

Qy         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147
              |||||||||||||| |||||||   || |||||||| |||||||  |||  |||||||
Db         86 GTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCTGGAGAAACAGTGAACCTCACC 145

Qy        148 TGCCATAC-CCCTGAAGAAGATGACATCACTTGGACCTCAGCGCAGAGCAGTGAAGTCCT 206
              ||  | || | |||||||||||||||||| |||||||||  |||||   || |||| |
Db        146 TGTGACACGCTCTGAAGAAGATGACATCACCTGGACCTCAGACCAGAGACATGGAGTCAT 205

Qy        207 AGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGGAGATGCTGGCCAGTATAC 266
              ||| ||||| || || |||||||||   |||||||| |||  ||||||||||||||| ||
Db        206 AGGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTTCTAGATGCTGGCCAGTACAC 265

Qy        267 CTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTGTTGATTCACAAAAAAGAAGA 326
              |||||| |||||||| ||  |||||||| |||||  ||| || | ||||| || ||| |
Db        266 CTGCCACAAAGGAGGCGAGACTCTGAGCCACTCACATCTGCTGCTCCACAAGAAGGAAAA 325

Qy        327 TGGAATTTGGTCCACTGATATCTTAAA 353
              |||||||||||||||||| || |||||
Db        326 TGGAATTTGGTCCACTGAAATTTTAAA 352
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```
RESULT 3
AZ853726/c
LOCUS       AZ853726                 569 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0157M01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0157M01 F, DNA sequence.
ACCESSION   AZ853726
VERSION     AZ853726.1  GI:13042136
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 569)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0157  row: M  column: 01
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 569.
FEATURES             Location/Qualifiers
     source          1. .569
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0157M01"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT      143 a    137 c    153 g    136 t
ORIGIN

  Query Match             16.9%;  Score 166.6;  DB 17;  Length 569;
  Best Local Similarity   80.0%;  Pred. No. 1.2e-34;
  Matches  196;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy         88 GTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCCGGAGAAATGGTGGTCCTCACC 147
              ||||||||||||||| ||||||||   || |||||||| |||||||  |||  |||||||
Db        283 GTTTATGTTGTAGAGGTGGACTGGACTCCCGATGCCCCTGGAGAAACAGTGAACCTCACC 224

Qy        148 TGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCAGCGCAGAGCAGTGAAGTCCTA 207
              ||  | || ||||||||||||||||||||| |||||||||  |||||   || |||| ||
Db        223 TGTGACACGCCTGAAGAAGATGACATCACCTGGACCTCAGACCAGAGACATGGAGTCATA 164

Qy        208 GGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTTGGAGATGCTGGCCAGTATACC 267
              || ||||| || || |||||||||   |||||||| |||  ||||||||||||||| |||
Db        163 GGCTCTGGAAAGACCCTGACCATCACTGTCAAAGAGTTTCTAGATGCTGGCCAGTACACC 104

Qy        268 TGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTGTTGATTCACAAAAAAGAAGAT 327
              ||||| ||||||||| ||  |||||||| |||||  ||| || | ||||| || ||| |
Db        103 TGCCACAAAGGAGGCGAGACTCTGAGCCACTCACATCTGCTGCTCCACAAGAAGGAAAAG 44

Qy        328 GGAAT 332
              | | |
Db         43 GAATT 39


RESULT 4
AG079702/c
LOCUS       AG079702                 668 bp    DNA     linear   GSS 03-NOV-2001
DEFINITION  Pan troglodytes DNA, clone: PTB-075I07.R, genomic survey sequence.
ACCESSION   AG079702
VERSION     AG079702.1  GI:16631504
KEYWORDS    GSS.
SOURCE      Pan troglodytes male lymphoblast DNA, clone_lib:PTB Chimpanzee Male
            BAC Library clone:PTB-075I07.R.
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     BAC end sequences of Library PTB
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 668)
  AUTHORS   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
            Totoki,Y., Watanabe,H. and Sakaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
            and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
            1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
            Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT     Clones are derived from the chimpanzee BAC library PTB This BAC end
            was generated during the R&D process and may have higher chance of
            clone tracking errors.
             PRIMERS
                 Sequencing: M13Rev
             LIBRARY
                 Vector    : pKS145
                 R.Site 1  : SacI
                 R.Site 2  : SacI.
FEATURES             Location/Qualifiers
     source          1. .668
                     /organism="Pan troglodytes"
                     /db_xref="taxon:9598"
                     /clone="PTB-075I07.R"
                     /sex="male"
                     /cell_type="lymphoblast"
                     /clone_lib="PTB Chimpanzee Male BAC Library"
BASE COUNT      180 a    138 c    137 g    213 t
ORIGIN

  Query Match             9.5%;  Score 93.6;  DB 17;  Length 668;
  Best Local Similarity   79.3%;  Pred. No. 1.3e-14;
  Matches  111;  Conservative    0;  Mismatches   29;  Indels    0;  Gaps    0;

Qy        345 TATCTTAAAGGAACAGAAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAA 404
              | | || |    | |   |||| ||| |  ||| | |||| | | ||| ||| | |||||
Db        561 TTTGTTTATTTCAAATCCAGAACCCAGAGCTAACACCTTTGTAAGATGCGAGACCAAGAA 502

Qy        405 TTATTCTGGACGTTTCACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAG 464
```

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                ||||||  |||||||||||  ||||||||||||||  ||||||||||||||||||  ||||||
Db        501 TTATTCAGGACGTTTCACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAG 442

Qy        465 TGTCAAAAGTAGCAGAGGCT 484
              |||||||||  ||||||||  |
Db        441 TGTCAAAAGCAGCAGAGGGT 422


RESULT 5
AQ981401/c
LOCUS       AQ981401               324 bp    DNA     linear   GSS 29-JAN-2000
DEFINITION  RPCI-23-304O12.TJ RPCI-23 Mus musculus genomic clone RPCI-23-304O12
            , DNA sequence.
ACCESSION   AQ981401
VERSION     AQ981401.1  GI:6813702
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akinret
            ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Krol,M., de Jong,P.
            and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-23
  JOURNAL   Unpublished (1999)
COMMENT     Other_GSSs: RPCI-23-304O12.TV
            Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-23. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
            or from Resea ch Genetics (info@resgen.com). BAC end page:
            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 304  row: O  column: 12
            Seq primer: SP6
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .324
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-23-304O12"
                     /clone_lib="RPCI-23"
                     /sex="Female"
                     /lab_host="DH10B"
                     /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
                     EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
                     brain genomic DNA was isolated and  partially digested
                     with a combination of EcoRI and EcoRI Methylase.   Size
                     selected DNA was cloned into the pBACe3.6 vector at the
                     EcoRI  sites.  The ligation products were transformed into
                     DH10B  electrocompetent cells (BRL Life Technologies)."
BASE COUNT      100 a     56 c     60 g    104 t      4 others
ORIGIN

  Query Match             6.5%;  Score 64;  DB 17;  Length 324;
  Best Local Similarity   59.6%;  Pred. No. 1.3e-06;
  Matches  106;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366
              ||  || |  ||||  ||  |   |  |  | | |  | | ||      | |   |||
Db        317 TTTCTTTATTAAAAGAAAACTCCTAAATATTTAATTTTTCTTTTCTTTTCAAATGCAGAT 258

Qy        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426
              | ||||||  ||||  ||  |||||  |||||  |||   |||||  ||  |||||  |||||  |||
Db        257 TTCAAAAACAAGACTTTCCTGAAGTGTGAAGCACCAAATTACTCCGGACGGTTCACGTGC 198

Qy        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCT 484
              |  ||||||  |  ||  |  |  ||  |||||  ||||   ||  |  ||  ||  ||  |  |
Db        197 TCATGGCTGGTGCAAAGAAACATGGACTTGAAGTTCANCATCNAGAGCAGTAGCAGGT 140


RESULT 6
BI688400
LOCUS       BI688400               796 bp    mRNA    linear   EST 18-SEP-2001
DEFINITION  603316319F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5356036 5',
            mRNA sequence.
ACCESSION   BI688400
VERSION     BI688400.1  GI:15651016
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 796)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Jeffrey Green M.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11905  row: f  column: 05
            High quality sequence stop: 779.
FEATURES             Location/Qualifiers
     source          1. .796
                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:5356036"
                     /clone_lib="NCI_CGAP_Mam6"
                     /sex="female, virgin"
                     /tissue_type="infiltrating ductal carcinoma"
                     /dev_stage="5 months"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT      280 a    158 c    175 g    183 t
ORIGIN

  Query Match             4.5%;  Score 44.6;  DB 13;  Length 796;
  Best Local Similarity   48.6%;  Pred. No. 0.38;
  Matches  122;  Conservative    0;  Mismatches  129;  Indels    0;  Gaps    0;

Qy        255 TGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTGTTGATTCA 314
              ||  ||||  |||||  | ||||  |    | | |       |   || || |       |
Db        434 TGTTCAGTCGACCTGATAAAAAGCAACGTATGGTAACTATTGAAAACGCCAGGCACCGAA 493

Qy        315 CAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAATCCAAAAA 374
              | || || ||| | |  ||  ||||| |   | | ||||| |  | | |   ||||||
Db        494 AACAAGAGCAGAAGCACCTTCATCCACAGCCTTATGAAAGGGAAGGTACAATGGCAAAAA 553

Qy        375 TAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGCTGGTGGCT 434
              || | ||   || |     ||  ||  | |    |  |      |    || | |  ||
Db        554 TACGGTCGCGCTAACGGAAGACACACGGCAAATCTTGAGCTAGAACTGGGGCAGTTACCT 613

Qy        435 GACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTCTGACCC 494
                ||    | ||||||||||||  ||| |||    ||  ||  ||  |    |  | |
Db        614 TTCGATCCTAAGTACTGATTTGTGATTAAGTTAGGAAGTTAAGAGCTGTGGATGCTATCT 673

Qy        495 CCAAGGGGTGA 505
              |  ||  |||
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Db        674 ACTTGGTTTGA 684


RESULT 7
AA004891
LOCUS       AA004891                 540 bp    mRNA    linear   EST 07-MAY-1997
DEFINITION  zh87g02.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:428306 5', mRNA sequence.
ACCESSION   AA004891
VERSION     AA004891.1  GI:1448568
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 540)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1160   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 460.
FEATURES             Location/Qualifiers
     source          1. .540
                     /organism="Homo sapiens"
                     /db_xref="GDB:1328075"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:428306"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.   1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      148 a    103 c    129 g    154 t      6 others
ORIGIN

  Query Match             4.2%;  Score 41.6;  DB 9;  Length 540;
  Best Local Similarity   52.7%;  Pred. No. 2.2;
  Matches   89;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        314 ACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAATCCAAAA 373
              ||  ||  |  || |||| | |   | ||||||  |  | |  |   |||  | |   ||
Db        101 ACTGAACTGTCGAAGGAAATAGCCGCTCTGATAGGTAGATGTGAGTAAAAAGAACAGGAA 160

Qy        374 ATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGCTGGTGGC 433
              | ||   |||  |  | ||     |||||||  |  |   ||    ||  |  |||  |
Db        161 AAAATTGCTTCTTTTATTGGTTTCCAAAGAAACAAACCAAACCAACCAGCTCTTGGATGT 220

Qy        434 TGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGG 482
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              |   ||  ||| ||  |||||||  || |  |||||| |  ||||
Db        221 GAAGATAAAATAGTGCTTTTTTGAAATGGAGAGGAAAAAGTNGGGGAGG 269


RESULT 8
BI983925
LOCUS       BI983925                 595 bp    mRNA    linear   EST 24-OCT-2001
DEFINITION  fu06c08.y3 Campbell zebrafish ovary Danio rerio cDNA clone 5304566
            5' similar to TR:Q9Y3B3 Q9Y3B3 CGI-109 PROTEIN. ;, mRNA sequence.
ACCESSION   BI983925
VERSION     BI983925.1  GI:16374884
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 595)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library constructed by Library constructed by Invitrogen and
            donated by R. Campbell (Marine Biology Laboratory, Woods Hole, MA).
            DNA Sequencing by: Washington University Genome Sequencing Center
            Clone distribution: the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 439.
FEATURES             Location/Qualifiers
     source          1. .595
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="5304566"
                     /clone_lib="Campbell zebrafish ovary"
                     /sex="female"
                     /dev_stage="4-5 months, 1 year and 2 years"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: ovary(pooled); Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Whole ovaries collected from zebrafish
                     aged 4-5 months, 1 year and 2 years.  Oligo-dT primed,
                     directionally cloned.  Average insert size 2 kb.  Library
                     constructed by Invitrogen and donated by R. Campbell
                     (Marine Biology Laboratory, Woods Hole, MA)."
BASE COUNT      126 a    179 c    161 g    129 t
ORIGIN

  Query Match             4.2%;  Score 41.4;  DB 13;  Length 595;
  Best Local Similarity   52.0%;  Pred. No. 2.6;
  Matches   93;  Conservative    0;  Mismatches   86;  Indels    0;  Gaps    0;

Qy        533 AGAGGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCA 592
              || |  ||   | ||||| ||         |  |||| |||| | |||| |||| || ||
Db        267 AGTGTTTCTATGAGGACATCACCATCGGCACCAAGTGCACACTCGAGTTCCAGGTGGTCA 326

Qy        593 GTGCCTGCCCCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACA 652
                |  ||| || || || |||  |||  |     ||   || || |   |   |  |||
Db        327 CCGGGGGCCACTATGACGTGGACTGCCGGCTGGAGGACCCCGAGGGGACGGTGCTCTACA 386

Qy        653 AGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGAC 711
              ||   | | |  |  | |||  ||||  |  ||||| |   |    || | | |  ||
Db        387 AGGAGATGAAGAAGCAGTACGACAGCTTCACCTTCAGCGCCGCTCGCAACGGAACCTAC 445
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RESULT 9
AA002214
LOCUS       AA002214                490 bp    mRNA    linear   EST 07-MAY-1997
DEFINITION  zh85a03.r1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:428044 5', mRNA sequence.
ACCESSION   AA002214
VERSION     AA002214.1  GI:1445109
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 490)
  AUTHORS   Hillier,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B.,
            Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins
            ,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore
            ,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T.,
            Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E.,
            Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M.
  TITLE     Generation and analysis of 280,000 human expressed sequence tags
  JOURNAL   Genome Res. 6 (9), 807-828 (1996)
  MEDLINE   97044478
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1136   Std Error: 0.00
            Seq primer: mob.REGA+ET
            High quality sequence stop: 355.
FEATURES             Location/Qualifiers
     source          1. .490
                     /organism="Homo sapiens"
                     /db_xref="GDB:1327813"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:428044"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.   1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      142 a     94 c    117 g    135 t      2 others
ORIGIN

  Query Match             4.2%;  Score 41;  DB 9;  Length 490;
  Best Local Similarity   52.7%;  Pred. No. 3.1;
  Matches   89;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        314 ACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAATCCAAAA 373
              ||  ||  |  || |||| | |   | ||||||  |  | |  |   |||  | |   ||
Db         86 ACTGAACTGTCGAAGGAAATAGCCGCTCTGATAGGTAGATGTGAGTAAAAAGAACAGGAA 145

Qy        374 ATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGCTGGTGGC 433
              | ||   |||  |  | ||     |||||||  |  |   ||    ||  |  |||  |
Db        146 AAAATTGCTTCTTTTATTGGTTTCCAAAGAAACAAACCAAACCAACCAGCTCTTGGATGT 205

Qy        434 TGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGG 482
                |    ||  ||| ||  ||||||||  ||-|  ||||||  |  ||||
Db        206 GAAGATAAAATAGTGCTTTTTTGAAATGGAGAGGAAAAAGTTGGGGAGG 254


RESULT 10
AI021962/c
LOCUS       AI021962                774 bp    mRNA    linear   EST 28-AUG-1998
DEFINITION  ox05d04.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA
            clone IMAGE:1655431 3' similar to gb:Z29328 UBIQUITIN-CONJUGATING
            ENZYME E2-21 KD (HUMAN);, mRNA sequence.
ACCESSION   AI021962
VERSION     AI021962.1  GI:3237575
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 774)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1053   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 246.
FEATURES             Location/Qualifiers
     source          1. .774
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1655431"
                     /clone_lib="Soares_fetal_liver_spleen_1NFLS_S1"
                     /sex="male"
                     /dev_stage="20 week-post conception fetus"
                     /lab_host="DH10B (ampicillin resistant)"
                     /note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
                     with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
                     This is a subtracted version of the original Soares fetal
                     liver spleen 1NFLS library.   1st strand cDNA was primed
                     with a Pac I - oligo(dT) primer [5'
                     AACTGGAAGAATTAATTAAAGATCTTTTTTTTTTTTTTTTTT 3'],
                     double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Pac I and cloned into the Pac I
                     and Eco RI sites of the modified pT7T3 vector.  Library
                     went through one round of normalization. Library
                     constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT      210 a     179 c     149 g     232 t       4 others
ORIGIN

  Query Match             4.2%;  Score 41;  DB 9;  Length 774;
  Best Local Similarity   52.7%;  Pred. No. 3.6;
  Matches   89;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        314 ACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAATCCAAAA 373
              ||  ||  |  || |||| | |   | ||||||  |  | |  |   |||  | |   ||
Db        256 ACTGAACTGTCGAAGGAAATAGCCGCTCTGATAGGTAGATGTGAGTAAAAAGAACAGGAA 197

Qy        374 ATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGCTGGTGGC 433
              | ||   |||  |  | ||     |||||||  |  |   ||    ||  |  |||  |
Db        196 AAAATTGCTTCTTTTATTGGTTTCCAAAGAAACAAACCAAACCAACCAGCTCTTGGATGT 137

Qy        434 TGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGG 482
                |    ||  ||| ||  ||||||||  || | .||||||  |  ||||
Db        136 GAAGATAAAATAGTGCTTTTTTGAAATGGAGAGGAAAAAGTTGGGGAGG 88


RESULT 11
AW077736
LOCUS       AW077736                590 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  fj36h09.y1 zebrafish adult brain Danio rerio cDNA 5' similar to
            WP:F57B10.5 CE11306 ;contains element TAR1 repetitive element ;,
            mRNA sequence.
```

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ACCESSION   AW077736
VERSION     AW077736.1  GI:6032888
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 590)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: T7
            High quality sequence stop: 492.
FEATURES             Location/Qualifiers
     source          1. .590
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone_lib="zebrafish adult brain"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
BASE COUNT      121 a    175 c    171 g    122 t      1 others
ORIGIN

  Query Match             4.1%;  Score 40.8;  DB 10;  Length 590;
  Best Local Similarity   53.8%;  Pred. No. 3.8;
  Matches   84;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        533 AGAGGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCA 592
              || |  ||   | ||||| ||        |  |||| |||| | ||||  |||| || ||
Db        148 AGTGTTTCTATGAGGACATCACCATCGGCACCAAGTGCACACTCGAGTTCCAGGTGGTCA 207

Qy        593 GTGCCTGCCCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACA 652
                |  ||| || || || ||| ||| |    ||  || || |   |  | |||
Db        208 CCGGGGGCCACTATGACGTGGACTGCCGGCTGGAGGACCCCGAGGGGACGGTGCTCTACA 267

Qy        653 AGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 688
              ||   | | |  | | ||| |||| |  |||||
Db        268 AGGAGATGAAGAAGCAGTACGACAGCTTCACCTTCA 303


RESULT 12
BI563149
LOCUS       BI563149                635 bp    mRNA    linear   EST 26-JUL-2002
DEFINITION  fr89b05.y1 zebrafish adult brain Danio rerio cDNA clone 4967768 5'
            similar to TR:Q9Y3B3 Q9Y3B3 CGI-109 PROTEIN. ;, mRNA sequence.
ACCESSION   BI563149
VERSION     BI563149.1  GI:15452341
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 635)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
            Matthew Clark. DNA Sequencing by: Washington University Genome
            Sequencing Center Clone distribution: Genome Systems, St. Louis,
            Missouri (web address: www.genomesystems.com) (email contact:
            info@genomesystems.com) and Research Genetics, Huntsville, Alabama
            (web address: www.resgen.com) (email contact: info@resgen.com) and
            RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
            www.rzpd.de)
            Seq primer: T7
            High quality sequence stop: 369.
FEATURES             Location/Qualifiers
     source          1. .635
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="4967768"
                     /clone_lib="zebrafish adult brain"
                     /sex="mixed male and female"
                     /tissue_type="brain"
                     /dev_stage="adult"
                     /lab_host="E. coli DH10B"
                     /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
                     Original library was constructed in lambdaZIPLOX.  Mass
                     excision of the cDNA library was performed to yield
                     pZIPLOX plasmids. Insert check was done in original
                     library."
BASE COUNT      125 a    191 c    185 g    134 t
ORIGIN

  Query Match             4.1%;  Score 40.8;  DB 13;  Length 635;
  Best Local Similarity   53.8%;  Pred. No. 3.9;
  Matches   84;  Conservative    0;  Mismatches   72;  Indels    0;  Gaps    0;

Qy        533 AGAGGGTCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCA 592
              || |  ||   | ||||| ||        |  |||| |||| | ||||  |||| || ||
Db        139 AGTGTTTCTATGAGGACATCACCATCGGCACCAAGTGCACACTCGAGTTCCAGGTGGTCA 198

Qy        593 GTGCCTGCCCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACA 652
                |  ||| || || || ||| ||| |    ||  || || |   |  | |||
Db        199 CCGGGGGCCACTATGACGTGGACTGCCGGCTGGAGGACCCCGAGGGGACGGTGCTCTACA 258

Qy        653 AGCTCAAGTATGAAAACTACACCAGCAGCTTCTTCA 688
              ||   | | |  | | ||| |||| |  |||||
Db        259 AGGAGATGAAGAAGCAGTACGACAGCTTCACCTTCA 294


RESULT 13
BM184881
LOCUS       BM184881                531 bp    mRNA    linear   EST 11-DEC-2001
DEFINITION  ft83f07.y3 Gong zebrafish ovary Danio rerio cDNA clone 5159964 5'
            similar to TR:Q9Y3B3 Q9Y3B3 CGI-109 PROTEIN. ;, mRNA sequence.
ACCESSION   BM184881
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VERSION     BM184881.1  GI:17515839
KEYWORDS    EST.
SOURCE      zebrafish.
  ORGANISM  Danio rerio
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes
            ; Cyprinidae; Danio.
REFERENCE   1  (bases 1 to 531)
  AUTHORS   Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy
            ,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood
            ,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B.,
            Swailer,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
            Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R.
            and Wilson,R.
  TITLE     WashU Zebrafish EST Project 1998
  JOURNAL   Unpublished (1998)
COMMENT     Other_ESTs: ft83f07.x1
            Contact: Stephen L. Johnson
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: zbrafish@watson.wustl.edu
            The library was constructed by Dr. Z. Gong. DNA Sequencing by:
            Washington University Genome Sequencing Center St. Louis. Please
            contact Zhiyuan Gong for further information on this library
            (National University of Singapore, Department of Biological
            Sciences, Lower Kent Ridge Road, Singapore 119260).
            Seq primer: T3 ET from Amersham
            High quality sequence stop: 394.
FEATURES             Location/Qualifiers
     source          1. .531
                     /organism="Danio rerio"
                     /db_xref="taxon:7955"
                     /clone="5159964"
                     /clone_lib="Gong zebrafish ovary"
                     /sex="female"
                     /dev_stage="4-5 month"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: ovary (pooled); Vector: pBluescript SK-;
                     Site_1: XhoI; Site_2: EcoRI; Poly A+ RNA was isolatd from
                     the ovaries of 2 female adult zebrafish (4-5 month  old).
                     cDNAs were made using oligo-dT primers and inserted into
                     lambda ZAP II vector  (Stratagene) by Dr. Z. Gong, in vivo
                     mass-excised to pBluescript SK- following the  Washington
                     University protocol
                     (http://genome.wustl.edu/est/lambda_protocol.shtml).
                     Please contact Zhiyuan Gong for further information on
                     this library (National University  of Singapore,
                     Department of Biological Sciences, Lower Kent Ridge Road,
                     Singapore 119260)."
BASE COUNT      110 a    165 c    157 g     99 t
ORIGIN
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  Query Match             4.1%;  Score 40.2;  DB 13;  Length 531;
  Best Local Similarity   52.0%;  Pred. No. 5.3;
  Matches   90;  Conservative    0;  Mismatches   83;  Indels    0;  Gaps    0;

Qy        539 TCAGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCT 598
              ||   | ||||| ||        |  |||| |||| | ||||  |||| || ||  |
Db          5 TCTATGAGGACATCACCATCGGCACCAAGTGCACACTCGAGTTCCAGGTGGTCACCGGGG 64

Qy        599 GCCCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCA 658
              ||| || || || |||  |||  |      ||   || || |   |   |  |||||   |
Db         65 GCCACTATGACGTGGACTGCCGGCTGGAGGACCCCGAGGGGACGGTGCTCTACAAGGAGA 124

Qy        659 AGTATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGAC 711
              | |  |  | |||  ||||  |  ||||| |   |    || |  | |  ||
Db        125 TGAAGAAGCAGTACGACAGCTTCACCTTCAGCGCCGCTCGCAACGGAACCTAC 177


RESULT 14
AA321223
```

```
LOCUS       AA321223               339 bp    mRNA    linear   EST 19-APR-1997
DEFINITION  EST23725 Bone marrow Homo sapiens cDNA 5' end similar to
            ubiquitin-conjugating enzyme UbcH2, 23 kDa, mRNA sequence.
ACCESSION   AA321223
VERSION     AA321223.1  GI:1973591
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 339)
  AUTHORS   Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A., Bult
            ,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D., White
            ,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wai,C., Clayton,R.A.,
            Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
            ,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodek,A.,
            Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.Jr., Kelley,J.M.,
            Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
            Moreno-Palanques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
            Phillips,C.A., Ryder,S.E., Scott,J.L., Saudek,D.M., Shirley,R.,
            Small,K.V., Spriggs,T.A., Utterback,T.R., Weidman,J.F., Li,Y.,
            Bednarik,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
            Dimke,D., Feng,D.-F., Ferrie,A., Fischer,C., Hastings,G.A., He,W.W.
            , Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
            Kunsch,C., Hungjun,J., Li,H., Meissner,P.S., Olsen,H., Raymond,L.,
            Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillion,P.J., Fannon
            ,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
            Venter,J.C.
  TITLE     Initial assessment of human gene diversity and expression patterns
            based upon 83 million nucleotides of cDNA sequence
  JOURNAL   Nature 377 (6547 Suppl), 3-174 (1995)
  MEDLINE   96026280
COMMENT     Other_ESTs: THC174363
            Contact: Kerlavage, AR
            Bioinformatics
            The Institute for Genomic Research
            9712 Medical Center Drive, Rockville, MD 20850 USA
            Tel: 3018699056
            Fax: 3018699423
            Email: arkerlav@tigr.org
            For clone availability, additional sequence and expression
            information related to this EST, please check the TIGR Human Gene
            Index (http://www.tigr.org/tdb/hgi/hgi.html)
            Seq primer: M13 Reverse.
FEATURES             Location/Qualifiers
     source          1. .339
                     /organism="Homo sapiens"
                     /db_xref="ATCC (inhost):121813"
                     /db_xref="taxon:9606"
                     /clone_lib="Bone marrow"
                     /sex="mixed"
                     /tissue_type="bone marrow"
                     /dev_stage="adult"
                     /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
                     XhoI"
BASE COUNT      101 a     60 c     92 g     84 t      2 others
ORIGIN
```

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  Best Local Similarity   52.1%;  Pred. No. 5.1;
  Matches   88;  Conservative    0;  Mismatches   81;  Indels    0;  Gaps    0;

Qy        314 ACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAATCCAAAA 373
              ||  ||  |  || |||| | |   | ||||||  |  | |  |   |||  | |   ||
Db         45 ACTGAACTGTCGAAGGAAATAGCCGCTCTGATAGGTAGATGTGAGTAAAAAGAACAGGAA 104

Qy        374 ATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGCTGGTGGC 433
              | ||   |||  |  | ||     |||||||  |  |   ||    ||  |  |||  |
Db        105 AAAATTGCTTCTTTTATTGGTTTCCAAAGAAACAAACCAAACCAACCAGCTCTTGGATGT 164

Qy        434 TGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGG 482
                |   ||  ||| ||  ||||||||  || |  |||| | |  ||||
Db        165 GAAGATAAAATAGTGCTTTTTTGAAATGGAGAGGAAAAACTNGGGGAGG 213
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```
RESULT 15
BE764332
LOCUS       BE764332                332 bp    mRNA    linear   EST 19-SEP-2000
DEFINITION  IL5-NT0071-180700-115-g02 NT0071 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE764332
VERSION     BE764332.1  GI:10194256
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 332)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=IL5-NT0071-180
            700-115-g02&t3=2000-07-18&t4=1)
            Seq primer: puc 18 forward
            High quality sequence stop: 233.
FEATURES             Location/Qualifiers
     source          1. .332
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="NT0071"
                     /dev_stage="Adult"
                     /note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
                     Site_2: SmaI; A mini-library was made by cloning products
                     derived from  ORESTES PCR (U.S. Letters Patent application
                     No. 196,716 -  Ludwig Institute for Cancer Research)
                     profiles into  the pUC 18 vector. Reverse transcription of
                     tissue mRNA and cDNA amplification were performed under
                     low stringency conditions."
BASE COUNT       92 a     66 c     84 g     90 t
ORIGIN

  Query Match             4.0%;  Score 39.6;  DB 12;  Length 332;
  Best Local Similarity   52.4%;  Pred. No. 6.6;
  Matches   87;  Conservative    0;  Mismatches   79;  Indels    0;  Gaps    0;

Qy        380 TCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGCTGGTGGCTGACGG 439
              | |||| ||||| || |     |   |||| |  |   |  |    | |   | |
Db         30 TATTTCAGAAATATGGGTTGGGGGTGTATTTTCTAAAATCAAGCAACAGTCTGTTTCAAC 89

Qy        440 CAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTCTCTGACCCCCAAG 499
              |||    |  ||||||| || | || ||||| || ||| | |   |    || |||||||
Db         90 CAAATGATTTTGATTTGGAAGTTAGAGTCAACAGAAGCTGTGTTGTGCACGAACCCCAAG 149

Qy        500 GGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGT 545
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Db        150 GCATCTCCTTTTCATTCTAGCCCATTTTTGCAAAGGGAGAAAGAGT 195


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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	983.8	99.7	990	4	US-09-079-984A-11	Sequence 11, Appl
	2	969.4	98.2	990	4	US-09-079-984A-1	Sequence 1, Appli
	3	772.6	78.3	987	1	US-08-186-529-1	Sequence 1, Appli
	4	772.6	78.3	987	1	US-08-640-386A-1	Sequence 1, Appli
	5	772.6	78.3	1018	2	US-08-184-009-194	Sequence 194, App
	6	772.6	78.3	1018	2	US-08-458-356-194	Sequence 194, App
	7	772.6	78.3	1018	4	US-08-460-736-194	Sequence 194, App
	8	772.6	78.3	1399	2	US-08-751-767A-3	Sequence 3, Appli
	9	772.6	78.3	1623	2	US-08-751-767A-9	Sequence 9, Appli
	10	772.6	78.3	2362	1	US-08-265-087-1	Sequence 1, Appli
	11	772.6	78.3	2362	1	US-08-621-493-1	Sequence 1, Appli
	12	772.6	78.3	2362	2	US-08-965-688-1	Sequence 1, Appli
	13	772.6	78.3	2362	4	US-09-260-173-1	Sequence 1, Appli
	14	772.6	78.3	6139	2	US-08-751-767A-7	Sequence 7, Appli
	15	771	78.1	987	4	US-08-848-760B-24	Sequence 24, Appl
	16	771	78.1	1870	4	US-09-310-842-4	Sequence 4, Appli
	17	771	78.1	2318	4	US-09-851-062-3	Sequence 3, Appli
	18	725.6	73.5	1560	2	US-08-751-767A-11	Sequence 11, Appl
	19	511.2	51.8	1061	2	US-08-385-335A-13	Sequence 13, Appl
	20	509.6	51.6	6295	2	US-08-659-206A-4	Sequence 4, Appli
	21	509.6	51.6	7287	2	US-08-659-206A-1	Sequence 1, Appli
c	22	49	5.0	7218	1	US-08-232-463-14	Sequence 14, Appl
c	23	39.4	4.0	625	4	US-09-328-111-593	Sequence 593, App
	24	34.2	3.5	2768	1	US-08-321-478-1	Sequence 1, Appli
	25	34.2	3.5	2768	1	US-08-321-478-3	Sequence 3, Appli
	26	34.2	3.5	2768	1	US-08-321-478-5	Sequence 5, Appli
	27	33.8	3.4	1921	3	US-08-482-677-3	Sequence 3, Appli
	28	33.8	3.4	1926	1	US-08-152-019A-43	Sequence 43, Appl
	29	33.8	3.4	2691	4	US-09-298-924-5	Sequence 5, Appli
	30	33.2	3.4	90050	4	US-09-245-041-5	Sequence 5, Appli
c	31	33	3.3	6048	4	US-09-634-920-3	Sequence 3, Appli
	32	33	3.3	6306	1	US-08-466-390-3	Sequence 3, Appli
	33	33	3.3	6306	1	US-08-470-950-3	Sequence 3, Appli
	34	33	3.3	6306	1	US-08-467-781-3	Sequence 3, Appli
	35	33	3.3	6306	1	US-08-195-487-3	Sequence 3, Appli
	36	33	3.3	6306	2	US-08-483-924-3	Sequence 3, Appli
	37	33	3.3	6306	5	PCT-US93-06160-3	Sequence 3, Appli
	38	32.8	3.3	598	4	US-09-453-702B-25	Sequence 25, Appl
	39	32.8	3.3	646	4	US-09-328-111-802	Sequence 802, App
	40	32.8	3.3	703	4	US-08-998-416-828	Sequence 828, App
c	41	32.4	3.3	1751	4	US-09-149-476-68	Sequence 68, Appl
	42	32.2	3.3	3107	1	US-07-846-181-4	Sequence 4, Appli
	43	32.2	3.3	3107	1	US-07-845-989-4	Sequence 4, Appli
	44	32.2	3.3	3468	1	US-07-951-715A-4	Sequence 4, Appli
	45	32.2	3.3	3468	2	US-08-459-448A-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-079-984A-11
; Sequence 11, Application US/09079984A
; Patent No. 6231850
; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
; APPLICANT: Yamada, Katsushige
; TITLE OF INVENTION: Canine interleukin 12, a production method
; TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
; TITLE OF INVENTION: method using it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miller & Christenbury Intellectual Property
; ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
; STREET: 1600 Market Street, 39th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,984A
; FILING DATE: 15-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Austin R. Miller
; REGISTRATION NUMBER: 16,602
; REFERENCE/DOCKET NUMBER: 1051-98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-1810
; TELEFAX: (215) 568-6946
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 990 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: Canine IL12
; LOCATION: 1 to 987
; IDENTIFICATION METHOD: Similarity
US-09-079-984A-11

Query Match 99.7%; Score 983.8; DB 4; Length 990;

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  Best Local Similarity   99.8%;  Pred. No. 4.5e-311;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||||||| ||||||
Db        961 AGCGACTGGGCATCTGTGTCCTGCAGT 987


RESULT 2
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US-09-079-984A-1
; Sequence 1, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-1

  Query Match             98.2%;  Score 969.4;  DB 4;  Length 990;
  Best Local Similarity   98.9%;  Pred. No. 2.3e-306;
  Matches  976;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  ||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
                |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
                ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
                |||||||||||||||||| | ||||||
Db        961 AGCGACTGGGCATCTGTGCCCTGCAGT 987


RESULT 3
US-08-186-529-1
; Sequence 1, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-186-529-1

  Query Match             78.3%;  Score 772.6;  DB 1;  Length 987;
  Best Local Similarity   87.1%;  Pred. No. 4e-242;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| |||||||||||||| ||||| ||||| ||| | || |||
Db         61 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||||  | ||||||||||||||| ||||| |||
Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        181 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| ||||| || |||||||| ||||||| |||| ||
Db        241 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| |||||||||||||||||||||||||| |||||||| |||
Db        301 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| |||| ||||||||||||||||||||
Db        361 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        421 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||| || ||||| |  |||| || |||||||| |||
Db        481 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    |||| |||||||||| ||||||| ||||||||||
Db        541 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 597

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| ||||||||||  ||||||||||||||
Db        598 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 657

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
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                ||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        658 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 717

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
                ||| ||||||||||||||| || |||||||||| |||||||||||||||||| |||||
Db        718 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 777

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
                |||||||||||  || ||||||||||||||||||||||||| ||| | |||| |||||||
Db        778 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 837

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
                |||| ||| |||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        838 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 897

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
                |||| |||  ||||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db        898 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 957

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db        958 AGCGAATGGGCATCTGTGCCCTGCAGT 984


RESULT 4
US-08-640-386A-1
; Sequence 1, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-640-386A-1
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  Query Match             78.3%;  Score 772.6;  DB 1;  Length 987;
  Best Local Similarity   87.1%;  Pred. No. 4e-242;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        181 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| |||||  || |||||||| ||||||| ||||  ||
Db        241 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||| |||||||| |||
Db        301 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        361 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        421 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        481 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        541 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 597

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| ||||| ||||||||||  ||||||||||||||
Db        598 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 657

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        658 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 717

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || |||||||||| |||||||||||||||||| |||||
Db        718 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 777

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||  || |||||||||||||||||||||||||||||||| ||| | |||| |||||||
Db        778 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 837

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        838 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 897

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  ||||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db        898 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 957

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        958 AGCGAATGGGCATCTGTGCCCTGCAGT 984
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RESULT 5
US-08-184-009-194
; Sequence 194, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-194

  Query Match             78.3%;  Score 772.6;  DB 2;  Length 1018;
  Best Local Similarity   87.1%;  Pred. No. 4.1e-242;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         32 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 91

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db         92 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 151

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||||  | ||||||||||||||  ||||| |||
Db        152 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 211

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        212 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 271

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || ||||||||||||||||||| ||||| || |||||||||| ||||||| ||||  ||
Db        272 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 331

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||| |||||||| |||
Db        332 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 391

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| |||||||||||||||||||||

Db        392 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 451

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        452 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 511

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        512 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 571

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        572 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 628

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| ||||||||||  ||||||||||||||
Db        629 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 688

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        689 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 748

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || |||||||||| ||||||||||||||||| |||||
Db        749 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 808

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||| || |||||||||||||||||||||||||| ||| | |||| |||||||
Db        809 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 868

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        869 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 928

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  ||||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db        929 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 988

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        989 AGCGAATGGGCATCTGTGCCCTGCAGT 1015


RESULT 6
US-08-458-356-194
; Sequence 194, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-194

  Query Match            78.3%;  Score 772.6;  DB 2;  Length 1018;
  Best Local Similarity  87.1%;  Pred. No. 4.1e-242;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         32 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 91

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db         92 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 151

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        152 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 211

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        212 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 271

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| ||||| || ||||||||| ||||||| ||||  ||
Db        272 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 331

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||| |||||||| |||
Db        332 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 391

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        392 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 451

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| ||||||||||||||||| |||||||||||||| ||||||
Db        452 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 511

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        512 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 571

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        572 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 628

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db        629 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 688

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||||  ||||||||||
Db        689 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 748

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||| || |||||||||| ||||||||||||||| |||||
Db        749 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 808

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || |||||||||||||||||||||||||| ||| | |||| |||||||
Db        809 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 868

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        869 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 928

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  |||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db        929 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 988

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        989 AGCGAATGGGCATCTGTGCCCTGCAGT 1015


RESULT 7
US-08-460-736-194
; Sequence 194, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-194

  Query Match            78.3%;  Score 772.6;  DB 4;  Length 1018;
  Best Local Similarity  87.1%;  Pred. No. 4.1e-242;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         32 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 91

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db         92 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 151
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        152 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 211

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        212 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 271

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||||| ||||| || |||||||||| |||||||  ||||  ||
Db        272 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 331

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||| |||||||| |||
Db        332 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 391

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        392 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 451

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||||| |||||||||||||| ||||||
Db        452 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 511

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        512 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 571

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| |||||||| ||||||||||
Db        572 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 628

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db        629 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 688

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        689 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 748

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || |||||||||| ||||||||||||||||| ||||||
Db        749 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 808

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || ||||||||||||||||||||||||||| ||| | |||| |||||||
Db        809 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 868

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        869 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 928

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  |||||  ||  |||||  |||| ||||||||||||| ||||| |||
Db        929 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 988

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        989 AGCGAATGGGCATCTGTGCCCTGCAGT 1015


RESULT 8
US-08-751-767A-3
; Sequence 3, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1399 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  43..1026
US-08-751-767A-3

  Query Match            78.3%;  Score 772.6;  DB 2;  Length 1399;
  Best Local Similarity  87.1%;  Pred. No. 5e-242;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         43 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 102

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db        103 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 162

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        163 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 222

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        223 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 282

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||||| ||||| || |||||||||| |||||||  ||||  ||
Db        283 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 342

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| |||||||||||||||||||||||||| |||||||| |||
Db        343 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 402

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        403 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 462

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||||| |||||||||||||| ||||||
Db        463 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 522

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        523 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 582
```

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Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        583 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 639

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| ||||||||||  |||||||||||||
Db        640 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 699

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        700 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 759

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || |||||||||||| |||||||||||||||||| |||||
Db        760 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 819

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||  || ||||||||||||||||||||||||||| ||| | |||| |||||||
Db        820 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 879

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  ||||||||||||||||| |||| |
Db        880 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 939

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  ||||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db        940 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 999

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db       1000 AGCGAATGGGCATCTGTGCCCTGCAGT 1026


RESULT 9
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1623 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1620
US-08-751-767A-9

  Query Match             78.3%;  Score 772.6;  DB 2;  Length 1623;
  Best Local Similarity   87.1%;  Pred. No. 5.5e-242;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db          1 ATGGGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| |||||||||||||| ||||| ||||| ||| | || |||
Db         61 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||  | ||||||||||||||  ||||| |||
Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        181 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||||| |||| || |||||||| ||||| |||  ||
Db        241 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||| |||||||| |||
Db        301 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        361 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||| ||||||
Db        421 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        481 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        541 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 597

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| ||||||||||  |||||||||||||
Db        598 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 657

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        658 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 717

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || |||||||||||| |||||||||||||||||| |||||
Db        718 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 777

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||  || ||||||||||||||||||||||||||| ||| | |||| |||||||
Db        778 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 837

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  ||||||||||||||||| |||| |
Db        838 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 897

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  ||||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db        898 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 957
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Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        958 AGCGAATGGGCATCTGTGCCCTGCAGT 984


RESULT 10
US-08-265-087-1
; Sequence 1, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-265-087-1

  Query Match             78.3%;  Score 772.6;  DB 1;  Length 2362;
  Best Local Similarity   87.1%;  Pred. No. 7e-242;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   | ||||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         33 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 92

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| |||||||||||||| ||||| ||||| ||| | || |||
Db         93 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 152

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        153 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 212

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| |||| |||| ||||||||||||||||||
Db        213 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 272

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||||| |||| || |||||||| ||||||| ||||  ||
Db        273 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 332

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| |||||||||||||||||||||||||| |||||||| |||
Db        333 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 392

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| |||| |||||||||||||||||||||
Db        393 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 452

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        453 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 512

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        513 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 572

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        573 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 629

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db        630 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 689

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        690 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 749

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || |||||||||| |||||||||||||||| |||||
Db        750 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 809

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || |||||||||||||||||||||||| ||| | |||| |||||||
Db        810 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 869

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        870 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 929

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| ||| |||||| || |||||| |||| |||||||||||||| ||||| |||
Db        930 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 989

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        990 AGCGAATGGGCATCTGTGCCCTGCAGT 1016


RESULT 11
US-08-621-493-1
; Sequence 1, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-621-493-1

  Query Match             78.3%;  Score 772.6;  DB 1;  Length 2362;
  Best Local Similarity   87.1%;  Pred. No. 7e-242;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         33 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 92

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db         93 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 152

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        153 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 212

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        213 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 272

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| ||||| || ||||||||| ||||||| ||||  ||
Db        273 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 332

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| |||||||||||||||||||||||||| |||||||| |||
Db        333 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 392

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        393 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 452

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        453 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 512

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        513 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 572

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||

Db        573 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 629

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||
Db        630 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 689

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        690 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 749

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || |||||||||| |||||||||||||||| |||||
Db        750 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 809

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || ||||||||||||||||||||||||||| ||| | |||| |||||||
Db        810 GACACCTGGAGTACTCCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 869

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  ||||||||||||||||| |||| |
Db        870 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 929

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  |||||| || |||||| |||| ||||||||||||| ||||| |||
Db        930 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 989

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        990 AGCGAATGGGCATCTGTGCCCTGCAGT 1016


RESULT 12
US-08-965-688-1
; Sequence 1, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
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;       LENGTH:  2362 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  unknown
;     MOLECULE TYPE:  cDNA
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  33..1016
US-08-965-688-1

  Query Match             78.3%;  Score 772.6;  DB 2;  Length 2362;
  Best Local Similarity   87.1%;  Pred. No. 7e-242;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  ||||||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         33 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 92

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||| |||||||||||||||| ||||| |||| ||| | || |||
Db         93 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 152

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        153 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 212

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        213 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 272

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| ||||| || ||||||||| ||||||| ||||  ||
Db        273 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 332

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| |||||||||||||||||||||||| ||||||| |||
Db        333 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 392

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        393 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 452

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||||| |||||||||||||| ||||||
Db        453 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 512

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        513 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 572

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        573 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 629

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| ||||||||||  ||||||||||||||
Db        630 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 689

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db        690 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 749

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| ||||||||||||||| || |||||||||| ||||||||||||||||| |||||
Db        750 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 809

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || |||||||||||||||||||||||||| ||| | |||| |||||||
Db        810 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 869

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||| ||| |  ||||||||||||||| |||| |
Db        870 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 929
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  |||||| ||  |||||| |||| ||||||||||||| ||||| |||
Db        930 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 989

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        990 AGCGAATGGGCATCTGTGCCCTGCAGT 1016


RESULT 13
US-09-260-173-1
; Sequence 1, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;       APPLICANT: Scott, Phillip
;                  Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 1:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2362 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
;       MOLECULE TYPE: cDNA
;       FEATURE:
;            NAME/KEY:  CDS
;            LOCATION:  33..1016
;       SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-260-173-1

  Query Match             78.3%;  Score 772.6;  DB 4;  Length 2362;
  Best Local Similarity   87.1%;  Pred. No. 7e-242;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  ||||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         33 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 92
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Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db         93 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 152

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        153 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 212

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  | |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        213 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 272

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||||| ||||| || ||||||||| ||||||| ||||  ||
Db        273 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 332

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||| |||||||| |||
Db        333 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 392

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        393 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 452

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || ||||||||||||| |||||||||||||||||| |||||||||||||| ||||||
Db        453 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 512

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        513 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 572

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        573 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 629

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db        630 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 689

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||||  ||||||||||
Db        690 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 749

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||| || |||||||||| ||||||||||||||||  |||||
Db        750 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 809

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || |||||||||||||||||||||||||| ||| | |||| ||||||
Db        810 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 869

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        870 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 929

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  |||||  ||  |||||| |||| |||||||||||||| |||| |||
Db        930 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 989

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        990 AGCGAATGGGCATCTGTGCCCTGCAGT 1016
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RESULT 14
US-08-751-767A-7
; Sequence 7, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  7:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

  Query Match             78.3%;  Score 772.6;  DB 2;  Length 6139;
  Best Local Similarity   87.1%;  Pred. No. 1.3e-241;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db       3222 ATGGGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 3281

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db       3282 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 3341

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              |||||  |||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db       3342 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 3401

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  | |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db       3402 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 3461

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||||| ||||| || ||||||||| ||||||| ||||  ||
Db       3462 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 3521

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||| |||||||| |||
Db       3522 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 3581

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db       3582 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 3641

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || ||||||||||||| |||||||||||||||||| |||||||||||||| ||||||
Db       3642 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 3701
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Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || |||||  |  ||||| || ||||||||  |||
Db       3702 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 3761

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| |||||| ||||||||||
Db       3762 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 3818

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| ||||||||||  ||||||||||||||
Db       3819 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 3878

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| ||||||||||||| ||||||||||
Db       3879 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 3938

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || ||||||||||| ||||||||||||||||| |||||
Db       3939 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 3998

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || ||||||||||||||||||||||||| ||| | |||| |||||||
Db       3999 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 4058

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| |
Db       4059 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 4118

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  |||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db       4119 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 4178

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db       4179 AGCGAATGGGCATCTGTGCCCTGCAGT 4205


RESULT 15
US-08-848-760B-24
; Sequence 24, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
;             STATE: Florida
;             COUNTRY: United States of America
;             ZIP: 32606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/848,760B
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: 09-APR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: PACE, DORAN R.
;             REGISTRATION NUMBER: 38,261
;             REFERENCE/DOCKET NUMBER: CNG-100C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (352) 375-8100
;             TELEFAX: (352) 372-5800
;   INFORMATION FOR SEQ ID NO: 24:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 987 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-08-848-760B-24

  Query Match            78.1%;  Score 771;  DB 4;  Length 987;
  Best Local Similarity  87.0%;  Pred. No. 1.3e-241;
  Matches  859;  Conservative    0;  Mismatches  125;  Indels    3;  Gaps    1;

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Job time : 55.4241 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:38:23 ; Search time 193.144 Seconds
(without alignments)
8158.492 Million cell updates/sec

Title: US-09-917-265-58
Perfect score: 987
Sequence: 1 atgcaccctcagcagttggt.....gggcatctgtgtcatgcagt 987

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1114047 seqs, 798260406 residues

Total number of hits satisfying chosen parameters: 2228094

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	3	987	100.0	1599	10	US-09-917-265-61	Sequence 61, Appl
c	4	987	100.0	1599	10	US-09-917-265-63	Sequence 63, Appl
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	45	39.4	4.0	2723	9	US-10-098-841-216	Sequence 216, App

ALIGNMENTS

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RESULT 1
US-09-917-265-58
; Sequence 58, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-58

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  Best Local Similarity   100.0%;  Pred. No. 1.8e-312;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
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; Sequence 60, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
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;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-60

  Query Match             100.0%;  Score 987;  DB 10;  Length 987;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-312;
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 148

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 28

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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                    ||||||||||||||||||||||||||
Db          27 AGCGACTGGGCATCTGTGTCATGCAGT 1


RESULT 3
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match             100.0%;  Score 987;  DB 10;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-312;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||||||||||||||||||||||||
Db        961 AGCGACTGGGCATCTGTGTCATGCAGT 987


RESULT 4
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match             100.0%;  Score 987;  DB 10;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-312;
  Matches  987;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1599 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1420

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1419 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1359 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1300
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Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1299 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1179 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1120

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        999 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 940

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        939 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 880

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        879 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 760

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        759 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 640

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||||||||||||||
Db        639 AGCGACTGGGCATCTGTGTCATGCAGT 613
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RESULT 5
US-09-917-265-107
; Sequence 107, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 107
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (154)..(1140)
;   OTHER INFORMATION:
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US-09-917-265-107

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  Query Match             99.7%;  Score 983.8;  DB 10;  Length 2267;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-311;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 213

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 273

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 333

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 393

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 453

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 513

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 573

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 633

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 693

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        694 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 753

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 813

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 873

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 933

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 993

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 1053

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1054 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 1113

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||||||| ||||||
Db       1114 AGCGACTGGGCATCTGTGTCCTGCAGT 1140
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RESULT 6
US-09-917-265-109/c
; Sequence 109, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
;   LENGTH: 2267
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-109

  Query Match             99.7%;  Score 983.8;  DB 10;  Length 2267;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-311;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2114 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 2055

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       2054 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1995

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1994 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 1935

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1934 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 1875

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1874 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 1815

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1814 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 1755

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1754 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1695

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1694 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 1635

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1634 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1575

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1574 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1515

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1514 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 1455

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1454 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 1395

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1394 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 1335

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1334 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 1275

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1274 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 1215

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1214 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 1155

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||||| ||||||
Db       1154 AGCGACTGGGCATCTGTGTCCTGCAGT 1128


RESULT 7
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match             93.3%;  Score 921;  DB 10;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1e-290;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        967 TGGGCATCTGTGTCATGCAGT 987
                |||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGT 921


RESULT 8
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             93.3%;  Score 921;  DB 10;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 1e-290;
  Matches  921;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        967 TGGGCATCTGTGTCATGCAGT 987
                |||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGT 613


RESULT 9
US-09-917-265-52
; Sequence 52, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
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;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(921)
;   OTHER INFORMATION:
US-09-917-265-52

  Query Match             93.2%;  Score 919.4;  DB 10;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 2.4e-290;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        967 TGGGCATCTGTGTCATGCAGT 987
              ||||||||||||||| ||||||
Db        901 TGGGCATCTGTGTCCTGCAGT 921


RESULT 10
US-09-917-265-54/c
; Sequence 54, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
;   LENGTH: 921
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-54

  Query Match             93.2%;  Score 919.4;  DB 10;  Length 921;
  Best Local Similarity   99.9%;  Pred. No. 2.4e-290;
  Matches  920;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        921 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 862

Qy        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        861 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 802

Qy        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        801 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 742

Qy        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        741 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 682

Qy        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 622

Qy        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 562

Qy        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 502

Qy        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 442

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 382

Qy        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 322
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Qy        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 262

Qy        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 202

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 142

Qy        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 82

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 22

Qy        967 TGGGCATCTGTGTCATGCAGT 987
              ||||||||||||||| ||||||
Db         21 TGGGCATCTGTGTCCTGCAGT 1


RESULT 11
US-09-917-265-29
; Sequence 29, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(987)
;   OTHER INFORMATION:
US-09-917-265-29

  Query Match            89.5%;  Score 883;  DB 10;  Length 987;
  Best Local Similarity  93.4%;  Pred. No. 2.1e-278;
  Matches  922;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||||||||||| |||||||||||| |||||||||||  ||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              |||||||||||||||||||||||||||||| |||| ||||||||||||||||||| |||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  ||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||  ||

Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||  |||| |||||||| |||||||||||||||||||||||||||||||| |||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||||||||||| |||||||||| |||||| |||||||||| ||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| |||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              || |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||| |||||||||||||||| |||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||| |||||||||| ||||| ||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


RESULT 12
US-09-917-265-31/c
; Sequence 31, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
;   LENGTH: 987
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-31

  Query Match            89.5%;  Score 883;  DB 10;  Length 987;
```

Best Local Similarity 94.4%; Pred. No. 2.1e-278;
Matches 922; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

```
Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||||||||||| |||||||||||| |||||||||||  ||||||||
Db        987 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 928

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db        927 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 868

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||| |||| |||||||||||||||||| |||
Db        867 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 808

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  |||||||||||||||||||| |||| |||||||||||||||||||| |||
Db        807 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 748

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||  ||
Db        747 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 688

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||| |||| |||||||| ||||||||||||||||||||||||||||||| |||||||
Db        687 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 628

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        627 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 568

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||||||||| |||||||||||| ||||||||| |||||
Db        567 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 508

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||| ||||||||||| || |||||| |||||| |||||||||| ||||
Db        507 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 448

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 388

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              || |||||||||||||||||||| || |||||||||| |||||||||||||||||||||
Db        387 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 328

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              || |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 268

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 AACCTGCAACTGAATCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 208

Qy        781 GACACCTGGAGCACCCCACACTTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        207 GACACCTGGAGCACCCCACACTTCCTACTTCTCCCTTAACATTTGGCGTACAGGTCCAGGGC 148

Qy        841 AAGAACAAATAGAGAAAAGAAAGATAGACCTCTGCGTGGACAAGACCCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 88

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         87 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 28

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||||||||||||||||||||||||||
Db         27 AGCAACTGGGCATCCGTGTCCTGCAGT 1
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RESULT 13

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US-09-917-265-55
; Sequence 55, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 55
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(984)
;   OTHER INFORMATION:
US-09-917-265-55
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Query Match 89.3%; Score 881; DB 10; Length 985;
Best Local Similarity 93.4%; Pred. No. 9.7e-278;
Matches 920; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

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Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||||||||||| |||||||||||| |||||||||||  ||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||| |||| |||||||||||||||||| |||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  |||||||||||||||||||| |||| |||||||||||||||||||| |||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||  ||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||| |||| |||||||| ||||||||||||||||||||||||||||||| |||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||||||||| |||||||||||| ||||||||| |||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||| ||||||||||| || |||||| |||||| |||||||||| ||||
Db        481 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              || |||||||||||||||||||| || |||||||||| |||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
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                 || |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||| |||||||||||||| |||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCA 985
              ||| |||||||||| ||||| ||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCA 985


RESULT 14
US-09-917-265-57/c
; Sequence 57, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 57
;   LENGTH: 985
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-57

  Query Match             89.3%;  Score 881;  DB 10;  Length 985;
  Best Local Similarity   93.4%;  Pred. No. 9.7e-278;
  Matches  920;  Conservative    0;  Mismatches   65;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||||||||| |||||||||||| |||||||||| ||||||||
Db        985 ATGCATCCTCAGCAGTTGGTCATCGCCTGGTTTTCCCTGGTTTTGCTGGCACCTCCCCTC 926

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||||| | ||||||||||||||||||||||||||||||||
Db        925 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 866

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              |||||||||||||||||||||||||||||| |||| ||||||||||||||||||| |||
Db        865 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 806

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  |||||||||||||||||| ||||||||||||||||||||||||||||||
Db        805 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 746

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||  ||
Db        745 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 686

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||  |||| |||||||| |||||||||||||||||||||||||||||| |||||||
Db        685 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 626
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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db        625 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 566

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db        565 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 506

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||||||||||||| |||||||||| ||||| |||||||||| ||||
Db        505 GGCTCCTCTGACCCCCAAGGGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 446

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        445 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 386

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| |||||||||||||||||||
Db        385 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 326

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              || |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        325 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 266

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        265 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 206

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        205 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 146

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| |||||||||||||||||||||||||||
Db        145 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 86

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Db         85 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 26

Qy        961 AGCGACTGGGCATCTGTGTCATGCA 985
              ||| |||||||||| ||||| ||||
Db         25 AGCAACTGGGCATCCGTGTCCTGCA 1


RESULT 15
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

  Query Match             89.1%;  Score 879.8;  DB 10;  Length 1599;
  Best Local Similarity   93.2%;  Pred. No. 3.2e-277;
  Matches  920;  Conservative    0;  Mismatches   67;  Indels    0;  Gaps    0;
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Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
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Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
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Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
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Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
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Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db        961 AGCAACTGGGCATCCGTGTCCTGCAGT 987


Search completed: July 16, 2003, 13:16:28
Job time : 194.144 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:54:38 ; Search time 33.0724 Seconds
(without alignments)
1325.559 Million cell updates/sec

Title: US-09-917-265-59
Perfect score: 1764
Sequence: 1 MHPQQLVISWFSLVLLASPL.....QARDRYYSSSWSDWASVSCS 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1764	100.0	329	19	AAW41791	Canine IL-12 P40 s
2	1764	100.0	329	20	AAY02342	Canine Interleukin
3	1764	100.0	329	20	AAW84373	Canine interleukin
4	1764	100.0	329	22	AAG66482	Canine protein #3.
5	1735	98.4	329	19	AAW41790	Canine IL-12 P40 s
6	1735	98.4	329	20	AAY02339	Canine Interleukin
7	1735	98.4	329	20	AAW84371	Canine interleukin
8	1735	98.4	329	22	AAG66480	Canine protein #1.
9	1729.5	98.0	330	20	AAW74322	Canine full length
10	1651	93.6	329	19	AAW76173	Feline FLAFp40 pro
11	1618.5	91.8	308	20	AAW74323	Canine mature CLAF
12	1567	88.8	329	22	AAE08602	Modified human cyt
13	1557	88.3	327	22	AAE08599	Modified human cyt
14	1554	88.1	307	19	AAW76174	Feline FLAFp40 mat
15	1515	85.9	327	21	AAB15391	Bovine interleukin
16	1512	85.7	327	22	AAE08598	Modified human cyt
17	1504	85.3	327	22	AAE08597	Modified human cyt
18	1502.5	85.2	328	23	AAU75579	Human interleukin
19	1502.5	85.2	526	23	AAE19818	Human IL-12.0 prot
20	1502.5	85.2	527	23	AAE19817	Human IL-12.1 prot
21	1502.5	85.2	537	23	AAE19820	Human IL-12.2 prot
22	1502.5	85.2	540	21	AAY54921	Interleukin-12 fus
23	1502.5	85.2	542	23	AAE19819	Human IL-12.3 prot
24	1502.5	85.2	547	23	AAE19821	Human IL-12.4 prot
25	1501.5	85.1	328	13	AAR22769	Natural killer cel
26	1501.5	85.1	328	16	AAR79186	Human interleukin-
27	1501.5	85.1	328	17	AAW07398	Human interleukin-
28	1501.5	85.1	328	18	AAW24235	40 kDa subunit of
29	1501.5	85.1	328	18	AAW36941	40 kDa subunit of
30	1501.5	85.1	328	18	AAW36939	40 kDa subunit of
31	1501.5	85.1	328	19	AAW62992	Human interleukin-
32	1501.5	85.1	328	19	AAW58725	Cytotoxic lymphocy
33	1501.5	85.1	328	19	AAW51311	Human Interleukin-
34	1501.5	85.1	328	19	AAW57482	Human interleukin-
35	1501.5	85.1	328	19	AAW51221	Human interleukin-
36	1501.5	85.1	328	19	AAW44324	Heterodimeric huma
37	1501.5	85.1	328	20	AAY42487	Human interleukin
38	1501.5	85.1	328	21	AAB23796	Human interleukin
39	1501.5	85.1	328	21	AAY54919	Human p40 protein
40	1501.5	85.1	328	21	AAY44181	Human interleukin-
41	1501.5	85.1	328	22	AAE11198	Human interleukin-
42	1501.5	85.1	328	22	AAE08603	Human cytokine p40
43	1501.5	85.1	328	22	AAB67262	IL-12 vaccine adju
44	1501.5	85.1	328	22	AAB36649	Human cytokine rec
45	1495.5	84.8	328	22	AAE11193	Human interleukin

ALIGNMENTS

RESULT 1
AAW41791
ID AAW41791 standard; peptide; 329 AA.
XX
AC AAW41791;
XX
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P40 subunit.
XX
KW Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW antiviral; vaccine adjuvant.
XX
OS Canis sp.
XX
PN JP10036397-A.
XX
PD 10-FEB-1998.
XX
PF 08-NOV-1996; 96JP-0296789.
XX
PR 23-MAY-1996; 96JP-0128104.
PR 08-NOV-1995; 95JP-0289729.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1998-174914/16.
DR N-PSDB; AAV13817.
XX
PT Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT activities are expected
XX

PS Claim 2; Pages 10-11; 12pp; Japanese.
XX
CC The present sequence is a canine interleukin-12 (IL-12) P40
CC subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC of inducing an antiviral activating factor and the expression of
CC class II MHC molecules in canine tumour cells, stimulating
CC proliferation of canine blastogenic lymphocytes and activating
CC canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC can be used in veterinary medicines, e.g. antitumour, antivirus and
CC vaccine adjuvant activities are expected.
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1764; DB 19; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.3e-148;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
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Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
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Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
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Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
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Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
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RESULT 2
AAY02342
ID AAY02342 standard; Protein; 329 AA.
XX
AC AAY02342;
XX
DT 09-JUL-1999 (first entry)
XX
DE Canine Interleukin-12 (IL-12) protein sequence.
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease.
XX
OS Canis sp.
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-308068/26.
DR N-PSDB; AAX35625.
XX
PT A prevention and treating agent containing interleukin 12 (CaIL12) -
PT for prevention and treatment of dog and cat immune diseases
XX
PS Claim 1; Page 14-15; 16pp; Japanese.
XX
CC The present sequence represents canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment
CC of dog and cat immune diseases. The treatment used an agent comprising
CC dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC useful for preventing and treating dog and cat immune diseases,
CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.
XX
SQ Sequence 329 AA;

Query Match 100.0%; Score 1764; DB 20; Length 329;
Best Local Similarity 100.0%; Pred. No. 1.3e-148;
Matches 329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
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Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
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Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
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Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||||||||
Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
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RESULT 3
AAW84373
ID AAW84373 standard; Protein; 329 AA.
XX
AC AAW84373;
XX
DT 30-MAR-1999 (first entry)
XX
DE Canine interleukin 12 protein.
XX
KW Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW skin disease; viral infection; allergic disease; breast tumour;
KW oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW feline leukaemia; allergy; pollinosis.
XX
OS Canis sp.
XX
PN WO9851327-A1.
XX
PD 19-NOV-1998.
XX
PF 07-MAY-1998; 98WO-JP02031.
XX
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX

```
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03162.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 30-32; 45pp; Japanese.
XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   329 AA;

  Query Match             100.0%;  Score 1764;  DB 20;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-148;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
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Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||||||||
Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 4
AAG66482
ID   AAG66482 standard; Protein; 329 AA.
XX
AC   AAG66482;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #3.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Signal_peptide
FT   Protein         23..329
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64388.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Disclosure; Page 17; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence   329 AA;

  Query Match             100.0%;  Score 1764;  DB 22;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-148;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||||||||
Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 5
AAW41790
ID   AAW41790 standard; peptide; 329 AA.
XX
AC   AAW41790;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant.
XX
OS   Canis sp.
```

```
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   N-PSDB; AAV13816.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 2; Page 8; 12pp; Japanese.
XX
CC   The present sequence is a canine interleukin-12 (IL-12) P40
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence   329 AA;

  Query Match            98.4%;  Score 1735;  DB 19;  Length 329;
  Best Local Similarity  99.4%;  Pred. No. 4.8e-146;
  Matches  324;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 LKPLENSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              ||||||||||||||||||||| ||
Db        304 DAKIRVQARDRYYSSSWSDWASVPCS 329


RESULT 6
AAY02339
ID   AAY02339 standard; Protein; 329 AA.
XX
AC   AAY02339;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Canine Interleukin-12 (IL-12) protein sequence.
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease.
XX
OS   Canis sp.
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   N-PSDB; AAX35615.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 12; 16pp; Japanese.
XX
CC   The present sequence represents canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence   329 AA;

  Query Match            98.4%;  Score 1735;  DB 20;  Length 329;
  Best Local Similarity  99.4%;  Pred. No. 4.8e-146;
  Matches  324;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 LKPLENSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              ||||||||||||||||||||| ||
Db        304 DAKIRVQARDRYYSSSWSDWASVPCS 329


RESULT 7
AAW84371
ID   AAW84371 standard; Protein; 329 AA.
XX
AC   AAW84371;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Canine interleukin 12 protein.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
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KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis.
XX
OS   Canis sp.
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03152.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 23-25; 45pp; Japanese.
XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   329 AA;

  Query Match             98.4%;  Score 1735;  DB 20;  Length 329;
  Best Local Similarity   99.4%;  Pred. No. 4.8e-146;
  Matches  324;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 LKPLENSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||| ||
Db        304 DAKIRVQARDRYYSSSWSDWASVPCS 329
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RESULT 8
AAG66480
ID   AAG66480 standard; Protein; 329 AA.
XX
AC   AAG66480;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #1.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Signal_peptide
FT   Protein         23..329
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64378.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Disclosure; Page 14; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence   329 AA;

  Query Match             98.4%;  Score 1735;  DB 22;  Length 329;
  Best Local Similarity   99.4%;  Pred. No. 4.8e-146;
  Matches  324;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 LKPLENSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
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Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              ||||||||||||||||||||||| ||
Db        304 DAKIRVQARDRYYSSSWSDWASVPCS 329


RESULT 9
AAW74322
ID   AAW74322 standard; Protein; 330 AA.
XX
AC   AAW74322;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p40 subunit.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   N-PSDB; AAX18176.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 1; Page 22-24; 51pp; Japanese.
XX
CC   This sequence is the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence   330 AA;

  Query Match             98.0%;  Score 1729.5;  DB 20;  Length 330;
  Best Local Similarity   98.5%;  Pred. No. 1.5e-145;
  Matches  325;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLL-IHKKEDGIWSTDILKE 119
              |||||||||||||||||||||||||||||||||||||||||    ||:||||||||||
Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLFDSTKKKDGIWSTDILKE 120

Qy        120 QKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAER 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAER 180

Qy        180 VRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPP 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPP 240

Qy        240 TNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKV 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKV 300

Qy        300 VCHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||||||||
Db        301 VCHKDAKIRVQARDRYYSSSWSDWASVSCS 330


RESULT 10
AAW76173
ID   AAW76173 standard; Protein; 329 AA.
XX
AC   AAW76173;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 protein.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= signal
FT   Protein         23..329
FT                   /label= FLAFp40
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   N-PSDB; AAV56625.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 1; Page 45-47; 94pp; Japanese.
XX
CC   This sequence represents a novel feline cytokine protein, FLAFp40. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence   329 AA;

  Query Match             93.6%;  Score 1651;  DB 19;  Length 329;
  Best Local Similarity   93.3%;  Pred. No. 1.5e-138;
  Matches  307;  Conservative   10;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              ||||||||:|| ||||| ||||||||||:||||||||||||||||||||:|||||||||
Db          1 MHPQQLVIAWFYLVLLAPPLMAIWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||||||||||| ||||||||||:||| | |||||||||||||||:||
Db         61 TSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQ 120
```

```
Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              ||||||||||||||||||||||||||||||||||||||:||||||  |||||||||| |||||:|
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              |||||||||||||||||||||||||||||||| :| ||||||||||| |||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||:|||||||
Db        301 CHKDAKIRVQARDRYYSSSWSNWASVSCS 329
```

RESULT 11
AAW74323
ID AAW74323 standard; Protein; 308 AA.
XX
AC AAW74323;
XX
DT 07-MAY-1999 (first entry)
XX
DE Canine mature CLAF p40 subunit.
XX
KW CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis.
XX
OS Canis sp.
XX
PN WO9855511-A1.
XX
PD 10-DEC-1998.
XX
PF 26-MAY-1998; 98WO-JP02295.
XX
PR 03-JUN-1997; 97JP-0161936.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Eda Y, Imamura T, Maeda H, Tokiyoshi S;
XX
DR WPI; 1999-070260/06.
DR N-PSDB; AAX18177.
XX
PT Canine cytokine protein which activates canine cytotoxic T
PT lymphocytes - is useful for treatment of viral and autoimmune
PT diseases in dogs
XX
PS Claim 1; Page 24-26; 51pp; Japanese.
XX
CC This sequence is the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs.
XX
SQ Sequence 308 AA;

Query Match 91.8%; Score 1618.5; DB 20; Length 308;
Best Local Similarity 98.4%; Pred. No. 1e-135;
Matches 303; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

```
Qy         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60

Qy         83 GDAGQYTCHKGGKVLSRSLLL-IHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFT 141
              |||||||||||||||||||    ||:|||||||||||||||||||||||||||||||||||
Db         61 GDAGQYTCHKGGKVLSRSLLFDSTKKKDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFT 120

Qy        142 CWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP 180

Qy        202 SAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPD 261
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPD 240

Qy        262 TWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 321
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 300

Qy        322 DWASVSCS 329
              ||||||||
Db        301 DWASVSCS 308
```

RESULT 12
AAE08602
ID AAE08602 standard; Protein; 329 AA.
XX
AC AAE08602;
XX
DT 01-NOV-2001 (first entry)
XX
DE Modified human cytokine p40 from clone R16-51.
XX
KW Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW human; p40; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Cleavage-site 1..22
FT /label= Leader_peptide
FT Protein 23..329
FT /note= "Mature modified p40"
XX
PN WO200140257-A2.
XX
PD 07-JUN-2001.
XX
PF 30-NOV-2000; 2000WO-US32664.
XX
PR 02-DEC-1999; 99US-0169035.
PR 28-NOV-2000; 2000US-0169035.
XX
PA (MAXY-) MAXYGEN INC.
XX
PI Leong SR, Punnonen J;
XX
DR WPI; 2001-502381/55.
DR N-PSDB; AAD15209.
XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT p40 and p35 polypeptides), useful for treating various diseases e.g.
PT diabetic retinopathy and cancer -
XX
PS Claim 38; Fig 1; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and

```
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein.
XX
SQ   Sequence   329 AA;

  Query Match             88.8%;  Score 1567;  DB 22;  Length 329;
  Best Local Similarity   89.6%;  Pred. No. 4.4e-131;
  Matches  292;  Conservative   14;  Mismatches   20;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| ||||||:|||||||:||||||||:|||||||||| | ||||| |||||
Db          4 QQLVISWFSLVFLASPLVAIWELEKNVYVVELDWYPDAPGEMVVLACDTPEEDGITWTSD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||:|||||| |||||||||||| ||| |||:||||:|||||||||||||:|||
Db         64 QSSEVLGTGKTLTIHVKEFGDAGQYTCRKGGAVLSQSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              |||||||||||||||||||||||||||||:|||||| ||||||||||||||||||| :|
Db        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAVTLSAERVSMD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              :|:| |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        184 HREYNKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||||||:||||||||| ||||||| | :| |||| |||||||| ||||||||||
Db        244 LKPLKNSRHVEISWEYPDTWSIPHSYFSLMFGVQVQGKNKREKKDRLSVDKTSAKVVCHK 303

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||:|||| ||
Db        304 DAKIRVQARDRYYSSSWSEWASVPCS 329


RESULT 13
AAE08599
ID   AAE08599 standard; Protein; 327 AA.
XX
AC   AAE08599;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p40 from clone B1-81.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p40; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Cleavage-site   1..22
FT                   /label= Leader_peptide
FT   Protein         23..327
FT                   /note= "Mature modified p40"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   N-PSDB; AAD15206.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 38; Fig 1; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p40 protein.
XX
SQ   Sequence   327 AA;

  Query Match             88.3%;  Score 1557;  DB 22;  Length 327;
  Best Local Similarity   87.5%;  Pred. No. 3.4e-130;
  Matches  288;  Conservative   20;  Mismatches   19;  Indels    2;  Gaps    1;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              |||||||:|||||||||||:|||||||:||||||||:|||||| ||| | ||||| |||
Db          1 MHPQQLVVSWFSLVLLASPLVAIWELEKNVYVVELDWYPDAPGETVVLACDTPEEDGITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||:|||||| |||||||||||| ||| |||:||||:|||||||||||||:|
Db         61 TSDQSSEVLGTGKTLTIHVKEFGDAGQYTCRKGGAVLSQSLLLLHKKEDGIWSTDILKDQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              |: ||||||||||||||||||||||||||||||:|||||| ||||||||||||||||||
Db        121 KKPKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              :|:|:| ||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        181 SMDHREYNKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSRFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||:|||||||||:|||||||||||||||||:| |||| |||| | :|:|||||
Db        241 NLQLRPLKNSRHVEISWEYPDTWSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVT 298

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||:|||||:|||| ||
Db        299 CHKDAKIRVQARDRYHSSSWSEWASVPCS 327


RESULT 14
AAW76174
ID   AAW76174 standard; Protein; 307 AA.
XX
AC   AAW76174;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp40 mature protein.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
```

```
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   N-PSDB; AAV56626, AAV56627.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 3; Page 47-49; 94pp; Japanese.
XX
CC   This sequence represents a novel feline cytokine mature protein, FLAFp40.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment
CC   of feline autoimmune diseases e.g. as caused by feline herpes virus
CC   or feline calcivirus.
XX
SQ   Sequence   307 AA;

  Query Match             88.1%;  Score 1554;  DB 19;  Length 307;
  Best Local Similarity   93.8%;  Pred. No. 5.7e-130;
  Matches  288;  Conservative    9;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82
              |||||||:|||||||||||||||||||||:|||||||||| |||||||||||||||||||
Db          1 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 60

Qy         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142
              |||||||||||:||| | |||||||||||||||:||||||||||||||||||||||||||
Db         61 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 120

Qy        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202
              ||||||||||||:|||||| |||||||||| |||||:|||||||||||||||||||||:
Db        121 WWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 180

Qy        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262
              |||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 240

Qy        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322
              |||||||||||| :| |||||||||||| ||||||||||||||||||||||||||||:
Db        241 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 300

Qy        323 WASVSCS 329
              |||||||
Db        301 WASVSCS 307


RESULT 15
AAB15391
ID   AAB15391 standard; Protein; 327 AA.
XX
AC   AAB15391;
XX
DT   15-DEC-2000  (first entry)
XX
DE   Bovine interleukin-12 p40 subunit protein.
XX
KW   Antiinfective; bovine; interleukin 12; IL12; heterodimer; infection.
XX
OS   Bos taurus.
XX
PN   JP2000157274-A.
XX
PD   13-JUN-2000.
XX
PF   20-NOV-1998;   98JP-0331052.
XX
PR   20-NOV-1998;   98JP-0331052.
XX
PA   (DAUC ) DAIICHI PHARM CO LTD.
XX
DR   WPI; 2000-468201/41.
DR   N-PSDB; AAA70709.
XX
PT   Preparation of bovine interleukin 12 comprising using a vector
PT   containing the gene encoding it, useful for the prevention and
PT   treatment of chronic and opportunistic infections -
XX
PS   Example 1; Page 9; 11pp; Japanese.
XX
CC   The invention relates to a method for the preparation of bovine
CC   interleukin 12 (BoIL12). BoIL12 consists of a heterodimer of p35
CC   and p40 subunits. BoIL12 is produced by introducing into a host cell,
CC   recombinant vectors containing genes encoding the p35 and p40 subunits.
CC   This sequence represents the bovine IL12 p40 subunit. Interleukin 12
CC   is used for the prevention and treatment of chronic infections and
CC   opportunistic infections.
XX
SQ   Sequence   327 AA;

  Query Match             85.9%;  Score 1515;  DB 21;  Length 327;
  Best Local Similarity   84.8%;  Pred. No. 1.8e-126;
  Matches  279;  Conservative   25;  Mismatches   23;  Indels    2;  Gaps    1;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              |||||||:|||||||||||::|:|||||:|||||||:|||||| ||||| |||| |||
Db          1 MHPQQLVVSWFSLVLLASPIVAMWELEKNVYVVELDWYPDAPGETVVLTCDTPEEDGITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||||||||||||||||||||||||: |||||||:|||||||||||||:|
Db         61 TSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLLLLHKKEDGIWSTDILKDQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              || | | ||||||||:||| ||||||||||||||||||||| |||:|||||  ||||:|
Db        121 KEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSRGSSDPRGVTCGAALLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
               :::|:| |||||||||||||:||||| |||||:|:|||||||||||||||||||||||
Db        181 SLEHREYNKYTVECQEGSACPAAEESLLIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||:|||||| ||||||||||||||||||||||:| |||| |||| | :|:|||||
Db        241 NLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVT 298

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              ||||| :|||||||||| ||:|||||||
Db        299 CHKDANVRVQARDRYYSSFWSEWASVSCS 327


Search completed: July 15, 2003, 11:02:54
Job time : 35.0724 secs
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:49 ; Search time 14.4202 Seconds
(without alignments)
2193.328 Million cell updates/sec

Title: US-09-917-265-59
Perfect score: 1764
Sequence: 1 MHPQQLVISWFSLVLLASPL.....QARDRYYSSSWSDWASVSCS 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1501.5	85.1	328	2	A38957	interleukin 12B pr
2	1141.5	64.7	335	2	I72789	interleukin 12 p40
3	193	10.9	468	1	A41242	interleukin-6 rece
4	178	10.1	362	2	S60614	growth promoting a
5	177.5	10.1	372	2	I58141	ciliary neurotroph
6	177.5	10.1	440	2	JL0144	interleukin-6 rece
7	177.5	10.1	460	2	JL0145	interleukin-6 rece
8	170	9.6	372	1	UHHUCN	ciliary neurotroph
9	149.5	8.5	422	2	I37891	interleukin-11 rec
10	146.5	8.3	432	2	I48343	interleukin-11 rec
11	132	7.5	812	2	H96544	hypothetical prote
12	122.5	6.9	1277	2	T30532	neural cell adhesi
13	120	6.8	831	2	JQ1655	prolactin receptor
14	118	6.7	977	2	I45877	protein-tyrosine k
15	111.5	6.3	310	2	A29884	prolactin receptor
16	111.5	6.3	412	2	A41070	prolactin receptor
17	111.5	6.3	610	2	A34631	lactogen receptor
18	111.5	6.3	610	2	A36116	prolactin receptor
19	111	6.3	279	2	B32985	somatotropin-bindi
20	111	6.3	638	2	A33505	somatotropin recep
21	110.5	6.3	462	1	A37986	interleukin-6 rece
22	108.5	6.2	1197	2	T30581	neural cell adhesi
23	108	6.1	581	2	I45971	prolactin receptor
24	107.5	6.1	638	2	S12136	somatotropin recep
25	106	6.0	288	2	B59405	prolactin receptor
26	106	6.0	376	2	A59405	prolactin receptor
27	106	6.0	622	2	A40144	prolactin receptor
28	106	6.0	1323	2	PN0568	connectin 3B - chi
29	104.5	5.9	638	2	B28176	somatotropin recep
30	104.5	5.9	677	2	S33608	somatotropin-bindi
31	104.5	5.9	978	1	A49814	protein-tyrosine k
32	103	5.8	579	2	B45266	MPL-K protein prec
33	103	5.8	616	2	A30304	prolactin receptor
34	103	5.8	635	2	A45266	MPL-P protein prec
35	102	5.8	292	2	I77525	prolactin receptor
36	102	5.8	303	2	I77524	prolactin receptor
37	102	5.8	608	2	I53269	prolactin receptor
38	102	5.8	7962	2	I38346	elastic titin - hu
39	101	5.7	696	2	G71620	hypothetical prote
40	100.5	5.7	1232	2	T43027	neural cell adhesi
41	100	5.7	296	2	A87000	probable thiosulfa
42	100	5.7	5175	2	T20992	hypothetical prote
43	100	5.7	5198	2	T43290	hemicentin precurs
44	99.5	5.6	1825	2	C88400	protein H19M22.1 [
45	99.5	5.6	1825	2	T32828	hypothetical prote

ALIGNMENTS

RESULT 1
A38957
interleukin 12B precursor [validated] - human
N;Alternate names: cytotoxic lymphocyte maturation factor 40K chain; natural killer c
C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Nov-2000
C;Accession: A38957; B39359; S21688; B36055
R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.
i, G.; Perussia, B.
J. Immunol. 146, 3074-3081, 1991
A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric
A;Reference number: A38957; MUID:91201875; PMID:1673147
A;Accession: A38957
A;Molecule type: mRNA
A;Residues: 1-328 <WOL>
A;Cross-references: GB:M65290
R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nab
Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
A;Title: Coexpression of two distinct genes is required to generate secreted bioactiv
A;Reference number: A39359; MUID:91239523; PMID:1674604
A;Accession: B39359
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-328 <GUB>
A;Cross-references: GB:M65272; GB:M38444; NID:g180625; PIDN:AAA35695.1; PID:g180626
R;Podlaski, F.J.; Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Levin, W.; Danho, W.; Chi
Arch. Biochem. Biophys. 294, 230-237, 1992
A;Title: Molecular characterization of interleukin 12.
A;Reference number: S21688; MUID:92198015; PMID:1347984
A;Accession: S21688
A;Molecule type: protein
A;Residues: 23-28;46-59;74-80,'X',94-130;161-169,'X',171-180;213-235;240-250;289-299,
A;Experimental source: lymphoblastoid cell line NC-37
R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A;Title: Purification to homogeneity and partial characterization of cytotoxic lympho
A;Reference number: A36055; MUID:90370873; PMID:2204066
A;Accession: B36055
A;Molecule type: protein
A;Residues: 23-45 <STE>
A;Experimental source: lymphoblastoid cell line NC-37
C;Genetics:
A;Gene: GDB:IL12B; NKSF2
A;Cross-references: GDB:127870; OMIM:161561
A;Map position: 5q31.1-5q33.1
C;Keywords: cytokine; glycoprotein; heparin binding; heterodimer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-328/Product: interleukin 12B #status predicted <MAT>
F;27-30/Region: heparin binding #status predicted
F;125/Binding site: carbohydrate (Asn) (covalent) #status absent
F;135,303/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;222/Binding site: carbohydrate (Asn) (covalent) #status experimental

```
F;319/Modified site: 2'-mannosyl-tryptophan (Trp) (partial) #status experimental

  Query Match            85.1%;  Score 1501.5;  DB 2;  Length 328;
  Best Local Similarity  85.3%;  Pred. No. 1.3e-113;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| |||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |:::| :|:||||| ||||:|||||||||:|||:|||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:|||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 2
I72789
interleukin 12 p40 subunit - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I72789
R;Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K.;
J. Immunol. 148, 3433-3440, 1992
A;Title: Cloning and Expression of Murine IL-12.
A;Reference number: I56135; MUID:92268481; PMID:1350290
A;Accession: I72789
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-335 <RES>
A;Cross-references: GB:M86671; NID:g293663; PIDN:AAA39296.1; PID:g293664

  Query Match            64.7%;  Score 1141.5;  DB 2;  Length 335;
  Best Local Similarity  65.5%;  Pred. No. 1.5e-84;
  Matches  220;  Conservative   38;  Mismatches   65;  Indels   13;  Gaps    4;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              | ||:| |||::||| |||||:|||||||||||:|| |||||| | ||| |||||||||
Db          1 MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |   |:||||||||| |||| ||||||||||: || | ||:||||:|||||:||
Db         61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              |  ||| |||||| |||||||| ||   : ||||::|||    | : ||||  :|||||:|
Db        118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKV 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              :| |||:||:| |||   ||:|||:|||: ::|  : |||||::|||||||||||||
Db        178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
              |||:|||||: |||||||||:|||||||||| | :: | |  : |        |    |
Db        238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLV 296

Qy        293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
              :||| :| | |   : |||:||||:|| | || | |
Db        297 EKTSTEVQC-KGGNVCVQAQDRYYNSSCSKWACVPC 331


RESULT 3
A41242
interleukin-6 receptor precursor - human
N;Contains: interleukin-6 receptor, soluble form
C;Species: Homo sapiens (man)
C;Date: 27-Mar-1992 #sequence_revision 02-Dec-1994 #text_change 21-Jul-2000
C;Accession: A41242; JU0080; S17468; A61459; S14621
R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi,
Science 241, 825-828, 1988
A;Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor
A;Reference number: A41242; MUID:88305347; PMID:3136546
A;Accession: A41242
A;Molecule type: mRNA
A;Residues: 1-468 <YAM>
A;Cross-references: GB:M20566; NID:g33845; PIDN:CAA31312.1; PID:g33846
R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi,
Proc. Jpn. Acad. 64, 209-211, 1988
A;Title: Molecular structure of interleukin 6 receptor.
A;Reference number: JU0080
A;Accession: JU0080
A;Molecule type: mRNA
A;Residues: 1-468 <YA2>
R;Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinr
Biochem. J. 277, 659-664, 1991
A;Title: Structural and functional studies on the human hepatic interleukin-6 recepto
A;Reference number: S17468; MUID:91336983; PMID:1872801
A;Accession: S17468
A;Molecule type: mRNA
A;Residues: 1-468 <SCH>
A;Cross-references: EMBL:X58298; NID:g32580; PIDN:CAA41231.1; PID:g32581
A;Experimental source: hepatoma cell line HepG2
R;Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.
J. Exp. Med. 170, 1409-1414, 1989
A;Title: Soluble cytokine receptors are present in normal human urine.
A;Reference number: A61459; MUID:90010793; PMID:2529343
A;Accession: A61459
A;Molecule type: protein
A;Residues: 20-49 <NOV>
C;Comment: Through this receptor, interleukin-6 induces proliferation, activation, an
C;Comment: This growth factor receptor does not have a tyrosine kinase domain.
C;Genetics:
A;Gene: GDB:IL6R
A;Cross-references: GDB:127966; OMIM:147880
A;Map position: 1q21-1q21
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-468/Product: interleukin-6 receptor #status predicted <MAT>
F;20-363/Domain: extracellular #status predicted <EXT>
F;40-98/Domain: immunoglobulin homology <IMM2>
F;121-309/Domain: cytokine receptor homology <CRS>
F;364-386/Domain: transmembrane #status predicted <TMM>
F;387-468/Domain: intracellular #status predicted <INT>
F;47-96/Disulfide bonds: #status predicted
F;55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            10.9%;  Score 193;  DB 1;  Length 468;
  Best Local Similarity  22.2%;  Pred. No. 8.2e-08;
  Matches   69;  Conservative   59;  Mismatches  113;  Indels   70;  Gaps   13;

Qy         42 PGEMVVLTCHTPEEDD---ITW------TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK 92
              ||: | |||   | :|   : |       :  |   | |: | ::  :  |:| |:|::
Db         39 PGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYR 98

Qy         93 GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW-------L 145
                |:      ||:          |: |: :      | |  |:      | |       |
Db         99 AGRPAGTVHLLV----------DVPPEEPQ------LSCFRKSPLSNVVCEWGPRSTPSL 142

Qy        146 T--AISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS---AC 200
              |  |:    ||    :  | :|    |                    :|: | |: |   |
```

```
Db        143 TTKAVLLVRKFQNSPAEDFQEP----C------------------QYSQESQKFSCQLAV 180

Qy        201 PSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEY 259
              |  : |  |  :  |        : | :|    |::|||| |: :  : :| | : |:|: 
Db        181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPPANITVTAVARNPRWLSVTWQD 240

Qy        260 PDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDA------KIRVQARD 313
              | :|::  |:: | | :: : : ::     :  |     |:  ||       :::|::  
Db        241 PHSWNS--SFYRLRFELRYRAERSKTFTTWMVKDLQHHCVI--HDAWSGLRHVVQLRAQE 296

Qy        314 RYYSSSWSDWA 324
               :    ||:|:
Db        297 EFGQGEWSEWS 307


RESULT 4
S60614
growth promoting activity receptor alpha precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C;Accession: S60614
R;Heller, S.; Finn, T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pueschel, A.W.; Rohrer, H.
Development 121, 2681-2693, 1995
A;Title: Analysis of function and expression of the chick GPA receptor (GPARalpha) sugge
A;Reference number: S60614; MUID:95401882; PMID:7671828
A;Accession: S60614
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-362 <HEL>
A;Cross-references: EMBL:Z48168; NID:g971417; PIDN:CAA88184.1; PID:g3063774
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C;Keywords: growth factor receptor
F;2-89/Domain: immunoglobulin homology <IMM>
F;114-294/Domain: cytokine receptor homology <CRS>

  Query Match             10.1%;  Score 178;  DB 2;  Length 362;
  Best Local Similarity   23.9%;  Pred. No. 9.6e-07;
  Matches   73;  Conservative   48;  Mismatches  112;  Indels   72;  Gaps   14;

Qy         43 GEMVVLTCHTPEED-DITWTSAQSSEVLGS---GKTLTIQVKEFGDAGQYTCHKGGKVLS 98
              |  | : | : : |  :||| |  :::  |   |  | ::  :   :|||:|::|
Db         37 GADVTMKCGSMDWDAAVTWT-ANGTDIDDSHLNGSYLILKNVDLTQSGQYSCYEGSS--- 92

Qy         99 RSLLLIHKKEDGIWSTDILKEQKESK-----NKIFLKCEAKNYSGRFTCWWLTAISTDLK 153
                          |    || |   :      : | | : |:   | | |     | :
Db         93 ------------WH---LKYQTYLRVGVPPKEPVLMCRSNNYPKGFYCSWHLPSPTYIP 136

Qy        154 FSVKSSRGFSDPQGVTCGAVTLSAER-VRVDNRDYKKYTVECQEGSACPSAEESLPIEVV 212
               |   |       |  |   :  |: :   || : :|                ::  :|
Db        137 NSFNIS--------VIHGTREMVCEKDIFPKNRCHIRYL----------QLFSTVKYKVT 178

Qy        213 VDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNS-RHVEVSWEYPDTWSTPHSYFS 271
              :   : |   : | :|    |:|||||  ::  ||: |: | :||||: | :|  | | |
Db        179 LTVTNALGKNSTTLTFDEFAIVKPDPPESVVAKPVPNNPRRLEVSWQNPSSWPDPES-FP 237

Qy        272 LTFCIQAQGKNNREKKDRLCVDK-----------TSAKVVCHKDAKIRVQARDRYYSSS 319
              | | :: :          | :|:            |       |:  |:| |:|     :
Db        238 LKFFLRYR---------PLILDQWQHVELSDGTSHTITDAYAGKEYIIQVAAKDNDI-GT 287

Qy        320 WSDWA 324
              ||||:
Db        288 WSDWS 292


RESULT 5
I58141
ciliary neurotrophic factor receptor alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C;Accession: I58141; A47387
R;Ip, N.Y.; McClain, J.; Barrezueta, N.X.; Aldrich, T.H.; Pan, L.; Li, Y.; Wiegand, S.J.
Neuron 10, 89-102, 1993
A;Title: The alpha component of the CNTF receptor is required for signaling and defines
A;Reference number: I58141; MUID:93152175; PMID:8381290
A;Accession: I58141
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-372 <IPN>
A;Cross-references: GB:S54212; NID:g265055; PIDN:AAB25290.1; PID:g265056
R;Clatterbuck, R.E.; Price, D.L.; Koliatsos, V.E.
Proc. Natl. Acad. Sci. U.S.A. 90, 2222-2226, 1993
A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult
A;Reference number: A47387; MUID:93211934; PMID:8460125
A;Accession: A47387
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 185-260,'D',262-277 <CLA>
A;Cross-references: GB:S57711; NID:g299331; PIDN:AAB25918.1; PID:g299332
A;Experimental source: Sprague-Dawley, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:128471, NCBIP:128472)
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: growth factor receptor
F;39-91/Domain: immunoglobulin homology <IMM>
F;116-296/Domain: cytokine receptor homology <CRS>

  Query Match             10.1%;  Score 177.5;  DB 2;  Length 372;
  Best Local Similarity   22.4%;  Pred. No. 1.1e-06;
  Matches   77;  Conservative   51;  Mismatches  136;  Indels   79;  Gaps   15;

Qy          8 ISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAP-------GEMVVLTCHTPEED-DIT 59
              : |    :||:   |::  :            :||       |  | | | |   |  :|
Db          5 VPWACCAVLAAAAAAVYTQKHS--------PQEAPHVQYERLGTDVTLPCGTASWDAAVT 56

Qy         60 W--TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDIL 117
              |       :  | :|  | ::  | | :| | |         |  :|:|    |:
Db         57 WRVNGTDLAPDLLNGSQLILRSLELGHSGLYACFHRDSWHLRHQVLLHV---GL------ 107

Qy        118 KEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL--KFSVKSSRGFSDPQGVTCGAVTL 175
                    :  | | :  |   | | |  :  | :   |:|          |  |:  :
Db        108 -----PPREPVLSCRSNTYPKGFYCSWHLSAPTYIPNTFNVT----------VLHGSKMM 152

Qy        176 SAER-VRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDII 234
                |:   : || : :|                ::  :| :   : | :     :|    |:
Db        153 VCEKDPALKNRCHIRYM----------HLFSTIKYKVSISVSNALGHNTTAITFDEFTIV 202

Qy        235 KPDPPTNLQLKPL-KNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVD 293
              |||| |:  :|:  | | :||:|: | ||  | | | | | :: :          | :|
Db        203 KPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPES-FPLKFFLRYR---------PLILD 252

Qy        294 K------------TSAKVVCHKDAKIRVQARDRYYSSSWSDWA 324
              :            |       |:  |:| |:|     :||||:
Db        253 QWQHVELSNGTAHTITDAYAGKEYIIQVAAKDNEI-GTWSDWS 294


RESULT 6
JL0144
interleukin-6 receptor precursor (clone lambda P1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C;Accession: JL0144
R;Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto,
J. Exp. Med. 171, 2001-2009, 1990
A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle
A;Reference number: JL0144; MUID:90278354; PMID:2112585
A;Accession: JL0144
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-440 <SUG>
A;Cross-references: GB:X51976; NID:g53548; PIDN:CAA36238.1; PID:g53549
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-440/Product: interleukin-6 receptor #status predicted <MAT>
F;40-94/Domain: immunoglobulin homology <IMM>
F;117-306/Domain: cytokine receptor homology <CRS>
F;358-385/Domain: transmembrane #status predicted <TRA>
```

```
  Query Match             10.1%;  Score 177.5;  DB 2;  Length 440;
  Best Local Similarity   22.0%;  Pred. No. 1.3e-06;
  Matches   74;  Conservative   58;  Mismatches  139;  Indels   65;  Gaps   14;

Qy         13 LVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPE-EDDIT----WTSAQSSE 67
              : |||:| :|:         |         ||  | | |   |   ::|    :: :|: |
Db         10 VALLAAPAVALVLGSCRALEVANGTVTSLPGATVTLICPGKEAAGNVTIHWVYSGSQNRE 69

Qy         68 VLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKI 127
                :| || ::  :  | | | |     ::    ||:          |:  |: :
Db         70 WTTTGNTLVLRDVQLSDTGDYLCSLNDHLVGTVPLLV----------DVPPEEPK----- 114

Qy        128 FLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDY 187
               | |  ||       | |               |  | | |   |     | |:::   |
Db        115 -LSCFRKNPLVNAICEW--------------RPSSTPSPTT--KAVLFAKKINTTN-GK 155

Qy        188 KKYTVECQEGSACPSAEESLPIEVVV-DAIHKL----------KYENYTSSFFIRDIIKP 236
               : | ||       |   |  :|::  | :: :             ::  :|    :::|
Db        156 SDFQVPCQYSQQLKSF--SCQVEILEGDKVYHIVSLCVANSVGSKSSHNEAFHSLKMVQP 213

Qy        237 DPPTNLQLKPLK-NSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRL----- 290
              ||| || :  :    | ::|||::|:||    ||: | | :: :   ::|    |
Db        214 DPPANLVVSAIPGRPRWLKVSWQHPETWDP--SYYLLQFQLRYRPVWSKEFTVLLLPVAQ 271

Qy        291 --CVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWA 324
                ||   : : | |    ::|: ::      ||:|:
Db        272 YQCVIHDALRGVKH---VVQVRGKEELDLGQWSEWS 304


RESULT 7
JL0145
interleukin-6 receptor precursor (clone lambda 301) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C;Accession: JL0145; S14543
R;Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle gen
A;Reference number: JL0144; MUID:90278354; PMID:2112585
A;Accession: JL0145
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-460 <SUG>
A;Cross-references: GB:X51975; NID:g49725; PIDN:CAA36237.1; PID:g49726
A;Experimental source: clone lambda 301
R;Fiorillo, M.T.; Ciliberto, G.; Dente, L.
submitted to the EMBL Data Library, July 1990
A;Description: Cloning and expression of murine IL-6 receptor.
A;Reference number: S14543
A;Accession: S14543
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373,'R',375-460 <FIO>
A;Cross-references: EMBL:X53802; NID:g52692; PIDN:CAA37810.1; PID:g52693
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C;Keywords: cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-460/Product: interleukin-6 receptor #status predicted <MAT>
F;40-94/Domain: immunoglobulin homology <IMM>
F;117-306/Domain: cytokine receptor homology <CRS>
F;358-385/Domain: transmembrane #status predicted <TRA>

  Query Match             10.1%;  Score 177.5;  DB 2;  Length 460;
  Best Local Similarity   22.0%;  Pred. No. 1.4e-06;
  Matches   74;  Conservative   58;  Mismatches  139;  Indels   65;  Gaps   14;

Qy         13 LVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPE-EDDIT----WTSAQSSE 67
              : |||:| :|:         |         ||  | | |   |   ::|    :: :|: |
Db         10 VALLAAPAVALVLGSCRALEVANGTVTSLPGATVTLICPGKEAAGNVTIHWVYSGSQNRE 69

Qy         68 VLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKI 127
                :| || ::  :  | | | |     ::    ||:          |:  |: :
Db         70 WTTTGNTLVLRDVQLSDTGDYLCSLNDHLVGTVPLLV----------DVPPEEPK----- 114

Qy        128 FLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDY 187
               | |  ||       | |               |  | | |   |     | |:::   |
Db        115 -LSCFRKNPLVNAICEW--------------RPSSTPSPTT--KAVLFAKKINTTN-GK 155

Qy        188 KKYTVECQEGSACPSAEESLPIEVVV-DAIHKL----------KYENYTSSFFIRDIIKP 236
               : | ||       |   |  :|::  | :: :             ::  :|    :::|
Db        156 SDFQVPCQYSQQLKSF--SCQVEILEGDKVYHIVSLCVANSVGSKSSHNEAFHSLKMVQP 213

Qy        237 DPPTNLQLKPLK-NSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRL----- 290
              ||| || :  :    | ::|||::|:||    ||: | | :: :   ::|    |
Db        214 DPPANLVVSAIPGRPRWLKVSWQHPETWDP--SYYLLQFQLRYRPVWSKEFTVLLLPVAQ 271

Qy        291 --CVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWA 324
                ||   : : | |    ::|: ::      ||:|:
Db        272 YQCVIHDALRGVKH---VVQVRGKEELDLGQWSEWS 304


RESULT 8
UHHUCN
ciliary neurotrophic factor receptor alpha precursor - human
N;Alternate names: CNTF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: A40854; A56526
R;Davis, S.; Aldrich, T.H.; Valenzuela, D.M.; Wong, V.; Furth, M.E.; Squinto, S.P.; Y
Science 253, 59-63, 1991
A;Title: The receptor for ciliary neurotrophic factor.
A;Reference number: A40854; MUID:91289158; PMID:1648265
A;Accession: A40854
A;Molecule type: mRNA
A;Residues: 1-372 <DAV>
A;Cross-references: GB:M73238
R;Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Brannan, C.I.; McClai
Genomics 25, 157-163, 1995
A;Title: Genomic organization and chromosomal localization of the human and mouse gen
A;Reference number: A56526; MUID:95293367; PMID:7774913
A;Accession: A56526
A;Molecule type: DNA
A;Residues: 1-346,'S',348-372 <VAL>
A;Cross-references: GB:L38025; NID:g608654; PIDN:AAA91337.1; PID:g608656
C;Comment: The CNTF receptor is attached to the membrane by a glycosylphosphatidylino
C;Comment: The CNTF receptor sequence appears to contain several PEST regions.
C;Genetics:
A;Gene: GDB:CNTFR
A;Cross-references: GDB:134652; OMIM:118946
A;Map position: 9p13-9p13
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: glycoprotein; growth factor receptor; membrane protein; phosphatidylinosi
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-372/Product: ciliary neurotrophic factor receptor #status predicted <MAT>
F;39-91/Domain: immunoglobulin homology <IMM>
F;116-296/Domain: cytokine receptor homology <CRS>
F;46-89/Disulfide bonds: #status predicted
F;60,70,142,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             9.6%;  Score 170;  DB 1;  Length 372;
  Best Local Similarity   23.0%;  Pred. No. 4.4e-06;
  Matches   69;  Conservative   42;  Mismatches  127;  Indels   62;  Gaps   12;

Qy         43 GEMVVLTCHTPEED-DITW--TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSR 99
              |  | | | |   |  :||       :  | :|  | :   | | :| | |       |
Db         39 GSDVTLPCGTANWDAAVTWRVNGTDLAPDLLNGSQLVLHGLELGHSGLYACFHRDSWHLR 98

Qy        100 SLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL--KFSVK 157
                :|:|    |:             :  | | :  |   | | |     | :   |:|
Db         99 HQVLLHV---GL----------PPREPVLSCRSNTYPKGFYCSWHLPTPTYIPNTFNVT 144

Qy        158 SSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIH 217
                |          : :  :   : || : :|                    ::  :| :   :
Db        145 VLHG---------SKIMVCEKDPALKNRCHIRYM----------HLFSTIKYKVSISVSN 185
```

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Qy        218 KLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEYPDTWSTPHSYFSLTFCI 276
Db        186 ALGHNATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPES-FPLKFFL 244

Qy        277 QAQGKNNREKKDRLCVDK------------TSAKVVCHKDAKIRVQARDRYYSSSWSDWA 324
Db        245 RYR---------PLILDQWQHVELSDGTAHTITDAYAGKEYIIQVAAKDNEI-GTWSDWS 294


RESULT 9
I37891
interleukin-11 receptor alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Dec-1999
C;Accession: I37891; G01970; G01971
R;Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minvielle,
Blood 86, 2534-2540, 1995
A;Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic cyt
A;Reference number: I37891; MUID:95399754; PMID:7670098
A;Accession: I37891
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-422 <RES>
A;Cross-references: EMBL:Z38102; NID:g995653; PIDN:CAA86224.1; PID:g995654
R;Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A;Reference number: G08959
A;Accession: G01970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-422 <VAN>
A;Cross-references: EMBL:U32323; NID:g975334; PIDN:AAB36491.1; PID:g975335
R;Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A;Reference number: G08961
A;Accession: G01971
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-422 <VA2>
A;Cross-references: EMBL:U32324; NID:g975336; PIDN:AAB36492.1; PID:g975337
C;Genetics:
A;Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 390/2; 418/1
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
F;120-310/Domain: cytokine receptor homology <CRS>

  Query Match             8.5%;  Score 149.5;  DB 2;  Length 422;
  Best Local Similarity   20.3%;  Pred. No. 0.00023;
  Matches   64;  Conservative   44;  Mismatches  143;  Indels   65;  Gaps   12;

Qy         37 WHPDA-----PGEMVVLTC-HTPEEDDITWTSAQSSEVL-----GSGKTLTIQVKEFGDA 85
Db         30 WGPPGVQYGQPGRSVKLCCPGVTAGDPVSWFRDGEPKLLQGPDSGLGHELVLAQADSTDE 89

Qy         86 GQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW- 144
Db         90 GTYIC---------------QTLDGALGGTVTLQLGYPPARPVVSCQAADYE-NFSCTWS 133

Qy        145 -----------LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDY-KKYTV 192
Db        134 PSQISGLPTRYLTSYRKKTVLGADSQRRSPSTGPWPCPQDPLGAARCVVHGAEFWSQYRI 193

Qy        193 ECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKN-SR 251
Db        194 NVTEVNPLGASTRLLDVS------------------LQSILRPDPPQGLRVESVPGYPR 234

Qy        252 HVEVSWEYPDTW-STPHSYFSLTFCIQAQGKNNR--EKKDRLCVDKTSAKVVCHKDAKIR 308
Db        235 RLRASWTYPASWPCQPH--FLLKFRLQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVR 292

Qy        309 VQARDRYYSSSWSDWA 324
Db        293 VSARDFLDAGTWSTWS 308


RESULT 10
I48343
interleukin-11 receptor alpha-chain precursor - mouse
N;Alternate names: cytokine type 1 receptor
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Jan-2000
C;Accession: I48343; S51619
R;Neuhaus, H.; Bettenhausen, B.; Bilinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gos
Dev. Biol. 166, 521-542, 1994
A;Title: et12, a novel putative type-1 cytokine receptor expressed during mouse embry
A;Reference number: I48343
A;Accession: I48343
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-432 <RES>
A;Cross-references: EMBL:X74953; NID:g673437; PIDN:CAA52908.1; PID:g673438
R;Hilton, D.J.; Hilton, A.A.; Raicevic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M
EMBO J. 13, 4765-4775, 1994
A;Title: Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for hi
A;Reference number: S51619; MUID:95045367; PMID:7957045
A;Accession: S51619
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-432 <HIL>
A;Cross-references: EMBL:U14412; NID:g576454; PIDN:AAA53248.1; PID:g576455
C;Genetics:
A;Gene: Et12/IL11
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: cytokine receptor
F;120-310/Domain: cytokine receptor homology <CRS>

  Query Match             8.3%;  Score 146.5;  DB 2;  Length 432;
  Best Local Similarity   20.9%;  Pred. No. 0.00042;
  Matches   68;  Conservative   44;  Mismatches  130;  Indels   83;  Gaps   14;

Qy         37 WHPDA-----PGEMVVLTC-----HTPEEDDITWTSAQSSEVL-----GSGKTLTIQVKE 81
Db         30 WGPPGVQYGQPGRPVMLCCPGVSAGTP----VSWFRDGDSRLLQGPDSGLGHRLVLAQVD 85

Qy         82 FGDAGQYTCH-----KGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNY 136
Db         86 SPDEGTYVCQTLDGVSGGMVTLKLGFPPARPE-------------------VSCQAVDY 125

Qy        137 SGRFTCWW------------LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDN 184
Db        126 E-NFSCTWSPGQVSGLPTRYLTSYRKKTLPGAESQRESPSTGPWPCPQDPLEASRCVVHG 184

Qy        185 RDY-KKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
Db        185 AEFWSEYRINVTEVNPLGASTCLLDVR------------------LQSILRPDPPQGLR 225

Qy        244 LKPLKN-SRHVEVSWEYPDTW-STPHSYFSLTFCIQAQGKNNR--EKKDRLCVDKTSAKV 299
Db        226 VESVPGYPRRLHASWTYPASWRRQPH--FLLKFRLQYRPAQHPAWSTVEPIGLEEVITDA 283

Qy        300 VCHKDAKIRVQARDRYYSSSWSDWA 324
Db        284 VAGLPHAVRVSARDFLDAGTWSAWS 308


RESULT 11
H96544
hypothetical protein F8A12.4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96544
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
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Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-812 <STO>
A;Cross-references: GB:AE005173; NID:g11094686; PIDN:AAG29622.1; GSPDB:GN00141
C;Genetics:
A;Gene: F8A12.4
A;Map position: 1

  Query Match             7.5%;  Score 132;  DB 2;  Length 812;
  Best Local Similarity   25.0%;  Pred. No. 0.014;
  Matches   71;  Conservative   33;  Mismatches  112;  Indels   68;  Gaps   15;

Qy         48 LTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKK 107
              ::| ||   | :|       |:|| |||   :   ||   :    | |:  ||
Db        426 ISCDTPMFCD-SW----RKRVVGSAKTLRTSI---GDDTSFV-PSGSKMNRRS------- 469

Qy        108 EDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL--------------- 152
              |||      : |    |   |:|   ||     |      || |
Db        470 EDG----RKIAEDSTKKRLKFMKSARKNDGS--TMGQKQVISDDADDDDSLTVAQITTLY 523

Qy        153 --KFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP-SAEESLPI 209
                |:|  |    |:| |           |:  ||   :     ||: |:     :|::|
Db        524 KKKYSENSGGNASEPLG--------KKIRLEADNNGLE----PCQKLSSIRYDGDETVPP 571

Qy        210 EVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSY 269
                :    | : |   |   :| :: |   :|    |:   | :::    |:|
Db        572 PEI-----KKRNEETGSKSGMRVVLSPFDESNSSKPPVDFGRAIDIVVSAPET------- 619

Qy        270 FSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKI-RVQAR 312
              :|||    | || |||  :  |    | : |:|  | |  ||
Db        620 --MTFCDDVYG-NNAEKKTMIDDDSEELKCLLHEDGTITREMAR 660


RESULT 12
T30532
neural cell adhesion molecule L1 homolog - Fugu rubripes
C;Species: Fugu rubripes
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Mar-2002
C;Accession: T30532
R;Riboldi Tunnicliffe, G.R.; Platzer, M.; Nyakatura, G.; Elgar, G.S.; Brenner, S.; Rosen
submitted to the EMBL Data Library, September 1997
A;Description: Analysis of the genomic loci of Fugu rubripes homologs of the human disea
A;Reference number: Z20848
A;Accession: T30532
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1277 <RIB>
A;Cross-references: EMBL:AF026198; NID:g3098263; PID:g3098264; PIDN:AAC15580.1
C;Genetics:
A;Introns: 42/1; 47/1; 81/2; 149/1; 190/1; 247/1; 285/2; 347/1; 391/1; 440/1; 477/2; 531
/2
A;Note: L1-CAM
C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; i

  Query Match             6.9%;  Score 122.5;  DB 2;  Length 1277;
  Best Local Similarity   22.9%;  Pred. No. 0.14;
  Matches   77;  Conservative   44;  Mismatches  122;  Indels   93;  Gaps   15;

Qy         41 APGEMVVLTCHTP--EEDDITWT------SAQSSE---VLGSGKTLTIQVKEFGDAGQYT 89
              |||| | | |        ||||      || | |    |   :| ::   |||   |
Db        361 APGETVKLDCQADGIPSPTITWTVNGVPLSATSLEPRRSLTESGSLILKDVIFGDTAIYQ 420

Qy         90 C---HKGGKVLSRSLLLIHK------KEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRF 140
              |   :| | :|: : : : :       |:|   | :         |  |:||
Db        421 CQASNKHGTILANTNVYVIELPPQILTENGNTYTFV------EGQKALLECETFGSPKPK 474

Qy        141 TCWWLTAIS---TDLKFSVKSSRGFS------DPQGV-TC----GAVTLSAERVRVDNRD 186
                ::  |||:|:|
Db        415 HH-GSWSEWSS 424
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              |  ::||    | : :: :: |        | :|: ||      ::::|| | | ||
Db        475 VTWESSSISLLLADPRVNLLTNGGLEIANVSHDDEGIYTCLVQGSNISVNAE-VEVLNRT 533

Qy        187 Y-------------------------------------------------KKYTVECQEGS 198
                                                              |||| :   |
Db        534 VILSPPQALRLQPGKTAIFTCLYVTDPKLSSPLLQWRKNDQKIFESHSDKKYTFD-GPGL 592

Qy        199 ACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWE 258
                 : |           | ||     :|:  : |  :|||| :||:   |: | | ::|
Db        593 IISNVEPGDEGVYTCQIITKLDMVEASSTLTLCD--RPDPPVHLQVTNAKH-RVVTLNWT 649

Qy        259 YPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDK 294
              |  ::|   : : |  |   :|  |:  |:  ||
Db        650 PGDDNNSPILEYVVEFEDQDMKENGWEELKRVAADK 685


RESULT 13
JQ1655
prolactin receptor precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C;Accession: JQ1655
R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA
A;Reference number: JQ1655; MUID:93075121; PMID:1445292
A;Accession: JQ1655
A;Molecule type: mRNA
A;Residues: 1-831 <TAN>
A;Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A;Experimental source: kidney
C;Superfamily: cytokine receptor homology
C;Keywords: glycoprotein; transmembrane protein
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
F;36-219/Domain: cytokine receptor homology <CRS1>
F;239-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TMM>
F;59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (cov

  Query Match             6.8%;  Score 120;  DB 2;  Length 831;
  Best Local Similarity   18.1%;  Pred. No. 0.13;
  Matches   67;  Conservative   57;  Mismatches  137;  Indels  110;  Gaps   16;

Qy          3 PQQLVISWFSLVLLASPLMAIWELEKDVYVVEL--DWHP----DAPGEMVVLTCH----- 51
              || : ::  |:|   ||:    | ::   :: |   | |    ||    :    |
Db        116 PQYVDVT--SIVQPGSPVNLTLETKRSANIMYLWAKWSPPLLADASSNHLY---HYELRI 170

Qy         52 TPEEDDITWTSAQSSEV------LGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIH 105
              ||| :   | :   :       | :|    :||:   | |:::
Db        171 KPEEKEEWETISVGVQTQCKINRLNAGMRYVVQVRCTLDPGEWS---------------- 214

Qy        106 KKEDGIWSTD----ILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRG 161
                  ||::    |   |   :    :|| :      |||||
Db        215 -----EWSSERHILIPSGQSPPEKPTIIKCRSPE-KETFTCWW---------------- 251

Qy        162 FSDPQGVTCGAVTLSAERVRVDNRDYKKYT-VECQEGS----ACPSAEESLPIEVVVDAI 216
                            :  :|      || :  :||      ||    : |     |
Db        252 ----------------KPGLDGGHPTNYTLLYSKEGEEQVYECPDYRTAGPNSCYFDKK 294

Qy        217 HKLKYENYTSS---------------FFIRDIIKPDPPTNLQL---KPLKNSRHVEVSW 257
              |   :  |  :                 :  |::|||| |: |   ||:    :: ::|
Db        295 HTSFWTIYNITVRATNEMGSNSSDPHYVDVTYIVQPDPPVNVTLELKKPINRKPYLVLTW 354

Qy        258 EYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAK---IRVQARDR 314
                |      : :| : :: : :   | :       :|  |:      |   |::  :
Db        355 SPPPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQQTQYKMFSLNPGKKYIIQIHCKPD 414

Qy        315 YYSSSWSDWAS 325
              ::  |||:|:|
Db        415 HH-GSWSEWSS 424
```

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RESULT 14
I45877
protein-tyrosine kinase (EC 2.7.1.112), receptor type kit precursor - aurochs
C;Species: Bos primigenius (aurochs)
C;Date: 19-Dec-1997 #sequence_revision 19-Dec-1997 #text_change 20-Apr-2000
C;Accession: I45877
R;Kubota, T.; Hikono, H.; Sasaki, E.; Sakurai, M.
Gene 141, 305-306, 1994
A;Title: Sequence of a bovine c-kit proto-oncogene cDNA.
A;Reference number: I45877; MUID:94215924; PMID:7512939
A;Accession: I45877
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-977 <KUB>
A;Cross-references: GB:D16680; NID:g516659; PIDN:BAA04084.1; PID:g516660
C;Superfamily: macrophage colony-stimulating factor 1 receptor; immunoglobulin homology;
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;329-395/Domain: immunoglobulin homology <IMM>
F;588-932/Domain: protein kinase homology <KIN>

  Query Match             6.7%;  Score 118;  DB 2;  Length 977;
  Best Local Similarity   26.5%;  Pred. No. 0.23;
  Matches   78;  Conservative   39;  Mismatches   91;  Indels   86;  Gaps   23;

Qy          9 SW-FSLVLLASPLMAIWELEKDVYVVELDW---HPDAPGEMVV-------LTCHTPEEDD 57
              :| |  |||    |:      :  |   ||     || |  |::|       | |  |
Db          7 AWDFLFVLLLLLLVQTGSSQPSVSPGELSLPSIHP-AKSELIVSVGDEIRLLCTDP--GF 63

Qy         58 ITWTSAQSSEVLG--SGKTLTIQVKEFGDA---GQYTC-HKGGKVLSRSLLLIHKKEDGI 111
              : ||     |:||  | ||    : |  :|   | |||:|||  || |: :  :  : :
Db         64 VKWT----FEILGQLSEKTNPEWITEKAEATNTGNYTCTNKGG--LSSSIYVFVRDPEKL 117

Qy        112 WSTDILKEQKESKNKIFLKC-----EAKNYSGRFTCWWLTA-----ISTDLKFSVKSSRG 161
              :  |:    || :|   ::|     |  |||       ||      :  || |
Db        118 FLIDLPLYGKE-ENDTLVRCPLTDPEVTNYS-------LTGCEGKPLPKDLTF------- 162

Qy        162 FSDPQ-GVTCGAVTLSAERVRVDNRDYKKYTVEC---QEGSACPSAEESLPIEVVVDA-- 215
               :||: |:|          :|   |:| :  : |    | | :  | : :| :   : |
Db        163 VADPKAGIT----------IRNVKREYHRLCLHCSANQRGKSMLSKKFTLKVRAAIKAVP 212

Qy        216 ---IHKLKY-----ENYTSSFFIRDI--------IKPD-PPTNLQLKPLKNSRH 252
                 : |  |     | :  :  |:|:        || :   |  | |  ||| |
Db        213 VVSVSKTSYLLREGEEFAVTCLIKDVSSSVDSMWIKENSQQTKAQTK--KNSWH 264


RESULT 15
A29884
prolactin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000
C;Accession: A29884
R;Boutin, J.M.; Jolicoeur, C.; Okamura, H.; Gagnon, J.; Edery, M.; Shirota, M.; Banville
Cell 53, 69-77, 1988
A;Title: Cloning and expression of the rat prolactin receptor, a member of the growth ho
A;Reference number: A29884; MUID:88165059; PMID:2832068
A;Accession: A29884
A;Molecule type: mRNA
A;Residues: 1-310 <BOU>
A;Cross-references: GB:M19304; NID:g206364; PIDN:AAA41937.1; PID:g206365
C;Superfamily: cytokine receptor homology
C;Keywords: transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-310/Product: prolactin receptor #status predicted <MAT>
F;31-216/Domain: cytokine receptor homology <CRS>

  Query Match             6.3%;  Score 111.5;  DB 2;  Length 310;
  Best Local Similarity   21.9%;  Pred. No. 0.18;
  Matches   51;  Conservative   42;  Mismatches   99;  Indels   41;  Gaps   10;

Qy        111 IWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTC 170
              :  :  :|| |          || : :    |||||     ||        |  :|
Db         11 VLNISLLKGQSPPGKPEIHKCRSPD-KETFTCWWNP--GTDGGLPTNYSLTYS------- 60

Qy        171 GAVTLSAERVRVDNRDYKKYTVECQE-----GSACPSAEESLPI-EVVVDAIHKLKYENY 224
                          :: :| | || :       ::|  :::   | :: :  ::
Db         61 -------------KEGEKTTYECPDYKTSGPNSCFFSKQYTSIWKIYIITVNATNQMGS 106

Qy        225 TSS----FFIRDIIKPDPPTN--LQLKPLKNSR-HVEVSWEYPDTWSTPHSYFSLTFCIQ 277
              :||      :  |::|:|| |  |::| ||: : :: | |  |         :|:: : |:
Db        107 SSSDPLYVDVTYIVEPEPPRNLTLEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIR 166

Qy        278 AQGKNNREKKDRLCVDKTSAKVV-CHKDAKIRVQAR---DRYYSSSWSDWASV 326
               : :   | :      :|  ||   :   |  || |   |  | | ||  :||
Db        167 LKPEEAEEWEIHFTGHQTQFKVFDLYPGQKYLVQTRCKPDHGYWSRWSQESSV 219


Search completed: July 15, 2003, 11:08:44
Job time : 15.4202 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:28 ; Search time 7.2101 Seconds
(without alignments)
1892.583 Million cell updates/sec

Title: US-09-917-265-59
Perfect score: 1764
Sequence: 1 MHPQQLVISWFSLVLLASPL.....QARDRYYSSSWSDWASVSCS 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1751	99.3	329	1	I12B_CANFA	Q28268 canis famil
2	1643	93.1	329	1	I12B_FELCA	O02744 felis silve
3	1551	87.9	329	1	I12B_HORSE	Q9xsq5 equus cabal
4	1527	86.6	327	1	I12B_CEREL	Q28234 cervus elap
5	1515	85.9	327	1	I12B_BOVIN	P46282 bos taurus
6	1511	85.7	327	1	I12B_SHEEP	O02815 ovis aries
7	1501.5	85.1	328	1	I12B_HUMAN	P29460 homo sapien
8	1493.5	84.7	328	1	I12B_MACMU	P48095 macaca mula
9	1477.5	83.8	324	1	I12B_PIG	Q28938 sus scrofa
10	1455.5	82.5	328	1	I12B_CERTO	P46658 cercocebus
11	1330	75.4	327	1	I12B_MARMO	Q61729 marmota mon
12	1141.5	64.7	335	1	I12B_MOUSE	P43432 mus musculu
13	193	10.9	468	1	IL6A_HUMAN	P08887 homo sapien
14	183	10.4	467	1	IL6A_PIG	O18796 sus scrofa
15	178	10.1	362	1	CNTR_CHICK	P51641 gallus gall
16	177.5	10.1	372	1	CNTR_RAT	Q08406 rattus norv
17	177.5	10.1	460	1	IL6A_MOUSE	P22272 mus musculu
18	170	9.6	372	1	CNTR_HUMAN	P26992 homo sapien
19	158.5	9.0	462	1	IL6A_RAT	P22273 rattus norv
20	120	6.8	831	1	PRLR_CHICK	Q04594 gallus gall
21	118	6.7	977	1	KIT_BOVIN	P43481 bos taurus
22	116.5	6.6	978	1	KIT_FELCA	Q28889 felis silve
23	115	6.5	978	1	KIT_CAPHI	Q28317 capra hircu
24	111.5	6.3	610	1	PRLR_RAT	P05710 rattus norv
25	111	6.3	638	1	GHR_RAT	P16310 rattus norv
26	110	6.2	611	1	GHR_COLLI	Q90375 columba liv
27	108	6.1	581	1	PRLR_BOVIN	Q28172 bos taurus
28	108	6.1	831	1	PRLR_MELGA	Q91094 meleagris g
29	107.5	6.1	638	1	GHR_PIG	P19756 sus scrofa
30	106	6.0	622	1	PRLR_HUMAN	P16471 homo sapien
31	105	6.0	581	1	PRLR_SHEEP	O46561 ovis aries
32	104.5	5.9	638	1	GHR_RABIT	P19941 oryctolagus
33	104.5	5.9	650	1	GHR_MOUSE	P16882 mus musculu
34	103	5.8	616	1	PRLR_RABIT	P14787 oryctolagus
35	103	5.8	635	1	TPOR_HUMAN	P40238 homo sapien
36	102	5.8	608	1	PRLR_MOUSE	Q08501 mus musculu
37	101	5.7	975	1	KIT_CANFA	O97799 canis famil
38	100	5.7	296	1	THT2_MYCLE	P46700 mycobacteri
39	98.5	5.6	468	1	IL9R_MOUSE	Q01114 mus musculu
40	98.5	5.6	608	1	GHR_CHICK	Q02092 gallus gall
41	98	5.6	581	1	PRLR_CEREL	Q28235 cervus elap
42	97.5	5.5	630	1	PRLR_ORENI	Q91513 oreochromis
43	97	5.5	975	1	KIT_MOUSE	P05532 mus musculu
44	96.5	5.5	739	1	VCA1_RAT	P29534 rattus norv
45	95.5	5.4	310	1	FCGB_HUMAN	P31994 homo sapien

ALIGNMENTS

RESULT 1
I12B_CANFA
ID I12B_CANFA STANDARD; PRT; 329 AA.
AC Q28268;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE maturation factor 40 kDa subunit) (CLMF p40).
GN IL12B.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98280561; PubMed=9617567;
RA Buettner M., Belke-Louis G.F., Rziha H.J., McInnes C., Kaaden O.R.;
RT "Detection, cDNA cloning and sequencing of canine interleukin 12.";
RL Cytokine 10:241-248(1998).
CC -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC BY RESTING PBMC (BY SIMILARITY).
CC -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC --
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CC --
DR EMBL; U49100; AAA92059.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 329 INTERLEUKIN-12 BETA CHAIN.
FT DOMAIN 43 97 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 236 321 FIBRONECTIN TYPE-III.
FT DISULFID 50 90 POTENTIAL.
FT DISULFID 200 200 INTERCHAIN (PROBABLE).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

```
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   329 AA;  37410 MW;  79F83ED02B5DA93C CRC64;

  Query Match             99.3%;  Score 1751;  DB 1;  Length 329;
  Best Local Similarity   99.1%;  Pred. No. 5.8e-136;
  Matches  326;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              |||||||||||||||||| || ||||||||||||||||||||||||||||||||||||||
Db          1 MHPQQLVISWFSLVLLASSLMTIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCVQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||||||||
Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 2
I12B_FELCA
ID   I12B_FELCA     STANDARD;      PRT;   329 AA.
AC   O02744; O46671;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=97246745; PubMed=9089110;
RA   Schijns V.E.C.J., Wierda C.M.H., Vahlenkamp T.W., Horzinek M.C.;
RT   "Molecular cloning of cat interleukin-12.";
RL   Immunogenetics 45:462-463(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98182592; PubMed=9522125;
RA   Fehr D., Dean G.A., Huder J., Fan Z., Huettner S., Higgins J.W.,
RA   Pedersen N.C., Lutz H.;
RT   "Nucleotide and predicted peptide sequence of feline interleukin-12
RT   (IL-12).";
RL   DNA Seq. 8:77-82(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y07762; CAA69068.1; -.
DR   EMBL; U83184; AAB93835.1; -.
DR   InterPro; IPR002996; CRIA.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    329       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    321       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    11     11       L -> F (IN REF. 2).
FT   CONFLICT    51     51       N -> D (IN REF. 2).
FT   CONFLICT   167    167       E -> G (IN REF. 2).
SQ   SEQUENCE   329 AA;  37374 MW;  12A069BC6322AE08 CRC64;

  Query Match             93.1%;  Score 1643;  DB 1;  Length 329;
  Best Local Similarity   93.0%;  Pred. No. 3.9e-127;
  Matches  306;  Conservative   10;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              ||||||||:| |||||| ||||||||||:||||||||||||||||||||:|||||||||
Db          1 MHPQQLVIAWLSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||||||||||| ||||||||||:||| | |||||||||||||||:||
Db         61 TSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              ||||||||||||||||||||||||||||||:|||||| |||| ||||| |||||:|
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              |||||||||||||||||||||||||||||| :| |||||||||||| |||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||:|||||||
Db        301 CHKDAKIRVQARDRYYSSSWSNWASVSCS 329


RESULT 3
I12B_HORSE
ID   I12B_HORSE     STANDARD;      PRT;   329 AA.
AC   Q9XSQ5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20009534; PubMed=10541814;
RA   Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA   Argyle D.J., Onions D.E.;
RT   "Cloning and sequencing of horse interleukin-12 and interleukin-18
RT   cDNAs.";
RL   Immunogenetics 50:94-97(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y11129; CAA72011.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    329       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   329 AA;  37442 MW;  7104BB0DFF8FA73C CRC64;

  Query Match             87.9%;  Score 1551;  DB 1;  Length 329;
  Best Local Similarity   87.7%;  Pred. No. 1.3e-119;
  Matches  286;  Conservative   21;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              | ||:|||||||||||||||||||||||||||||:|||||||||||||:||||: ||||||
Db          4 QWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGEMVVLTCNTPEEEGITWTSA 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||:|||||||||||||||| |||||||:||| | ||:|||||||||||||:||||
Db         64 QSNEVLGSGKTLTIQVKEFGDAGWYTCHKGGEVLSHSHLLLHKKEDGIWSTDILKDQKES 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| |||||||||||||||||||||||||||||||||| |||:|||||| |||||||  ||
Db        124 KNKTFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGSSDPRGVTCGAATLSAERVSVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              :|:|||||||||||||:|||||||:||||:|||||||||| |||||||||||| |||
Db        184 DREYKKYTVECQEGSACPAAEESLPIEIVVDAVHKLKYENYTSGFFIRDIIKPDPPKNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||:||||||||||||| || |||| :|:|||| :|:||| | |||
Db        244 LKPLKNSRQVEVSWEYPETWSTPHSYFSLTFSIQVQGKNKKERKDRLFMDETSATVTCHK 303

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
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              | :|||||||||||||||:|||||||
Db        304 DGQIRVQARDRYYSSSWSEWASVSCS 329


RESULT 4
I12B_CEREL
ID   I12B_CEREL     STANDARD;      PRT;   327 AA.
AC   Q28234;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99304506; PubMed=10376218;
RA   Lockhart E., Slobbe L., Buchan G.;
RT   "The characterisation of a cervine immunoregulatory cytokine,
RT   interleukin 12.";
RL   DNA Seq. 10:139-148(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U57752; AAB02258.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37145 MW;  53AF5BB288907F06 CRC64;

  Query Match             86.6%;  Score 1527;  DB 1;  Length 327;
  Best Local Similarity   85.4%;  Pred. No. 1.2e-117;
  Matches  281;  Conservative   24;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              |||||||:|||||||| ||::|||||||:|||||||:|||||| ||| | ||||| |||
Db          1 MHPQQLVVSWFSLVLLTSPIVAIWELEKNVYVVELDWYPDAPGETVVLRCDTPEEDGITW 60
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Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||||||||:|||||||||||||||||:||||||||:|||||||||||||||:|
Db         61 TSDQSSEVLGSGKTLTVQVKEFGDAGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              || | | ||||||:||| ||||||||||||||||||||| |||:|||||| :|| |:|
Db        121 KEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSRGSSDPRGVTCGAASLSTEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
               ||:|:|||||||||||||:|||||||||:|:|||||||||||||||||||||||||||
Db        181 IVDHREYKKYTVECQEGSACPAAEESLPIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||:|||||| |||||||||||||||||||||:| |||| |||| | :|:|||||
Db        241 NLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVT 298

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              ||||| |||||||||:| ||:|||||||
Db        299 CHKDASIRVQARDRYYNSFWSEWASVSCS 327


RESULT 5
I12B_BOVIN
ID   I12B_BOVIN     STANDARD;      PRT;   327 AA.
AC   P46282;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Holstein; TISSUE=Lymphoid;
RX   MEDLINE=95244628; PubMed=7727547;
RA   Zarlenga D.S., Canals A., Aschenbrenner R.A., Gasbarre L.C.;
RT   "Enzymatic amplification and molecular cloning of cDNA encoding the
RT   small and large subunits of bovine interleukin 12.";
RL   Biochim. Biophys. Acta 1270:215-217(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U11815; AAA85792.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37050 MW;  D484DA36EF6F3D9F CRC64;

  Query Match             85.9%;  Score 1515;  DB 1;  Length 327;
  Best Local Similarity   84.8%;  Pred. No. 1.1e-116;
  Matches  279;  Conservative   25;  Mismatches   23;  Indels    2;  Gaps    1;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              |||||||:|||||||||||::|:|||||:||||||||:|||||| ||||| ||||| |||
Db          1 MHPQQLVVSWFSLVLLASPIVAMWELEKNVYVVELDWYPDAPGETVVLTCDTPEEDGITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||||||||||||||||||||||||||: |||||||:|||||||||||||:|
Db         61 TSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLLLLHKKEDGIWSTDILKDQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              || | | ||||||:||| ||||||||||||||||||||| |||:|||||| ||||:|
Db        121 KEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSRGSSDPRGVTCGAALLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
               :::|:| |||||||||||||:||||| |||||:|:|||||||||||||||||||||||
Db        181 SLEHREYNKYTVECQEGSACPAAEESLLIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||:|||||| |||||||||||||||||||||:| |||| |||| | :|:|||||
Db        241 NLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVT 298

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              ||||| :|||||||||||| ||:|||||||
Db        299 CHKDANVRVQARDRYYSSFWSEWASVSCS 327


RESULT 6
I12B_SHEEP
ID   I12B_SHEEP     STANDARD;      PRT;   327 AA.
AC   O02815; O18989; Q9TT18;
DT   01-NOV-1997 (Rel. 35, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Ovis aries (Sheep), and
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940, 9925;
RN   [1]
RP   SEQUENCE FROM N.A., AND SUBUNIT.
RC   SPECIES=Sheep; TISSUE=Peripheral blood;
RX   MEDLINE=20480126; PubMed=11023671;
RA   Swinburne S.J., Russ G.R., Krishnan R.;
RT   "Ovine interleukin 12 has biological activity on ovine and human
RT   activated peripheral blood mononuclear cells.";
RL   Cytokine 12:1546-1552(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Sheep; STRAIN=Merino; TISSUE=Peripheral blood;
RX   MEDLINE=20344025; PubMed=10888112;
RA   De Rose R., Scheerlinck J.-P.Y., Casey G., Wood P.R., Tennent J.M.,
RA   Chaplin P.J.;
RT   "Ovine interleukin-12: analysis of biologic function and species
RT   comparison.";
RL   J. Interferon Cytokine Res. 20:557-564(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
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RC   SPECIES=C.hircus;
RA   Beyer J.C., Cheevers W.P., Kumpula-Mcwhirter N.M.;
RT   "Cloning of caprine IL-12 40 kDa subunit.";
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF004024; AAB61368.2; -.
DR   EMBL; AF209435; AAF20151.1; -.
DR   EMBL; AF007576; AAB62945.1; -.
DR   InterPro; IPR002996; CRlA.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      236    319       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    290    290       T -> A (IN REF. 2).
SQ   SEQUENCE   327 AA;  36936 MW;  DDCD983A10143A96 CRC64;

  Query Match             85.7%;  Score 1511;  DB 1;  Length 327;
  Best Local Similarity   85.1%;  Pred. No. 2.4e-116;
  Matches  280;  Conservative   25;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              |||||||:||||||||||::|||||||:|||||||:|:|||| ||||| |||| |||
Db          1 MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGETVVLTCDTPEEDGITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||||||||||||||||||||||||:||||||||:|||||||||||||||:|
Db         61 TSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              || | | |||||||:||| ||| ||||||||:|||||||||| |||:|||||| :||||:|
Db        121 KEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSRGSSDPRGVTCGAASLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
               :|:|:| ||||||||||||:||||||||||::|:|||||||||||||||||||||||
Db        181 SMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||:|||||| ||||||||||||||||||||:| |||| |||| |  |:|||||
Db        241 NLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKNKREKK--LFTDQTSAKVT 298

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              ||||| |||||||||||| ||:|||||||
Db        299 CHKDANIRVQARDRYYSSFWSEWASVSCS 327


RESULT 7
I12B_HUMAN
ID   I12B_HUMAN     STANDARD;      PRT;   328 AA.
AC   P29460;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40) (NK cell stimulatory
DE   factor chain 2) (NKSF2).
GN   IL12B OR NKSF2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91239523; PubMed=1674604;
RA   Gubler U., Chua A.O., Schoenhaut D.S., Dwyer C.M., McComas W.,
RA   Motyka R., Nabavi N., Wolitzky A.G., Quinn P.M., Familletti P.C.,
RA   Gately M.K.;
RT   "Coexpression of two distinct genes is required to generate secreted
RT   bioactive cytotoxic lymphocyte maturation factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:4143-4147(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91201875; PubMed=1673147;
RA   Wolf S.F., Temple P.A., Kobayashi M., Young D., Dicig M., Lowe L.,
RA   Dzialo R., Fitz L., Ferenz C., Hewick R.M., Kelleher K.,
RA   Herrmann S.H., Clark S.C., Azzoni L., Chan S.H., Trinchieri G.,
RA   Perussia B.;
RT   "Cloning of cDNA for natural killer cell stimulatory factor, a
RT   heterodimeric cytokine with multiple biologic effects on T and
RT   natural killer cells.";
RL   J. Immunol. 146:3074-3081(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   PubMed=11197695;
RA   Huang D., Cancilla M.R., Morahan G.;
RT   "Complete primary structure, chromosomal localization, and definition
RT   of polymorphisms of the gene encoding the human interleukin 12 p40
RT   subunit.";
RL   Genes Immun. 1:515-520(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Hongyuan J., Meiyun Z.;
RT   "Cloning and sequence analysis of IL-12 cDNA from Chinese.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 23-45.
RX   MEDLINE=90370873; PubMed=2204066;
RA   Stern A.S., Podlaski F.J., Hulmes J.D., Pan Y.C.E., Quinn P.M.,
RA   Wolitzky A.G., Familletti P.C., Stremlo D.L., Truitt T.,
RA   Chizzonite R., Gately M.K.;
RT   "Purification to homogeneity and partial characterization of
RT   cytotoxic lymphocyte maturation factor from human B-lymphoblastoid
RT   cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6808-6812(1990).
RN   [6]
RP   SIMILARITY TO IL-6 RECEPTOR.
RX   MEDLINE=91300556; PubMed=2070420;
RA   Gearing D.P., Cosman D.;
RT   "Homology of the p40 subunit of natural killer cell stimulatory
RT   factor (NKSF) with the extracellular domain of the interleukin-6
RT   receptor.";
RL   Cell 66:9-10(1991).
RN   [7]
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RP   CARBOHYDRATE-LINKAGE SITE TRP-319.
RX   MEDLINE=99225373; PubMed=10207176;
RA   Doucey M.A., Hess D., Blommers M.J., Hofsteenge J.;
RT   "Recombinant human interleukin-12 is the second example of a
RT   C-mannosylated protein.";
RL   Glycobiology 9:435-441(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED
CC       T AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC.
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS. NKSF IS ESSENTIALLY A COMPLEX OF CYTOKINE AND SOLUBLE
CC       RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: KNOWN TO BE C-MANNOSYLATED IN THE RECOMBINANT PROTEIN; IT IS
CC       NOT YET KNOWN FOR SURE IF THE WILD-TYPE PROTEIN IS ALSO MODIFIED.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M65272; AAA35695.1; -.
DR   EMBL; M65290; AAA59938.1; -.
DR   EMBL; AY008847; AAG32620.1; -.
DR   EMBL; AF180563; AAD56386.1; -.
DR   PIR; B39359; B39359.
DR   PIR; B36055; B36055.
DR   GlycoSuiteDB; P29460; -.
DR   Genew; HGNC:5970; IL12B.
DR   MIM; 161561; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22
FT   CHAIN       23    328       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     235    320       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   222    222       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   319    319       C-LINKED (MAN).
FT                               /FTId=CAR_000187.
FT   CONFLICT   239    239       K -> N (IN REF. 2).
SQ   SEQUENCE   328 AA;  37169 MW;  118FA801B8F5BB2F CRC64;

  Query Match             85.1%;  Score 1501.5;  DB 1;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 1.4e-115;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| |||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| |||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:||||||||:|||:|||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||:| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:|||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 8
I12B_MACMU
ID   I12B_MACMU     STANDARD;      PRT;   328 AA.
AC   P48095;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19841; AAB60397.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    328       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     235    320       FIBRONECTIN TYPE-III.
```

```
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD    125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     106    106       K -> I.
FT   VARIANT     206    206       L -> P.
FT   VARIANT     218    218       L -> P.
FT   VARIANT     289    289       I -> T.
FT   VARIANT     295    295       S -> P.
SQ   SEQUENCE   328 AA;  37273 MW;  A46198AAC6D2746B CRC64;

  Query Match             84.7%;  Score 1493.5;  DB 1;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 6.5e-115;
  Matches  277;  Conservative   20;  Mismatches   28;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||  |||||||||||:|||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              || |||||||||||||||||||||||||||: || ||||:||||||||||:||:|||
Db         64 QSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLLLLHKKEDGIWSTDVLKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |:|||||||||||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSNPQGVTCGAVTLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:||| |||||:|||||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEERLPIEVMVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||||| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQVQGKSKREKKDRIFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :|   |||:||||||||:|||| ||
Db        303 NASFSVQAQDRYYSSSWSEWASVPCS 328


RESULT 9
I12B_PIG
ID   I12B_PIG       STANDARD;      PRT;   324 AA.
AC   Q28938;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=97383978; PubMed=9239844;
RA   Foss D.L., Murtaugh M.P.;
RT   "Molecular cloning and mRNA expression of porcine interleukin-12.";
RL   Vet. Immunol. Immunopathol. 57:121-134(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U08317; AAA75356.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    324       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     231    316       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   195    195       INTERCHAIN (PROBABLE).
FT   CARBOHYD   125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   218    218       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   324 AA;  36828 MW;  F0E48B72F700086C CRC64;

  Query Match             83.8%;  Score 1477.5;  DB 1;  Length 324;
  Best Local Similarity   83.0%;  Pred. No. 1.3e-113;
  Matches  273;  Conservative   24;  Mismatches   27;  Indels    5;  Gaps    1;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              || ||||:|||||| |||||::|||||||:|||||||:|:|||||||||:||||| |||
Db          1 MHLQQLVVSWFSLVWLASPIVAIWELEKNVYVVELDWYPNAPGEMVVLTCNTPEEDGITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||:|||||| |||||||||||| ||| |||:||||:|||||||||||||:|
Db         61 TSDQSSEVLGTGKTLTIHVKEFGDAGQYTCRKGGAVLSQSLLLLHKKEDGIWSTDILKDQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              || ||| |||||||||||||||||||||||||||||||| :||:|||||  |||
Db        121 KEPKNKSFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGSTDPRGVTCGTATLSE--- 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
                |  :|||| |||||||||:||||||||||::|:|||||||||||||||||||||||||
Db        178 --DLGEYKKYRVECQEGSACPAAEESLPIEVVLEAVHKLKYENYTSSFFIRDIIKPDPPK 235

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              |||| ||||||||:|||||||||||||||| | :| |||| |||||:|  |: ||||
Db        236 NLQLNPLKNSRHVEISWEYPDTWSTPHSYFSLMFGVQVQGKNKREKKDKLFTDQISAKVT 295

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              ||||| |||||||||||||:||||||:
Db        296 CHKDANIRVQARDRYYSSSWSEWASVSCN 324


RESULT 10
I12B_CERTO
ID   I12B_CERTO     STANDARD;      PRT;   328 AA.
AC   P46658;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19834; AAA86701.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1    22       BY SIMILARITY.
FT   CHAIN       23   328       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43    97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     235   320       FIBRONECTIN TYPE-III.
FT   DISULFID    50    90       POTENTIAL.
FT   DISULFID   199   199       INTERCHAIN (PROBABLE).
FT   CARBOHYD   125   125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   135   135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   222   222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   303   303       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   328 AA;  37252 MW;  A2DE98E844435B14 CRC64;

  Query Match             82.5%;  Score 1455.5;  DB 1;  Length 328;
  Best Local Similarity   82.8%;  Pred. No. 8.3e-112;
  Matches  270;  Conservative   22;  Mismatches   33;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| |||||||||||:|||||||||:||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              || |||||||||||||||||||||||||: || |||| |||||||||||||:|||
Db         64 QSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLLLPHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||: ||:|||||||| |||||: ||||| ||: |||| |:|||||||| |||||||| |
Db        124 KNETFLRCEAKNYSGRITCWWLSTISTDLTFSIISSRGSSNPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:||| ||||||:|||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEERLPIEVMVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||||| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQVQGKSKREKKDRIFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
                 :|   |||:|||||||::| || ||
Db        303 NASFSVQAQDRYYSSSWNEWTSVPCS 328


RESULT 11
I12B_MARMO
ID   I12B_MARMO     STANDARD;      PRT;   327 AA.
AC   Q61729;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RA   Laxton C.D., Foster G.R., Shanmuganathan S., Mills J.S.,
RA   Ackrill A.M.;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X97019; CAA65747.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1    22       BY SIMILARITY.
FT   CHAIN       23   327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43    97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     235   319       FIBRONECTIN TYPE-III.
FT   DISULFID    50    90       POTENTIAL.
FT   DISULFID   199   199       INTERCHAIN (PROBABLE).
FT   CARBOHYD   134   134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   152   152       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37172 MW;  9A15445915AB90E6 CRC64;

  Query Match             75.4%;  Score 1330;  DB 1;  Length 327;
  Best Local Similarity   75.4%;  Pred. No. 1.5e-101;
  Matches  245;  Conservative   35;  Mismatches   43;  Indels    2;  Gaps    2;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||| ||| |||||:|||||||:|||||||||| ||| ||||| ||||| |||||
Db          4 QQLVISWVSLVWLASPLLAIWELEKNVYVVELDWHPDTPGEKVVLTCDTPEEDGITWTSE 63
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Qy          64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
               ||||||||||||||| |||| ||| ||| :||:||| |||:|| |||||||||| :||
Db          64 QSSEVLGSGKTLTILVKEFEDAGHYTCRRGGEVLSQMLLLLHKNEDGIWSTDILK-KKEP 122

Qy         124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
               :|| : |||||||| |||||||||||: ||||| || ||||||||  |||||||::::
Db         123 ENKNLVTCEAKNYSGRFTCWWLTAISTDVNFSVKSHRGSSDPQGVTCGEATLSAERVKIE 182

Qy         184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
                |:|||||:|:||| :|||:|||:||| |||||:|||||||| |||||||||||||| ||:
Db         183 QREYKKYSVQCQEDNACPTAEETLPITVVVDAVHKLKYENYISSFFIRDIIKPDPPKNLK 242

Qy         244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
               :|| |  : |||:|||||:|||||||||||| :| |||  ::: : | |||||  | | |
Db         243 MKPSKTPQQVEVTWEYPDSWSTPHSYFSLTFSVQVQGK-KKKRSNTLHVDKTSVTVTCQK 301

Qy         304 DAKIRVQARDRYYSSSWSDWASVSC 328
                ||: ||||||||:||||:||::||
Db         302 GAKVSVQARDRYYNSSWSEWATMSC 326


RESULT 12
I12B_MOUSE
ID   I12B_MOUSE     STANDARD;      PRT;   335 AA.
AC   P43432;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Spleen;
RX   MEDLINE=92268481; PubMed=1350290;
RA   Schoenhaut D.S., Chua A.O., Wolitzky A.G., Quinn P.M., Dwyer C.M.,
RA   Gately M.K., Gubler U.;
RT   "Cloning and expression of murine IL-12.";
RL   J. Immunol. 148:3433-3440(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96257799; PubMed=8647196;
RA   Tone Y., Thompson S.A., Babik J.M., Nolan K.F., Tone M., Raven C.,
RA   Waldmann H.;
RT   "Structure and chromosomal location of the mouse interleukin-12 p35
RT   and p40 subunit genes.";
RL   Eur. J. Immunol. 26:1222-1227(1996).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; M86671; AAA39296.1; -.
DR   EMBL; S82426; AAB37383.1; -.
DR   EMBL; S82421; AAB37383.1; JOINED.
DR   EMBL; S82422; AAB37383.1; JOINED.
DR   EMBL; S82424; AAB37383.1; JOINED.
DR   EMBL; S82425; AAB37383.1; JOINED.
DR   MGD; MGI:96540; Il12b.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    335       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     233    324       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   197    197       INTERCHAIN (PROBABLE).
FT   CARBOHYD    47     47       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   122    122       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   132    132       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   220    220       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DOMAIN     155    159       POLY-SER.
SQ   SEQUENCE   335 AA;  38235 MW;  19E4FA5EF0CFC82A CRC64;

  Query Match             64.7%;  Score 1141.5;  DB 1;  Length 335;
  Best Local Similarity   65.5%;  Pred. No. 3.9e-86;
  Matches  220;  Conservative   38;  Mismatches   65;  Indels   13;  Gaps    4;

Qy           1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
               | ||:| ||||::||| ||||||||||||||||:|| |||||| | ||| |||||||||
Db           1 MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy          61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
               || |   |:|||||||| |||| ||||||||||: || | ||:||||:|||||:||
Db          61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy         121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
               |  ||| |||||| |||||||| ||   : ||||::|||    | : ||||  :||||:|
Db         118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSSPDSRAVTCGMASLSAEKV 177

Qy         181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
               :| |||:||:| |||   ||:|||:||||: ::|  : ||||||:|||||||||||||
Db         178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237

Qy         241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
               |||:|||||: |||||||||:|||||||| | :: | |  : |        |    |
Db         238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLV 296

Qy         293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
               :||| :| | |   : |||:||||:|| | || | |
Db         297 EKTSTEVQC-KGGNVCVQAQDRYYNSSCSKWACVPC 331


RESULT 13
IL6A_HUMAN
ID   IL6A_HUMAN     STANDARD;      PRT;   468 AA.
AC   P08887; Q16202;
DT   01-NOV-1988 (Rel. 09, Created)
DT   01-NOV-1988 (Rel. 09, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1)
DE   (CD126 antigen).
GN   IL6R.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RX   MEDLINE=88305347; PubMed=3136546;
RA   Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,
RA   Taniguchi T., Hirano T., Kishimoto T.;
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RT   "Cloning and expression of the human interleukin-6 (BSF-2/IFN beta 2)
RT   receptor.";
RL   Science 241:825-828(1988).
RN   [2]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RA   Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B.,
RA   Taniguchi T., Hirano T., Kishimoto T.;
RT   "Molecular structure of interleukin 6 receptor.";
RL   Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:209-211(1988).
RN   [3]
RP   SEQUENCE FROM N.A. (LONG ISOFORM).
RX   MEDLINE=91336983; PubMed=1872801;
RA   Schooltink H., Stoyan T., Lenz D., Schmitz H., Hirano T.,
RA   Kishimoto T., Heinrich P.C., Rose-John S.;
RT   "Structural and functional studies on the human hepatic interleukin-6
RT   receptor. Molecular cloning and overexpression in HepG2 cells.";
RL   Biochem. J. 277:659-664(1991).
RN   [4]
RP   SEQUENCE OF 313-365 FROM N.A. (SHORT ISOFORM).
RX   MEDLINE=94333499; PubMed=8056053;
RA   Horiuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M.,
RA   Matsumoto A., Yamamoto M., Yamamoto N.;
RT   "Soluble interleukin-6 receptors released from T cell or
RT   granulocyte/macrophage cell lines and human peripheral blood
RT   mononuclear cells are generated through an alternative splicing
RT   mechanism.";
RL   Eur. J. Immunol. 24:1945-1948(1994).
RN   [5]
RP   PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.
RX   MEDLINE=99167486; PubMed=10066782;
RA   Cole A.R., Hall N.E., Treutlein H.R., Eddes J.S., Reid G.E.,
RA   Moritz R.L., Simpson R.J.;
RT   "Disulfide bond structure and N-glycosylation sites of the
RT   extracellular domain of the human interleukin-6 receptor.";
RL   J. Biol. Chem. 274:7207-7215(1999).
RN   [6]
RP   MUTAGENESIS.
RX   MEDLINE=93223711; PubMed=8467812;
RA   Yawata H., Yasukawa K., Natsuka S., Murakami M., Yamasaki K., Hibi M.,
RA   Taga T., Kishimoto T.;
RT   "Structure-function analysis of human IL-6 receptor: dissociation of
RT   amino acid residues required for IL-6-binding and for IL-6 signal
RT   transduction through gp130.";
RL   EMBO J. 12:1705-1712(1993).
CC   -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC       WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC       ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
CC       LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
CC       REACTIONS AND HEMATOPOIESIS.
CC   -!- FUNCTION: LOW CONCENTRATION OF A SOLUBLE FORM OF INTERLEUKIN-6
CC       RECEPTOR ACTS AS AN AGONIST OF IL-6 ACTIVITY.
CC   -!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST.
CC   -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM).
CC       SECRETED (SHORT FORM).
CC   -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
CC       SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC   -!- TISSUE SPECIFICITY: THE SHORT FORM IS EXPRESSED IN PERIPHERAL
CC       BLOOD MONONUCLEAR CELLS AND WEAKLY FOUND IN URINE AND SERUM.
CC   -!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
CC       N-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC   -!- PTM: A SHORT SOLUBLE FORM MAY ALSO BE RELEASED FROM THE MEMBRANE
CC       BY PROTEOLYSIS.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   -!- DATABASE: NAME=PROW; NOTE=CD guide CD126 entry;
CC       WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd126.htm".
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CC   ---------------------------------------------------------------------
DR   EMBL; X12830; CAA31312.1; -.
DR   EMBL; X58298; CAA41231.1; -.
DR   EMBL; S72848; AAC60635.1; -.
DR   PIR; A41242; A41242.
DR   PIR; JU0080; JU0080.
DR   PIR; S14621; S14621.
DR   PIR; S17468; S17468.
DR   Genew; HGNC:6019; IL6R.
DR   MIM; 147880; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW   Alternative splicing; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    468       INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT   DOMAIN      20    365       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM   366    386       POTENTIAL.
FT   DOMAIN     387    468       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN      40    103       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID    25    193
FT   DISULFID    47     96
FT   DISULFID   121    132
FT   DISULFID   165    176
FT   CARBOHYD    55     55       N-LINKED (GLCNAC. . .).
FT   CARBOHYD    93     93       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   221    221       N-LINKED (GLCNAC. . .).
FT   VARSPLIC   356    365       VQDSSSVPLP -> GSRRRGSCGL (IN SHORT
FT                               ISOFORM).
FT   VARSPLIC   366    468       MISSING (IN SHORT ISOFORM).
FT   MUTAGEN    121    121       C->S: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    122    122       F->A: NO CHANGE OF LIGAND-BINDING AND IL6
FT                               SIGNALING.
FT   MUTAGEN    132    132       C->A: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    134    134       W->L: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    140    140       P->G: NO CHANGE OF LIGAND-BINDING AND IL6
FT                               SIGNALING.
FT   MUTAGEN    153    153       F->L: NO CHANGE OF LIGAND-BINDING AND IL6
FT                               SIGNALING.
FT   MUTAGEN    165    165       C->L: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    174    174       F->L: NO CHANGE OF LIGAND-BINDING AND IL6
FT                               SIGNALING.
FT   MUTAGEN    176    176       C->A: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    184    184       D->T: 30% DECREASE OF LIGAND-BINDING AND
FT                               IL6 SIGNALING.
FT   MUTAGEN    190    190       V->G: 80% DECREASE OF LIGAND-BINDING AND
FT                               NO IL6 SIGNALING.
FT   MUTAGEN    193    193       C->D: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    211    211       C->A: NO CHANGE OF LIGAND-BINDING AND IL6
FT                               SIGNALING.
FT   MUTAGEN    217    217       D->V: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    232    232       R->S: 30% DECREASE OF LIGAND-BINDING AND
FT                               IL6 SIGNALING.
FT   MUTAGEN    233    233       W->Q: 30% DECREASE OF LIGAND-BINDING AND
FT                               INCREASE OF IL6 SIGNALING.
FT   MUTAGEN    254    254       E->A: 50% DECREASE OF LIGAND-BINDING AND
FT                               IL6 SIGNALING.
FT   MUTAGEN    277    277       C->D: 30% INCREASE OF LIGAND-BINDING AND
FT                               100% INCREASE IN IL6 SIGNALING.
FT   MUTAGEN    278    278       V->N: 50% DECREASE OF LIGAND-BINDING AND
FT                               50% INCREASE IN IL6 SIGNALING.
FT   MUTAGEN    279    279       I->D: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN    280    280       H->I: NO CHANGE OF LIGAND-BINDING AND NO
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FT                                IL6 SIGNALING.
FT   MUTAGEN      281    281      D->G: 70% DECREASE OF LIGAND-BINDING AND
FT                                NO IL6 SIGNALING.
FT   MUTAGEN      285    285      G->D: 80% DECREASE OF LIGAND-BINDING AND
FT                                NO IL6 SIGNALING.
FT   MUTAGEN      291    291      Q->K: COMPLETE LOSS OF LIGAND-BINDING.
FT   MUTAGEN      293    293      R->G: COMPLETE LOSS OF LIGAND-BINDING.
SQ   SEQUENCE   468 AA;  51547 MW;  62AA239FA14F1B8B CRC64;

  Query Match             10.9%;  Score 193;  DB 1;  Length 468;
  Best Local Similarity   22.2%;  Pred. No. 2e-08;
  Matches   69;  Conservative   59;  Mismatches  113;  Indels   70;  Gaps   13;

Qy         42 PGEMVVLTCHTPEEDD---ITW------TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK 92
              ||: | |||   | :|   : |       :  |   | |: | ::  :  |:| |:|::
Db         39 PGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYR 98

Qy         93 GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW-------L 145
               |:     ||:          |: |: :     | |  |:      | |       |
Db         99 AGRPAGTVHLLV----------DVPPEEPQ------LSCFRKSPLSNVVCEWGPRSTPSL 142

Qy        146 T--AISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS---AC 200
              |  |:    ||    :  | :|    |                  :|: | |: |   |
Db        143 TTKAVLLVRKFQNSPAEDFQEP----C-----------------QYSQESQKFSCQLAV 180

Qy        201 PSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEY 259
              |  : |  |  :  |       : | :|    |::|||| |: :  : :| | : |:|:
Db        181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240

Qy        260 PDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDA------KIRVQARD 313
              | :|::  |:: | | :: : : ::     :  |     |:   ||       ::::|::
Db        241 PHSWNS--SFYRLRFELRYRAERSKTFTTWMVKDLQHHCVI--HDAWSGLRHVVQLRAQE 296

Qy        314 RYYSSSWSDWA 324
              :    ||:|:
Db        297 EFGQGEWSEWS 307


RESULT 14
IL6A_PIG
ID   IL6A_PIG       STANDARD;      PRT;   467 AA.
AC   O18796;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).
GN   IL6R.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Morris K.R., Strom A.D.G.;
RT   "Cloning and expression of biologically active porcine IL-6 receptor
RT   alpha chain.";
RL   Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 123-186 FROM N.A.
RC   TISSUE=Liver;
RA   Klir J.J., Matteri R.L.;
RT   "Partial cDNA sequence of porcine interleukin 6 receptor.";
RL   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
CC       WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
CC       ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
CC       LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
CC       REACTIONS AND HEMATOPOIESIS.
CC   -!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
CC       SIMILARITY).
CC   -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
CC   -!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
CC       C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC   ---------------------------------------------------------------------
DR   EMBL; AF147881; AAF73109.1; -.
DR   EMBL; AF015116; AAB70916.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
KW   Signal.
FT   SIGNAL        1     19       BY SIMILARITY.
FT   CHAIN        20    467       INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT   DOMAIN       20    365       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    366    386       POTENTIAL.
FT   DOMAIN      387    467       CYTOPLASMIC (POTENTIAL).
FT   DOMAIN       40    103       IG-LIKE C2-TYPE DOMAIN.
FT   DISULFID     25    193       BY SIMILARITY.
FT   DISULFID     47     96       BY SIMILARITY.
FT   DISULFID    121    132       BY SIMILARITY.
FT   DISULFID    165    176       BY SIMILARITY.
FT   CARBOHYD     55     55       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     93     93       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    221    221       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    350    350       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   467 AA;  51066 MW;  A2B0B884EF21C502 CRC64;

  Query Match             10.4%;  Score 183;  DB 1;  Length 467;
  Best Local Similarity   22.0%;  Pred. No. 1.3e-07;
  Matches   75;  Conservative   58;  Mismatches  132;  Indels   76;  Gaps   14;

Qy         15 LLASPLMAI-------WELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDD---ITW---- 60
              |||:| ||:         |: :||           ||  | |||   |  |   | |
Db         12 LLAAPGMALAPRGCSKLEVAQDVLT-------SLPGASVTLTCPGGEPGDNATIHWVLRN 64

Qy         61 --TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILK 118
                | :      | |: | ::  :  |:| |:|:: |       ||:          |
Db         65 QVTGSPDGRPAGVGRRLLLKSVQLSDSGNYSCYQDGVPAGSVRLLV----------DAPP 114

Qy        119 EQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAE 178
              |: :      | |  |:      | |                    |   |  || |  :
Db        115 EEPQ------LSCFRKSPLSNVGCEWRP---------------RSPPSPTTKAVLLVRK 152

Qy        179 RVRVDNRDYK---KYTVECQE---GSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRD 232
                    |::   :|::| |      | |  : |  |  :  |       :   :|
Db        153 FQNSPVEDFQEPCQYSLEAQRFFCQLAVPEGDNSFHIVTLCVANSAGSQSSTPQTFEGYG 212

Qy        233 IIKPDPPTNLQLKPL-KNSRHVEVSWEYPDTWSTPHSYF-SLTFCIQAQGKNNR------ 284
              |::|||| |: :  : :| | : |:|: | :|   :|||  | | :: : : ::
Db        213 ILQPDPPVNITVSAVDRNPRWLSVTWQDPPSW---NSYFYRLQFELRYRAERSKTFTTWM 269

Qy        285 -EKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWA 324
               ::    |:   :   : |    ::::|:: :    ||:|:
Db        270 VKELQHHCIIHDAWSGMRH---VVQLRAQEEFGHGLWSEWS 307


RESULT 15
```

```
CNTR_CHICK
ID   CNTR_CHICK     STANDARD;      PRT;   362 AA.
AC   P51641;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Ciliary neurotrophic factor receptor alpha precursor (CNTFR alpha)
DE   (Growth promoting activity receptor alpha) (GPA receptor alpha) (GPAR
DE   alpha).
GN   CNTFR.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96064819; PubMed=7595532;
RA   Ip F.C.F., Fu A.K.Y., Tsim K.W.K., Ip N.Y.;
RT   "Cloning of the alpha component of the chick ciliary neurotrophic
RT   factor receptor: developmental expression and down-regulation in
RT   denervated skeletal muscle.";
RL   J. Neurochem. 65:2393-2400(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95401882; PubMed=7671828;
RA   Heller S., Finn T.P., Huber J., Nishi R., Geissen M., Pueschel A.W.,
RA   Rohrer H.;
RT   "Analysis of function and expression of the chick GPA receptor (GPAR
RT   alpha) suggests multiple roles in neuronal development.";
RL   Development 121:2681-2693(1995).
CC   -!- FUNCTION: BINDS TO CNTF (GPA). THE ALPHA CHAIN PROVIDES THE
CC       RECEPTOR SPECIFICITY.
CC   -!- SUBUNIT: HETEROTRIMER OF THE ALPHA CHAIN, LIFR AND GP130.
CC   -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
CC       similarity).
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN NERVOUS SYSTEM. ALSO FOUND
CC       IN SKELETAL MUSCLE.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U29245; AAA87838.1; -.
DR   EMBL; Z48168; CAA88184.1; -.
DR   HSSP; P16471; 1BP3.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     19       POTENTIAL.
FT   CHAIN        20    334       CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT                                ALPHA.
FT   PROPEP      335    362       REMOVED IN MATURE FORM (POTENTIAL).
FT   DOMAIN       37     94       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      199    300       FIBRONECTIN TYPE-III.
FT   DISULFID     44     87       POTENTIAL.
FT   CARBOHYD     58     58       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     68     68       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    140    140       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    188    188       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   LIPID       334    334       GPI-ANCHOR (POTENTIAL).
FT   CONFLICT    337    337       A -> V (IN REF. 2).
SQ   SEQUENCE   362 AA;  40307 MW;  5A90217EB48419F7 CRC64;

  Query Match             10.1%;  Score 178;  DB 1;  Length 362;
  Best Local Similarity   23.9%;  Pred. No. 2.5e-07;
  Matches   73;  Conservative   48;  Mismatches  112;  Indels   72;  Gaps   14;

Qy         43 GEMVVLTCHTPEED-DITWTSAQSSEVLGS---GKTLTIQVKEFGDAGQYTCHKGGKVLS 98
              |  | : | : : |  :||| |  :::  |   |  | ::  :   :|||:|::|
Db         37 GADVTMKCGSMDWDAAVTWT-ANGTDIDDSHLNGSYLILKNVDLTQSGQYSCYEGSS--- 92

Qy         99 RSLLLIHKKEDGIWSTDILKEQKESK-----NKIFLKCEAKNYSGRFTCWWLTAISTDLK 153
                        |    || |   :       :  | | : ||   | | |      | :
Db         93 ------------WH---LKYQTYLRVGVPPKEPVLMCRSNNYPKGFYCSWHLPSPTYIP 136

Qy        154 FSVKSSRGFSDPQGVTCGAVTLSAER-VRVDNRDYKKYTVECQEGSACPSAEESLPIEVV 212
               |   |        |  |   :  |: :   || : :|              ::  :|
Db        137 NSFNIS--------VIHGTREMVCEKDIFPKNRCHIRYL----------QLFSTVKYKVT 178

Qy        213 VDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNS-RHVEVSWEYPDTWSTPHSYFS 271
              :   : |   : | :|    |:|||| ::  ||: |: | :||||: | :|  | | |
Db        179 LTVTNALGKNSTTLTFDEFAIVKPDPPESVVAKPVPNNPRRLEVSWQNPSSWPDPES-FP 237

Qy        272 LTFCIQAQGKNNREKKDRLCVDK-----------TSAKVVCHKDAKIRVQARDRYYSSS 319
              | | :: :          | :|:           |       |:  |:| |:|     :
Db        238 LKFFLRYR---------PLILDQWQHVELSDGTSHTITDAYAGKEYIIQVAAKDNDI-GT 287

Qy        320 WSDWA 324
              ||||:
Db        288 WSDWS 292


Search completed: July 15, 2003, 11:07:02
Job time : 8.2101 secs
```

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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:57:19 ; Search time 29.1539 Seconds
(without alignments)
2325.231 Million cell updates/sec

Title: US-09-917-265-59
Perfect score: 1764
Sequence: 1 MHPQQLVISWFSLVLLASPL.....QARDRYYSSSWSDWASVSCS 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1343.5	76.2	332	11	Q924V5	Q924v5 cavia porce
2	1343	76.1	327	11	Q9ET05	Q9et05 marmota mon
3	1282	72.7	327	11	Q91ZK7	Q91zk7 sigmodon hi
4	1146.5	65.0	335	11	Q9QUM1	Q9qum1 mus musculu
5	1130.5	64.1	335	11	Q9R278	Q9r278 rattus norv
6	1035	58.7	195	6	Q95N82	Q95n82 canis famil
7	1010	57.3	268	11	Q62712	Q62712 rattus norv
8	1004.5	56.9	344	11	Q924K7	Q924k7 meriones un
9	818	46.4	174	6	Q28232	Q28232 cervus elap
10	799	45.3	150	6	Q9BG70	Q9bg70 canis famil
11	768	43.5	149	6	Q9TV09	Q9tv09 canis famil
12	727.5	41.2	169	11	Q9Z1Y8	Q9z1y8 cavia porce
13	695	39.4	143	6	O62779	O62779 felis silve
14	507	28.7	132	11	O70328	O70328 mesocricetu
15	438.5	24.9	111	11	P97731	P97731 rattus sp.
16	176.5	10.0	372	11	O88507	O88507 mus musculu
17	152.5	8.6	431	11	Q99MF4	Q99mf4 rattus norv
18	149.5	8.5	422	4	Q16542	Q16542 homo sapien
19	148.5	8.4	432	11	P70225	P70225 mus musculu
20	146.5	8.3	432	11	Q64385	Q64385 mus musculu
21	132	7.5	812	10	Q9C6J9	Q9c6j9 arabidopsis
22	129	7.3	229	4	Q14213	Q14213 homo sapien
23	127.5	7.2	622	6	Q9N0J7	Q9n0j7 callithrix
24	122.5	6.9	1277	13	Q98902	Q98902 fugu rubrip
25	118	6.7	229	4	O75269	O75269 homo sapien
26	115	6.5	628	11	Q9JKG1	Q9jkg1 cavia porce
27	113.5	6.4	1148	13	Q9IBA7	Q9iba7 gallus gall
28	113	6.4	428	5	Q8WPM7	Q8wpm7 oikopleura
29	112	6.3	628	11	Q9JKT1	Q9jkt1 cavia porce
30	111.5	6.3	978	6	Q9XS93	Q9xs93 canis famil
31	111	6.3	628	11	Q9JI97	Q9ji97 cavia porce
32	111	6.3	1146	13	Q9I8V6	Q9i8v6 gallus gall
33	109.5	6.2	538	13	Q9DFU0	Q9dfu0 sparus aura
34	109	6.2	838	13	Q90YM1	Q90ym1 brachydanio
35	108.5	6.2	455	4	Q9UIR0	Q9uir0 homo sapien
36	108.5	6.2	626	5	Q22040	Q22040 caenorhabdi
37	108.5	6.2	923	6	O97745	O97745 sus scrofa
38	108.5	6.2	964	6	O97744	O97744 sus scrofa
39	108.5	6.2	964	6	Q9TQQ1	Q9tqq1 sus scrofa
40	108.5	6.2	1197	13	Q90478	Q90478 brachydanio
41	108	6.1	386	6	Q95LF0	Q951f0 canis famil
42	108	6.1	638	6	Q9TU69	Q9tu69 canis famil
43	107.5	6.1	608	6	Q9N0Y7	Q9n0y7 monodelphis
44	106	6.0	206	4	Q16354	Q16354 homo sapien
45	106	6.0	268	4	Q8TD78	Q8td78 homo sapien

ALIGNMENTS

RESULT 1
Q924V5
ID Q924V5 PRELIMINARY; PRT; 332 AA.
AC Q924V5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Interleukin-12 p40 subunit (IL-12 p40).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARTLEY;
RA Shiratori I., Matsumoto M., Tsuji S., Nomura M., Toyoshima K.,
RA Seya T.;
RT "Molecular cloning and functional characterization of guinea pig
RT Interleukin -12.";
RL Int. Immunol. 0:0-0(2001).
DR EMBL; AB025724; BAB63963.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ SEQUENCE 332 AA; 37632 MW; B75D16B23DE8B9B4 CRC64;

Query Match 76.2%; Score 1343.5; DB 11; Length 332;
Best Local Similarity 77.4%; Pred. No. 2.4e-112;
Matches 254; Conservative 25; Mismatches 42; Indels 7; Gaps 3;

```
Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              :||: || |||||||||:|:|||:|||||||||||| ||||| |||||:| ||| |||||
Db          4 RQLISSWLSLVLLASPLLAMWELKKDVYVVELDWHTDAPGETVVLTCNTAEEDGITWTSD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
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```
Db         64 RKSDILGSGKTLTIQVKEFEDAGGYTCHKGGEVLSRSQLLLHKKEDEIWSTDILKEQKGS 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              |:|  ||:|||||  |||:|||||:|||||:|||||||||||:|||||||||||||||||
Db        180 NQEY-KYSVECQEDSACPTAEESLPIEVVVDAIHKFKYENYTSSFYIRDIIKPDPPKNLQ 238

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |:|  ||:|||||  |||:|||||:|||||:|||||:|||||:|||||||||||||||||
Db        239 LKPSVNSQQVEVSWEYPDTWSTPHSYFSLTFLVQTHGKNKNRREKKYELFTDKTSATVSC 298

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQG--KNNREKKDRLCVDKTSAKVVC 301
              |:|  ||:|||||  |||:|||||:|||||:|||||:|||||:|||||||||||||||||
Db        299 HKISKVEVRARDRYYSSSWSEWASVSCS 326


RESULT 2
Q9ET05
ID   Q9ET05      PRELIMINARY;      PRT;   327 AA.
AC   Q9ET05;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p40 subunit.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21424491; PubMed=11533170;
RA   Garcia-Navarro R., Blanco-Urgoiti B., Berraondo P.,
RA   Sanchez De La Rosa R., Vales A., Hervas-Stubbs S., Lasarte J.J.,
RA   Borras F., Ruiz J., Prieto J.;
RT   "Protection against Woodchuck Hepatitis Virus (WHV) Infection by Gene
RT   Gun Coimmunization with WHV Core and Interleukin-12.";
RL   J. Virol. 75:9068-9076(2001).
DR   EMBL; AF288519; AAG01023.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   327 AA;  37140 MW;  42782B3559C224DD CRC64;

  Query Match            76.1%;  Score 1343;  DB 11;  Length 327;
  Best Local Similarity  76.0%;  Pred. No. 2.7e-112;
  Matches  247;  Conservative   35;  Mismatches   41;  Indels    2;  Gaps    2;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||  ||| |||||:|||||||:|||||||||| ||| ||||| ||||| |||||
Db          4 QQLVISWVSLVWLASPLLAIWELEKNVYVVELDWHPDTPGETVVLTCDTPEEDGITWTSE 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||| |||| ||| ||||:||:|||: |||:|| |||||||||| :||
Db         64 QSSEVLGSGKTLTILVKEFEDAGHYTCHRGGEVLSQMLLLLHKNEDGIWSTDILK-KKEP 122

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              :||  : |||||||||||||||||||:||||||  || |||||||||  |||||||::::
Db        123 ENKNLVTCEAKNYSGRFTCWWLTAISTDVKFSVKSHRGSSDPQGVTCGEATLSAERVKIE 182

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |:||||:|:||| :|||:|||:||| |||||:|||||||| |||||||||||||| ||:
Db        183 QREYKKYSVQCQEDNACPTAEETLPITVVVDAVHKLKYENYISSFFIRDIIKPDPPKNLK 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              :|| |  : |||:|||||:|||||||||||| :| |||  ::: : | |||||  | | |
Db        243 MKPSKTPQQVEVTWEYPDSWSTPHSYFSLTFSVQVQGK-KKKRSNTLHVDKTSVTVTCQK 301

Qy        304 DAKIRVQARDRYYSSSWSDWASVSC 328
              ||: ||||||||:||||:||::||
Db        302 GAKVSVQARDRYYNSSWSEWATMSC 326


RESULT 3
Q91ZK7
ID   Q91ZK7      PRELIMINARY;      PRT;   327 AA.
AC   Q91ZK7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 12 p40 subunit.
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pletneva L.M., Bacot S., Blanco J.C., Langley R.J., Prince G.A.;
RT   "Sigmodon hispidus cytokines, chemokines and interferons.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF421395; AAL16936.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ   SEQUENCE   327 AA;  37119 MW;  F096702CC950FD56 CRC64;

  Query Match            72.7%;  Score 1282;  DB 11;  Length 327;
  Best Local Similarity  72.8%;  Pred. No. 7.9e-107;
  Matches  238;  Conservative   37;  Mismatches   48;  Indels    4;  Gaps    3;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |:| ||||::||| |||||||||||||||:|| | |||| ||||| | ||||| |||
Db          4 QKLTISWFAMVLLVSPLMAIWELEKDVYVVEVDWSPGAPGERVVLTCDTSEEDDIIWTSD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||:|||||| :|||||  |||||||||||: || | ||:|||||||||||||:||:
Db         64 QSSEVVGSGKTLIVQVKEFSDAGQYTCHKGGETLSHSRLLLHKKEDGIWSTDILKDQKDP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| |||||| ||||||||||||:|||||||:|||   || : |||||  :|| |:| ||
Db        124 KNKTFLKCEAANYSGRFTCWWLTAVSTDLKFSLKSSSSSSDSRSVTCGAASLSTEKVTVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              ||| ||:| |||   ||:|||:||||:|::| || |||||:: ||||||||||| |||
Db        184 QRDYNKYSVACQEDITCPTAEETLPIELVMEAQHKYKYENYSTGFFIRDIIKPDPPKNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKK-DRLCVDKTSAKVVCH 302
              |||||:|: |||||||||:|||||||||| | :|   |  :||| : | ||| |||: |
Db        244 LKPLKSSQ-VEVSWEYPDSWSTPHSYFSLKFFVQVYRK--KEKKGESLLVDKPSAKIRCS 300

Qy        303 KDAKIRVQARDRYYSSSWSDWASVSCS 329
              |  ::||:|:| ||:||||:||||||:
Db        301 KGGEVRVRAQDHYYNSSWSEWASVSCN 327


RESULT 4
Q9QUM1
ID   Q9QUM1      PRELIMINARY;      PRT;   335 AA.
AC   Q9QUM1;
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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 12B P40 subunit.
GN   IL12B OR LL12B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SJL/J, AND B10.S/J; TISSUE=SPLEEN;
RA   Ma R.Z., Teuscher C.;
RT   "Screening for candidate genes of mouse autoimmnue diseases.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF128215; AAF22556.1; -.
DR   EMBL; AF128214; AAF22555.1; -.
DR   MGD; MGI:96540; Il12b.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   335 AA;  38171 MW;  7D061E116C00FC4A CRC64;

  Query Match             65.0%;  Score 1146.5;  DB 11;  Length 335;
  Best Local Similarity   65.8%;  Pred. No. 1.2e-94;
  Matches  221;  Conservative   38;  Mismatches   64;  Indels   13;  Gaps    4;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              | ||:| ||||::||| ||||||:||||||||||||:|| |||||| | ||| ||||||||||
Db          1 MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |   |:||||||||| |||| ||||||||||||: || | ||:||||:||||||:||
Db         61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              |  ||| |||||| |||||||| ||   : ||||::|||    | : ||||  :||||:|
Db        118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGTASLSAEKV 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
               :| |||:||:| |||   ||:|||:||||: ::|  : |||||::||||||||||||
Db        178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
              |||:|||||: ||||||||||:|||||||||| | :: | |  : |         |  | |
Db        238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGALLV 296

Qy        293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
              :||| :| | |   : |||:||||:|| | || | |
Db        297 EKTSTEVQC-KGGNVCVQAQDRYYNSSCSKWACVPC 331


RESULT 5
Q9R278
ID   Q9R278      PRELIMINARY;      PRT;   335 AA.
AC   Q9R278;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p40.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER;
RX   MEDLINE=98273736; PubMed=9613680;
RA   Khalife J., Pierrot C., Cocude C., Cetre C., Godin C., Capron A.;
RT   "Molecular cloning and sequencing of the rat interleukin-12 p40
RT   gene.";
RL   Eur. Cytokine Netw. 9:69-73(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER;
RA   Khalife J., Pierrot C., Cocude C., Cetre C., Godin C., Capron A.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF133197; AAD24190.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   335 AA;  38413 MW;  39BF5B49AF191007 CRC64;

  Query Match             64.1%;  Score 1130.5;  DB 11;  Length 335;
  Best Local Similarity   65.2%;  Pred. No. 3.2e-93;
  Matches  217;  Conservative   41;  Mismatches   62;  Indels   13;  Gaps    4;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |:|  |||::||| |||||:||||||||||:|| |||||| | ||| :||||||||||
Db          4 QKLTFSWFAMVLLVSPLMAMWELEKDVYVVEVDWRPDAPGETVTLTCDSPEEDDITWTSD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |   |:||||||| |:|| ||||||||:||: || | ||:||||:|||||:||   |
Db         64 QRRGVIGSGKTLTITVREFLDAGQYTCHRGGETLSHSHLLLHKKENGIWSTEIL---KNF 120

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| |||||| |||||||| ||   :|||||::|||    : : |||| :||||:| ::
Db        121 KNKTFLKCEAPNYSGRFTCSWLVHRNTDLKFNIKSSSSSPESRAVTCGRASLSAEKVTLN 180

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
               |||:||:| |||   ||:|||:||||:||:|  : |||||::||||||||||| |||
Db        181 QRDYEKYSVACQEDVTCPTAEETLPIELVVEAQQQNKYENYSTSFFIRDIIKPDPPKNLQ 240

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKT 295
              :||||||: ||||||||||:|||||||||| | :: | |  : |         |    |:||
Db        241 VKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKTKETEEECNQKGAFLVEKT 299

Qy        296 SAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
              ||:| | | | | |||:||||:|| | |  | |
Db        300 SAEVQC-KGANICVQAQDRYYNSSCSKWTCVPC 331


RESULT 6
Q95N82
ID   Q95N82      PRELIMINARY;      PRT;   195 AA.
AC   Q95N82;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 subunit p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Fonfara S., Groene A., Koenig M., Baumgaertner W.;
RT   "Sequence of canine interleukin-12-p40 mRNA in DH82-cells.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF349536; AAK54070.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER       1      1
FT   NON_TER     195    195
SQ   SEQUENCE   195 AA;  21943 MW;  46D77A1570B2F8B9 CRC64;
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  Query Match           58.7%;  Score 1035;  DB 6;  Length 195;
  Best Local Similarity  100.0%;  Pred. No. 5.7e-85;
  Matches  195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 60

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 120

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 180

Qy        184 NRDYKKYTVECQEGS 198
              |||||||||||||||
Db        181 NRDYKKYTVECQEGS 195


RESULT 7
Q62712
ID   Q62712      PRELIMINARY;      PRT;   268 AA.
AC   Q62712;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin-12p40 (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER; TISSUE=CULTURED SPLENOCYTES;
RA   Goodman R.E., Toews G.B.;
RT   "A partial cDNA of the coding region of rat IL-12p40, cloned by RT/PCR
RT   from Staphlococcal endotoxin stimulated splenocytes.";
RL   Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U16674; AAA52229.1; -.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
KW   Immunoglobulin domain.
FT   NON_TER     268    268
SQ   SEQUENCE   268 AA;  30644 MW;  9370D4CD28D9C73F CRC64;

  Query Match           57.3%;  Score 1010;  DB 11;  Length 268;
  Best Local Similarity  70.3%;  Pred. No. 1.5e-82;
  Matches  189;  Conservative   34;  Mismatches   42;  Indels    4;  Gaps    2;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |:|  |||::||| |||||:|||||||||||:|| |||||| | ||| :|||||||||||
Db          4 QKLTFSWFAMVLLVSPLMAMWELEKDVYVVEVDWRPDAPGETVTLTCDSPEEDDITWTSD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |   |:||||||||| |:|| ||||||||:||: || | ||:||||:|||||:||   |
Db         64 QRRGVIGSGKTLTITVREFLDAGQYTCHRGGETLSHSHLLLHKKENGIWSTEIL---KNF 120

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||| || |||||||| ||   :|||||::|||    : : ||||| :||||:| ::
Db        121 KNKTFLKREAPNYSGRFTCSWLVHRNTDLKFNIKSSSSSPESRAVTCGAASLSAEKVTLN 180

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
               |||:||:| |||   ||:|||:||||:||:|  : |||||::|||||||||||| |||
Db        181 QRDYEKYSVACQEDVTCPTAEETLPIELVVEAQQQNKYENYSTSFFIRDIIKPDPPKNLQ 240

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSL 272
              :|||||: |||||||||:||||||||||
Db        241 VKPLKNSQ-VEVSWEYPDSWSTPHSYFSL 268


RESULT 8
Q924K7
ID   Q924K7      PRELIMINARY;      PRT;   344 AA.
AC   Q924K7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin-12 p40 subunit.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gaucher D., Chadee K.;
RT   "Molecular cloning of gerbil interleukin-12, and its expression as a
RT   bioactive single-chain protein.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288612; AAK83061.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ   SEQUENCE   344 AA;  39375 MW;  21B513448D73E8CB CRC64;

  Query Match           56.9%;  Score 1004.5;  DB 11;  Length 344;
  Best Local Similarity  57.8%;  Pred. No. 6.7e-82;
  Matches  199;  Conservative   54;  Mismatches   68;  Indels   23;  Gaps    8;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |:| ||||::|||||||||||||||:|||||:||   |  | ||||| | || |||||
Db          4 QKLTISWFAVVLLASPLMAIWELEKNVYVVEMDWRSGA-NESVVLTCDTSEEGDITWTKD 62

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |:::|  ||||:||:||:| :||||||||| : ||   ||:|||::| || :|||: | |
Db         63 QTTKVEQSGKTVTIEVKDFNEAGQYTCHKGDQTLSHFRLLLHKKKNGYWSNEILKQDKNS 122

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              :|: |||||| |||||||| ||    ||||||:|:|:|    | : ||||||:|:||:|: |
Db        123 ENQTFLKCEAANYSGRFTCSWLVE-RTDLKFSIKNSSSSPDSRAVTCGAVSLTAEKVKGD 181

Qy        184 NRD--YKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTN 241
               :|   |:|:| |||   ||:|||::|| :|::|  : |||||::|||||||| |||| |
Db        182 EKDGKLKQYSVTCQEDITCPTAEETVPIGLVLEAQEQNKYENYSTSFFIRDIITPDPPKN 241

Qy        242 LQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQG---------KNNREKKDR-LC 291
              |::|||| : |||||||||:||||||||:| | :  :           :|:| | |  |
Db        242 LKVKPLKNDK-VEVSWEYPDSWSTPHSYFALKFYVWTESNKENKMRNTNSNKENKMRNAC 300

Qy        292 -------VDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
                    || || || | || :: |:|:||||:| :|  | | |
Db        301 IQNGTWLVDTTSTKVRC-KDGRVCVEAQDRYYNSLYSKHACVPC 343


RESULT 9
Q28232
ID   Q28232      PRELIMINARY;      PRT;   174 AA.
AC   Q28232;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 (Fragment).
GN   IL-12.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
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RP   SEQUENCE FROM N.A.
RA   Lockhart E.A.;
RT   "Cloning and sequencing of cervine IL-12.";
RL   Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U10160; AAA19658.1; -.
DR   InterPro; IPR002996; CR1A.
FT   NON_TER       1       1
FT   NON_TER     174     174
SQ   SEQUENCE   174 AA;  19684 MW;  389260B3A9067F2E CRC64;

  Query Match             46.4%;  Score 818;  DB 6;  Length 174;
  Best Local Similarity   86.8%;  Pred. No. 1.5e-65;
  Matches  151;  Conservative   14;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         85 AGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW 144
              |||||||||||:||||||||:|||||||||||||||:||| | | |||||||:||| |||||
Db          1 AGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWW 60

Qy        145 LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAE 204
              |||||||||||||||| |||:|||||||::|| |:| ||:|:|||||||||||||||:||
Db         61 LTAISTDLKFSVKSSRGSSDPRGVTCGAMSLSTEKVIVDHREYKKYTVECQEGSACPAAE 120

Qy        205 ESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWE 258
              |||||||||:|:|||||||||||||||||||||| ||||:|||||| ||||||
Db        121 ESLPIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWE 174


RESULT 10
Q9BG70
ID   Q9BG70      PRELIMINARY;      PRT;   150 AA.
AC   Q9BG70;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Interleukin 12 subunit p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Markus S., Baumgaertner W.;
RT   "Expression of canine interleukin-12 subunit p40 mRNA in a continuous
RT   macrophage cell line.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF333121; AAK01441.1; -.
DR   InterPro; IPR003600; Ig_like.
DR   SMART; SM00410; IG_like; 1.
FT   NON_TER       1       1
FT   NON_TER     150     150
SQ   SEQUENCE   150 AA;  16780 MW;  A867903EF16083BA CRC64;

  Query Match             45.3%;  Score 799;  DB 6;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 6e-64;
  Matches  150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         49 TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKE 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKE 60

Qy        109 DGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGV 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGV 120

Qy        169 TCGAVTLSAERVRVDNRDYKKYTVECQEGS 198
              |||||||||||||||||||||||||||||
Db        121 TCGAVTLSAERVRVDNRDYKKYTVECQEGS 150


RESULT 11
Q9TV09
ID   Q9TV09      PRELIMINARY;      PRT;   149 AA.
AC   Q9TV09;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Interleukin-12 p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RT   "Cloning and sequencing of canine IL-12 p40 mRNA.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF091134; AAD46992.1; -.
FT   NON_TER       1       1
FT   NON_TER     149     149
SQ   SEQUENCE   149 AA;  16453 MW;  20E2686B0AA37E26 CRC64;

  Query Match             43.5%;  Score 768;  DB 6;  Length 149;
  Best Local Similarity   98.6%;  Pred. No. 3.6e-61;
  Matches  146;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         69 LGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIF 128
              ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LGAGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIF 60

Qy        129 LKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYK 188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYN 120

Qy        189 KYTVECQEGSACPSAEESLPIEVVVDAI 216
              |||||||||||||||||||||||||||
Db        121 KYTVECQEGSACPSAEESLPIEVVVDAI 148


RESULT 12
Q9Z1Y8
ID   Q9Z1Y8      PRELIMINARY;      PRT;   169 AA.
AC   Q9Z1Y8;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   Interleukin 12p40 (Fragment).
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069279; PubMed=9824482;
RA   Wicher V., Scarozza A.M., Ramsingh A.I., Wicher K.;
RT   "Cytokine gene expression in skin of susceptible guinea-pig infected
RT   with Treponema pallidum.";
RL   Immunology 95:242-247(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99144670; PubMed=10025978;
RA   Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;
RT   "Spontaneous cytokine gene expression in normal guinea pig blood and
RT   tissues.";
RL   Cytokine 10:851-859(1998).
DR   EMBL; AF097507; AAC83805.1; -.
FT   NON_TER       1       1
FT   NON_TER     169     169
SQ   SEQUENCE   169 AA;  19128 MW;  0A2DE7480C1281F5 CRC64;

  Query Match             41.2%;  Score 727.5;  DB 11;  Length 169;
  Best Local Similarity   79.3%;  Pred. No. 1.8e-57;
  Matches  138;  Conservative   11;  Mismatches   20;  Indels    5;  Gaps    2;

Qy         91 HKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIST 150
              ||||:||||| ||:||||| |||||||||||  |  | ||||||::||||||||||||  |
Db          1 HKGGEVLSRSQLLLHKKEDEIWSTDILKEQKGSNGKTFLKCEARSYSGRFTCWWLTAFGT 60
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Qy        151 DLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIE 210
              |:|||||| ||| ||| |||||     ||||  ||::| ||:||||| ||||:||||||||
Db         61 DVKFSVKGSRGSSDPSGVTCG----EAERVSGDNQEY-KYSVECQEDSACPTAEESLPIE 115

Qy        211 VVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWS 264
              |||||||| |||||||||:|||||||||| ||||||  ||: ||||||||||||
Db        116 VVVDAIHKFKYENYTSSFYIRDIIKPDPPKNLQLKPSVNSQQVEVSWEYPDTWS 169


RESULT 13
O62779
ID   O62779      PRELIMINARY;      PRT;   143 AA.
AC   O62779;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 p40 subunit (Fragment).
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99322318; PubMed=10391845;
RA   Harley R., Helps C.R., Harbour D.A., Gruffydd-Jones T.J., Day M.J.;
RT   "Cytokine mRNA expression in lesions in cats with chronic
RT   gingivostomatitis.";
RL   Clin. Diagn. Lab. Immunol. 6:471-478(1999).
DR   EMBL; AF054607; AAC15980.1; -.
DR   InterPro; IPR002996; CR1A.
FT   NON_TER       1      1
FT   NON_TER     143    143
SQ   SEQUENCE   143 AA;  16122 MW;  E107DF253F5D4D40 CRC64;

  Query Match             39.4%;  Score 695;  DB 6;  Length 143;
  Best Local Similarity   90.9%;  Pred. No. 1.2e-54;
  Matches  130;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         90 CHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIS 149
              |||| :||| | :|| :|||||||||||:|||||||||||||||||||||||||||||
Db          1 CHKGXEVLSHSXVLIXEKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAIS 60

Qy        150 TDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPI 209
              |||||:|||||| |||||||||| |||||:|||||||||||||||||||:|||||||
Db         61 TDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPI 120

Qy        210 EVVVDAIHKLKYENYTSSFFIRD 232
              |||||||||||||||||||||||
Db        121 EVVVDAIHKLKYENYTSSFFIRD 143


RESULT 14
O70328
ID   O70328      PRELIMINARY;      PRT;   132 AA.
AC   O70328;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE   Interleukin-12p40 (Fragment).
OS   Mesocricetus auratus (Golden hamster).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC   Mesocricetus.
OX   NCBI_TaxID=10036;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SPLEEN;
RX   MEDLINE=98234044; PubMed=9573100;
RA   Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT   "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT   analysis of cytokine mRNA expression in experimental visceral
RT   leishmaniasis.";
RL   Infect. Immun. 66:2135-2142(1998).
DR   EMBL; AF046211; AAC40096.1; -.
FT   NON_TER       1      1
FT   NON_TER     132    132
SQ   SEQUENCE   132 AA;  14882 MW;  57355AEA95E57D7E CRC64;

  Query Match             28.7%;  Score 507;  DB 11;  Length 132;
  Best Local Similarity   70.5%;  Pred. No. 8e-38;
  Matches   93;  Conservative   18;  Mismatches   21;  Indels    0;  Gaps    0;

Qy         95 KVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKF 154
              | || | ||:||||:||||||||||:||: ||| |||||| ||||||||||||||||||
Db          1 KTLSHSRLLLHKKENGIWSTDILKDQKDPKNKTFLKCEAANYSGRFTCWWLTAISTDLKF 60

Qy        155 SVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVD 214
              :||||   || : ||||| :||||:| || :||:||:| |||   ||:|||:||| :|::
Db         61 NVKSSSSSSDSRAVTCGAASLSAEKVTVDRKDYQKYSVACQEDITCPTAEETLPIGLVME 120

Qy        215 AIHKLKYENYTS 226
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Db        121 AQHKYKYENYST 132


RESULT 15
P97731
ID   P97731      PRELIMINARY;      PRT;   111 AA.
AC   P97731;
DT   01-MAY-1997 (TrEMBLrel. 03, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin-12 (Fragment).
OS   Rattus sp.
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10118;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96285631; PubMed=8693286;
RA   Mathieson P.W., Gillespie K.M.;
RT   "Cloning of a partial cDNA for rat interleukin-12 (IL-12) and analysis
RT   of IL-12 expression in vivo.";
RL   Scand. J. Immunol. 44:11-14(1996).
DR   EMBL; S82489; AAB37425.2; -.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
KW   Immunoglobulin domain.
FT   NON_TER     111    111
SQ   SEQUENCE   111 AA;  12689 MW;  BFE9372413B20CB8 CRC64;

  Query Match             24.9%;  Score 438.5;  DB 11;  Length 111;
  Best Local Similarity   73.5%;  Pred. No. 8.9e-32;
  Matches   83;  Conservative   10;  Mismatches   17;  Indels    3;  Gaps    1;

Qy         21 MAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVK 80
              ||:|||||||||||:|| |||||| | ||| :|||||| ||| |   |:||||||| |:
Db          1 MAMWELEKDVYVVEVDWRPDAPGETVTLTCDSPEEDDIHWTSDQRRGVIGSGKTLTITVR 60

Qy         81 EFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEA 133
              || ||||||||:||: || | ||:||||:|||||:||   |  ||| ||||||
Db         61 EFLDAGQYTCHRGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEA 110


Search completed: July 15, 2003, 11:06:10
Job time : 30.1539 secs
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:59:19 ; Search time 11.2854 Seconds
(without alignments)
857.760 Million cell updates/sec

Title: US-09-917-265-59
Perfect score: 1764
Sequence: 1 MHPQQLVISWFSLVLLASPL.....QARDRYYSSSWSDWASVSCS 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1502.5	85.2	540	2	US-08-751-767A-8	Sequence 8, Appli
2	1502.5	85.2	540	2	US-08-751-767A-10	Sequence 10, Appl
3	1501.5	85.1	328	1	US-08-265-087-2	Sequence 2, Appli
4	1501.5	85.1	328	1	US-08-186-529-2	Sequence 2, Appli
5	1501.5	85.1	328	1	US-08-621-493-2	Sequence 2, Appli
6	1501.5	85.1	328	1	US-08-640-386A-2	Sequence 2, Appli
7	1501.5	85.1	328	2	US-08-965-688-2	Sequence 2, Appli
8	1501.5	85.1	328	2	US-08-751-767A-4	Sequence 4, Appli
9	1501.5	85.1	328	4	US-09-260-173-2	Sequence 2, Appli
10	1422.5	80.6	519	2	US-08-751-767A-12	Sequence 12, Appl
11	1418.5	80.4	306	1	US-08-424-682A-1	Sequence 1, Appli
12	1142.5	64.8	335	2	US-08-385-335A-15	Sequence 15, Appl
13	1132.5	64.2	335	2	US-08-659-206A-3	Sequence 3, Appli
14	1132.5	64.2	335	2	US-08-659-206A-6	Sequence 6, Appli
15	193	10.9	323	6	5171840-6	Patent No. 5171840
16	193	10.9	323	6	5480796-6	Patent No. 5480796
17	193	10.9	344	6	5171840-7	Patent No. 5171840
18	193	10.9	344	6	5480796-7	Patent No. 5480796
19	193	10.9	468	4	US-08-795-473B-5	Sequence 5, Appli
20	193	10.9	468	4	US-09-439-856-5	Sequence 5, Appli
21	193	10.9	468	6	5171840-2	Patent No. 5171840
22	193	10.9	468	6	5480796-2	Patent No. 5480796
23	170	9.6	372	1	US-07-865-878A-4	Sequence 4, Appli
24	170	9.6	372	1	US-07-676-647-2	Sequence 2, Appli
25	170	9.6	372	1	US-08-449-329-2	Sequence 2, Appli
26	170	9.6	372	2	US-08-445-073-2	Sequence 2, Appli
27	170	9.6	372	2	US-08-585-258-2	Sequence 2, Appli
28	170	9.6	372	2	US-08-603-010-4	Sequence 4, Appli
29	170	9.6	372	4	US-09-211-590-2	Sequence 2, Appli
30	170	9.6	372	5	PCT-US91-03896-2	Sequence 2, Appli
31	149.5	8.5	422	4	US-09-151-102-2	Sequence 2, Appli
32	149.5	8.5	422	4	US-08-929-846-2	Sequence 2, Appli
33	146.5	8.3	432	4	US-08-702-665A-3	Sequence 3, Appli
34	146.5	8.3	441	4	US-09-151-102-4	Sequence 4, Appli
35	146.5	8.3	441	4	US-08-929-846-4	Sequence 4, Appli
36	145	8.2	423	4	US-08-702-665A-5	Sequence 5, Appli
37	129	7.3	229	1	US-08-383-750-6	Sequence 6, Appli
38	124.5	7.1	230	5	PCT-US93-09636-6	Sequence 6, Appli
39	121.5	6.9	386	6	5171840-5	Patent No. 5171840
40	121.5	6.9	386	6	5480796-5	Patent No. 5480796
41	120.5	6.8	210	4	US-09-043-785-1	Sequence 1, Appli
42	118	6.7	229	2	US-08-684-687-2	Sequence 2, Appli
43	118	6.7	229	3	US-08-352-678-6	Sequence 6, Appli
44	109.5	6.2	201	6	5171840-11	Patent No. 5171840
45	107.5	6.1	592	4	US-09-000-145-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-08-751-767A-8
; Sequence 8, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, ROBERT J.
; APPLICANT: GRANT, HUGH
; APPLICANT: MACDONALD, IAN D.
; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,767A
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164091
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-751-767A-8

Query Match 85.2%; Score 1502.5; DB 2; Length 540;
Best Local Similarity 84.8%; Pred. No. 1.3e-140;
Matches 279; Conservative 22; Mismatches 27; Indels 1; Gaps 1;

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Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
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Db          1 MGHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
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Db         61 TLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Db        121 KEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
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Db        181 RGDNKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPK 239

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
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Db        240 NLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVI 299

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
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Db        300 CRKNASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 2
US-08-751-767A-10
; Sequence 10, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  540 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-10

  Query Match             85.2%;  Score 1502.5;  DB 2;  Length 540;
  Best Local Similarity   84.8%;  Pred. No. 1.3e-140;
  Matches  279;  Conservative   22;  Mismatches   27;  Indels    1;  Gaps    1;

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              |  |||||||||| |||||:|||||:||||||||||:|||||||||||| ||||| |||
Db          1 MGHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              |  |||||||||||||||||||||||||||||:||| |||||:|||||||||||||:|
Db         61 TLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              || ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||
Db        121 KEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              | ||::| :|:|||||| ||||:|||||||||:|||:|||||||||||||||||||||
Db        181 RGDNKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPK 239

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              |||||||||| ||||||||||||||||||||||:| |||: ||||||:  ||||| |:
Db        240 NLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVI 299

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              | |:| | |:|:|||||||||:|||| ||
Db        300 CRKNASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 3
US-08-265-087-2
; Sequence 2, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-265-087-2

  Query Match             85.1%;  Score 1501.5;  DB 1;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 7.9e-141;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| |||||:|||||:|||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||||||||||||||||||||||||:||| |||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123
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Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:||||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:|||| |||:|||||||||:|||:|||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:|||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 4
US-08-186-529-2
; Sequence 2, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-186-529-2

  Query Match             85.1%;  Score 1501.5;  DB 1;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 7.9e-141;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| ||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| |||||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:||||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:|||| |||:|||||||||:|||:|||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:|||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 5
US-08-621-493-2
; Sequence 2, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-621-493-2

  Query Match             85.1%;  Score 1501.5;  DB 1;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 7.9e-141;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| ||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| |||||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
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           ||| ||:|||||||||||||||| ||||| |||||||| ||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:|||||||||:|||:|||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||:| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:||||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 6
US-08-640-386A-2
; Sequence 2, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-640-386A-2

  Query Match             85.1%;  Score 1501.5;  DB 1;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 7.9e-141;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| |||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| |||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||| ||||| |||||||| ||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:|||||||||:|||:|||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||:| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:||||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 7
US-08-965-688-2
; Sequence 2, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-965-688-2

  Query Match             85.1%;  Score 1501.5;  DB 2;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 7.9e-141;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| |||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| |||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123
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Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:||||||||||||||||| ||||| |||||||| |||||||||| ||||||||
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:|||||| |||||:|||||||||:|||:|||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||||:| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:||||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328
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RESULT 8
US-08-751-767A-4
; Sequence 4, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-4

  Query Match             85.1%;  Score 1501.5;  DB 2;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 7.9e-141;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| ||||||:|||||:||||||||||:|||||||||||| ||||| |||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:||||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183
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Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:|||||| |||||:|||||||||:|||:|||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||||:| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:||||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328
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RESULT 9
US-09-260-173-2
; Sequence 2, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;       APPLICANT: Scott, Phillip
;                  Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 328 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-260-173-2

  Query Match             85.1%;  Score 1501.5;  DB 4;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 7.9e-141;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| ||||||:|||||:||||||||||:|||||||||||| ||||| |||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63
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Qy          64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
               ||||||||||||||||||||||||||||||:||| ||||:||||||||||||||:|||
Db          64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy         124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
               ||| ||:|||||||||||||||| ||||| |||||||| |||||||| |||||||| |
Db         124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy         184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
               |::| :|:||||| |||||:||||||||:|||:|||||||||||||||||||| |||
Db         184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy         244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
               |||||||| |||||||||||||||||||||:| |||: ||||||:  ||||| |:| |
Db         243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy         304 DAKIRVQARDRYYSSSWSDWASVSCS 329
               :| | |:|:|||||||||:|||| ||
Db         303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 10
US-08-751-767A-12
; Sequence 12, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  519 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-12

  Query Match           80.6%;  Score 1422.5;  DB 2;  Length 519;
  Best Local Similarity   85.1%;  Pred. No. 1.1e-132;
  Matches  262;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          22 AIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKE 81
               |||||:|||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||
Db           1 AIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKE 60

Qy          82 FGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFT 141
               |||||||||||||:||| ||||:||||||||||||||:||| ||| ||:||||||||||
Db          61 FGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFT 120

Qy         142 CWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP 201
               ||||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||
Db         121 CWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACP 179

Qy         202 SAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPD 261
               :|||||||||:|||:|||||||||||||||||||||||| |||||||||| |||||||||
Db         180 AAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPD 239

Qy         262 TWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 321
               |||||||||||||:| |||: ||||||:  ||||| |:| |:| | |:|:|||||||||
Db         240 TWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWS 299

Qy         322 DWASVSCS 329
               :|||| ||
Db         300 EWASVPCS 307


RESULT 11
US-08-424-682A-1
; Sequence 1, Application US/08424682A
; Patent No. 5650492
;  GENERAL INFORMATION:
;    APPLICANT:  Gately, Maurice K
;    APPLICANT:  Hakimi, John
;    APPLICANT:  Ling, Ping
;    TITLE OF INVENTION:  P40 HOMODIMER OF INTERLEUKIN-12
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/424,682A
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/087,832
;      FILING DATE:  02-JUL-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  306 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-424-682A-1

  Query Match           80.4%;  Score 1418.5;  DB 1;  Length 306;
  Best Local Similarity   85.0%;  Pred. No. 1.2e-132;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82
               ||||:|||||||||:|||||||||||| ||||| |||| |||||||||||||||||||
Db           1 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 60

Qy          83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142
               |||||||||||:||| ||||:||||||||||||||:||| ||| ||:||||||||||||
Db          61 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 120
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Qy        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        121 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 179

Qy        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262
              |||||||||:|||:|||||||||||||||||||||||| |||||||||| ||||||||||
Db        180 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 239

Qy        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        240 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 299

Qy        323 WASVSCS 329
              |||| ||
Db        300 WASVPCS 306
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RESULT 12
US-08-385-335A-15
; Sequence 15, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-385-335A-15

  Query Match             64.8%;  Score 1142.5;  DB 2;  Length 335;
  Best Local Similarity   65.5%;  Pred. No. 3.3e-105;
  Matches  220;  Conservative   38;  Mismatches   65;  Indels   13;  Gaps    4;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              | ||:| ||||::||| |||||:||||||||||:|| |||||| | ||| |||||||||
Db          1 MGPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |   |:||||||||| |||| |||||||||||: || | ||:||||:|||||:||
Db         61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              |  ||| |||||| |||||||| ||   : ||||::|||    | : |||| :|||||:|
Db        118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKV 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              :| |||:||:| |||   ||:|||:|||||: ::|  : |||||::||||||||||||||
Db        178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
              |||:|||||: |||||||||:|||||||||| | :: | |  : |         |    |
Db        238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLV 296

Qy        293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
              :||| :| | |   : |||:||||:|| | || | |
Db        297 EKTSTEVQC-KGGNVCVQAQDRYYNSSCSKWACVPC 331
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RESULT 13
US-08-659-206A-3
; Sequence 3, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-3

  Query Match             64.2%;  Score 1132.5;  DB 2;  Length 335;
  Best Local Similarity   65.2%;  Pred. No. 3.3e-104;
  Matches  219;  Conservative   38;  Mismatches   66;  Indels   13;  Gaps    4;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              | ||:| ||||::||| |||||:||||||||||:|| |||||| | ||| |||||||||
Db          1 MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |   |:||||||||| |||| |||||||||||: || | ||:||||:|||||:||
Db         61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              |  ||| |||||| |||||||| ||   : ||||::|||    | : |||| :|||||:|
Db        118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKV 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              :| |||:||:| |||   ||:|||:|||||: ::|  : |||||::||||||||||||||
Db        178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237
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Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
              |||:||||||: |||||||||:|||||||||| | :: | |  : |        |    |
Db        238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLV 296

Qy        293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
              :||| :| | |   : |||:|| |:|| | || | |
Db        297 EKTSTEVQC-KGGNVCVQAQDRCYNSSCSKWACVPC 331


RESULT 14
US-08-659-206A-6
; Sequence 6, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-6

  Query Match             64.2%;  Score 1132.5;  DB 2;  Length 335;
  Best Local Similarity   65.2%;  Pred. No. 3.3e-104;
  Matches  219;  Conservative   38;  Mismatches   66;  Indels   13;  Gaps    4;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              | ||:| ||||::||| |||||:||||||||||||:|| |||||| | ||| |||||||||
Db          1 MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |   |:||||||| |||| |||||||||||: || | ||:||||:|||||:||
Db         61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              |  ||| |||||| |||||||| ||   : ||||::|||    | : ||||  :||||:|
Db        118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKV 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
               :| |||:||:| |||   ||:|||:||||: ::|  : ||||||||||||||||||
Db        178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
              |||:||||||: |||||||||:|||||||||| | :: | |  : |        |    |
Db        238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLV 296

Qy        293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
              :||| :| | |   : |||:|| |:|| | || | |
Db        297 EKTSTEVQC-KGGNVCVQAQDRCYNSSCSKWACVPC 331


RESULT 15
5171840-6
;Patent No. 5171840
;    APPLICANT: KISHIMOTO, TADAMITSU
;    TITLE OF INVENTION: RECEPTOR PROTEIN FOR HUMAN B CELL
;STIMULATORY FACTOR-2
;    NUMBER OF SEQUENCES: 11
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/298,694
;      FILING DATE: 19-JAN-1989
;SEQ ID NO:6:
;      LENGTH: 323
5171840-6

  Query Match             10.9%;  Score 193;  DB 6;  Length 323;
  Best Local Similarity   22.2%;  Pred. No. 4.9e-11;
  Matches   69;  Conservative   59;  Mismatches  113;  Indels   70;  Gaps   13;

Qy         42 PGEMVVLTCHTPEEDD---ITW------TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK 92
              ||: | |||   | :|   : |       :  |   | |: | ::  :  |:| |:|::
Db         39 PGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYR 98

Qy         93 GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW-------L 145
               |:      ||:          |:  |: :      | |  |:      | |       |
Db         99 AGRPAGTVHLLV----------DVPPEEPQ------LSCFRKSPLSNVVCEWGPRSTPSL 142

Qy        146 T--AISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS---AC 200
             |  |:    ||    :  | :|    |                   :|: | |: |   |
Db        143 TTKAVLLVRKFQNSPAEDFQEP----C------------------QYSQESQKFSCQLAV 180

Qy        201 PSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEY 259
              |  : |  |  :  |       : | :|    |::|||| |: :  : :| | : |:|:
Db        181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240

Qy        260 PDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDA------KIRVQARD 313
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Qy        314 RYYSSSWSDWA 324
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Search completed: July 15, 2003, 11:10:01
Job time : 12.2854 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 11:03:04 ; Search time 15.3606 Seconds
(without alignments)
2493.521 Million cell updates/sec

Title: US-09-917-265-59
Perfect score: 1764
Sequence: 1 MHPQQLVISWFSLVLLASPL.....QARDRYYSSSWSDWASVSCS 329

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1764	100.0	329	10	US-09-917-265-59	Sequence 59, Appl
2	1764	100.0	329	10	US-09-917-265-108	Sequence 108, App
3	1764	100.0	533	10	US-09-917-265-62	Sequence 62, Appl
4	1657	93.9	329	10	US-09-917-265-30	Sequence 30, Appl
5	1653	93.7	307	10	US-09-917-265-53	Sequence 53, Appl
6	1653	93.7	328	10	US-09-917-265-56	Sequence 56, Appl
7	1653	93.7	511	10	US-09-917-265-67	Sequence 67, Appl
8	1651	93.6	329	12	US-10-079-616-1	Sequence 1, Appli
9	1643	93.1	533	10	US-09-917-265-39	Sequence 39, Appl
10	1554	88.1	307	12	US-10-079-616-2	Sequence 2, Appli
11	1546	87.6	307	10	US-09-917-265-27	Sequence 27, Appl
12	1546	87.6	511	10	US-09-917-265-44	Sequence 44, Appl
13	1502.5	85.2	328	9	US-10-172-399-8	Sequence 8, Appli
14	1502.5	85.2	526	10	US-09-828-825-4	Sequence 4, Appli
15	1502.5	85.2	527	10	US-09-828-825-2	Sequence 2, Appli
16	1502.5	85.2	537	10	US-09-828-825-8	Sequence 8, Appli
17	1502.5	85.2	537	10	US-09-828-825-16	Sequence 16, Appl
18	1502.5	85.2	542	10	US-09-828-825-6	Sequence 6, Appli
19	1502.5	85.2	542	10	US-09-828-825-14	Sequence 14, Appl
20	1502.5	85.2	547	10	US-09-828-825-10	Sequence 10, Appl
21	1502.5	85.2	547	10	US-09-828-825-12	Sequence 12, Appl
22	1501.5	85.1	328	9	US-10-247-463-6	Sequence 6, Appli
23	1501.5	85.1	328	10	US-09-754-014-1	Sequence 1, Appli
24	1501.5	85.1	328	10	US-09-836-866-1	Sequence 1, Appli
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29	193	10.9	315	9	US-09-935-868-16	Sequence 16, Appl
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32	193	10.9	360	9	US-10-287-035-15	Sequence 15, Appl
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34	193	10.9	592	9	US-09-935-868-8	Sequence 8, Appli
35	193	10.9	592	9	US-10-287-035-8	Sequence 8, Appli
36	193	10.9	1158	9	US-09-935-868-26	Sequence 26, Appl
37	193	10.9	1158	9	US-10-287-035-26	Sequence 26, Appl
38	193	10.9	1168	9	US-09-935-868-24	Sequence 24, Appl
39	193	10.9	1168	9	US-10-287-035-24	Sequence 24, Appl
40	177.5	10.1	460	9	US-10-247-463-13	Sequence 13, Appl
41	149.5	8.5	422	9	US-10-247-463-11	Sequence 11, Appl
42	149.5	8.5	422	10	US-09-924-338-2	Sequence 2, Appli
43	148.5	8.4	432	9	US-10-247-463-10	Sequence 10, Appl
44	146.5	8.3	441	10	US-09-924-338-4	Sequence 4, Appli
45	129	7.3	229	9	US-10-000-776-10	Sequence 10, Appl

ALIGNMENTS

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RESULT 1
US-09-917-265-59
; Sequence 59, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-59

  Query Match           100.0%;  Score 1764;  DB 10;  Length 329;
  Best Local Similarity  100.0%;  Pred. No. 3.7e-139;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

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Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
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Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 2
US-09-917-265-108
; Sequence 108, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-108

  Query Match             100.0%;  Score 1764;  DB 10;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-139;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
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Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYPSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
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Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 3
US-09-917-265-62
; Sequence 62, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-62

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Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
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Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
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Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 4
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; Sequence 30, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-30

  Query Match             93.9%;  Score 1657;  DB 10;  Length 329;
  Best Local Similarity   93.6%;  Pred. No. 3.1e-130;
  Matches  308;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

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Db          1 MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
                || |||||||||||||||| |||||||||:||| | |||||||||||||:||
Db         61 TSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
                ||||||||||||||||||||||||||||||:|||||| |||||||||| |||||:|
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
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Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
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Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
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Db        301 CHKDAKIRVQARDRYYSSSWSNWASVSCS 329


RESULT 5
US-09-917-265-53
; Sequence 53, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
;   LENGTH: 307
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-53

  Query Match             93.7%;  Score 1653;  DB 10;  Length 307;
  Best Local Similarity   100.0%;  Pred. No. 6.1e-130;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82
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Qy         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142
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Db         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120

Qy        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202
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Db        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Qy        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262
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Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Qy        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322
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Db        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300

Qy        323 WASVSCS 329
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Db        301 WASVSCS 307


RESULT 6
US-09-917-265-56
; Sequence 56, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
;   LENGTH: 328
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-56

  Query Match             93.7%;  Score 1653;  DB 10;  Length 328;
  Best Local Similarity   93.6%;  Pred. No. 6.6e-130;
  Matches  307;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
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Db          1 MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITW 60

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Db         61 TSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||||||||||||||||||||||||||||||||| :| |||||||||||| ||||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSC 328
              |||||||||||||||||||:||||||
Db        301 CHKDAKIRVQARDRYYSSSWSNWASVSC 328


RESULT 7
US-09-917-265-67
; Sequence 67, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-67

  Query Match             93.7%;  Score 1653;  DB 10;  Length 511;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-129;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60

Qy         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120

Qy        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Qy        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Qy        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300

Qy        323 WASVSCS 329
                 |||||||
Db        301 WASVSCS 307


RESULT 8
US-10-079-616-1
; Sequence 1, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 329 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: protein
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-079-616-1

  Query Match             93.6%;  Score 1651;  DB 12;  Length 329;
  Best Local Similarity   93.3%;  Pred. No. 9.7e-130;
  Matches  307;  Conservative   10;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
                 ||||||||:|| ||||| |||||||||:|||||||||||||||||||:|||||||||
Db          1 MHPQQLVIAWFYLVLLAPPLMAIWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
                 || |||||||||||||||| ||||||||||:||| | |||||||||||||||:||
Db         61 TSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
                 ||||||||||||||||||||||||||||||||:|||||| |||||||||| |||||:|
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
                 ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
                 |||||||||||||||||||||||||||||||| :| |||||||||||| |||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
                 |||||||||||||||||||||:|||||||
Db        301 CHKDAKIRVQARDRYYSSSWSNWASVSCS 329


RESULT 9
US-09-917-265-39
; Sequence 39, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-39

  Query Match             93.1%;  Score 1643;  DB 10;  Length 533;
  Best Local Similarity   93.0%;  Pred. No. 8.6e-129;
  Matches  306;  Conservative   10;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
                 ||||||||:| ||||| |||||||||:|||||||||||||||||||:|||||||||
Db          1 MHPQQLVIAWLSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
                 || |||||||||||||||| ||||||||||:||| | |||||||||||||||:||
Db         61 TSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
                 ||||||||||||||||||||||||||||||||:|||||| |||| ||||| |||||:|
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
                 ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
                 |||||||||||||||||||||||||||||||| :| |||||||||||| |||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
                 |||||||||||||||||||||:|||||||
Db        301 CHKDAKIRVQARDRYYSSSWSNWASVSCS 329
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```
RESULT 10
US-10-079-616-2
; Sequence 2, Application US/10079616
; Patent No. US20020107366A1
;  GENERAL INFORMATION:
;       APPLICANT: IMAMURA, Takayuki
;                  MAEDA, Hiroaki
;                  FUJIYASU, Takeshi
;                  IMAGAWA, Yoshitaka
;                  TOKIYOSHI, Sachio
;       TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;       NUMBER OF SEQUENCES: 26
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: BROWDY AND NEIMARK
;            STREET: 419 Seventh Street, N.W., Suite 300
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: USA
;            ZIP: 20004
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/079,616
;            FILING DATE: 22-Feb-2002
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 09/011,143
;            FILING DATE: 04-FEB-1998
;            APPLICATION NUMBER: PCT/JP97/01824
;            FILING DATE: 29-MAY-1997
;            APPLICATION NUMBER: JP 165249/1996
;            FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;            NAME: BROWDY, Roger L.
;            REGISTRATION NUMBER: 25,618
;            REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 202-628-5197
;            TELEFAX: 202-737-3528
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 307 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-079-616-2

  Query Match             88.1%;  Score 1554;  DB 12;  Length 307;
  Best Local Similarity   93.8%;  Pred. No. 1.1e-121;
  Matches  288;  Conservative    9;  Mismatches   10;  Indels    0;  Gaps    0;

Qy         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82
              ||||||:|||||||||||||||||||||:|||||||||| |||||||||||||||||||
Db          1 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 60

Qy         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142
               |||||||||||:||| | |||||||||||||||||:|||||||||||||||||||||||
Db         61 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 120

Qy        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202
              ||||||||||||:|||||| |||||||||| |||||:|||||||||||||||||||||:
Db        121 WWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 180

Qy        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 240

Qy        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322
              |||||||||||| :| |||||||||||| |||||||||||||||||||||||||||||:
Db        241 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 300

Qy        323 WASVSCS 329
              |||||||
Db        301 WASVSCS 307


RESULT 11
US-09-917-265-27
; Sequence 27, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 307
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-27

  Query Match             87.6%;  Score 1546;  DB 10;  Length 307;
  Best Local Similarity   93.5%;  Pred. No. 5.1e-121;
  Matches  287;  Conservative    9;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82
              ||||||:|||||||||||||||||||||:|||||||||| |||||||||||||||||||
Db          1 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 60

Qy         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142
               |||||||||||:||| | |||||||||||||||||:|||||||||||||||||||||||
Db         61 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 120

Qy        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202
              ||||||||||||:|||||| |||||||||| |||||:|||||||||||||||||||||:
Db        121 WWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 180

Qy        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 240

Qy        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322
              |||||||||||| :| |||||||||||| |||||||||||||||||||||||||||||:
Db        241 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 300

Qy        323 WASVSCS 329
              |||||||
Db        301 WASVSCS 307


RESULT 12
US-09-917-265-44
; Sequence 44, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
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;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-44

  Query Match             87.6%;  Score 1546;  DB 10;  Length 511;
  Best Local Similarity   93.5%;  Pred. No. 1e-120;
  Matches  287;  Conservative    9;  Mismatches   11;  Indels    0;  Gaps    0;

Qy         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82
              ||||||:||||||||||||||||||||:||||||||||| ||||||||||||||||||||
Db          1 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 60

Qy         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142
               |||||||||||:||| | ||||||||||||||||:||||||||||||||||||||||||
Db         61 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 120

Qy        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202
              ||||||||||||:|||||| |||| ||||| |||||:|||||||||||||||||||||||:
Db        121 WWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 180

Qy        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262
              ||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 240

Qy        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322
              |||||||||||| :| |||||||||||| ||||||||||||||||||||||||||||||:
Db        241 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 300

Qy        323 WASVSCS 329
              |||||||
Db        301 WASVSCS 307


RESULT 13
US-10-172-399-8
; Sequence 8, Application US/10172399
; Publication No. US20030045495A1
; GENERAL INFORMATION:
;  APPLICANT: Li, Chuan-Yuan
;  APPLICANT:  Dewhirst, Mark
;  APPLICANT:  Huang, Qian
;  TITLE OF INVENTION: A METHOD FOR SELECTIVE EXPRESSION OF THERAPEUTIC GENES BY HYPERTH
;  FILE REFERENCE: 180-129
;  CURRENT APPLICATION NUMBER: US/10/172,399
;  CURRENT FILING DATE:  2002-06-14
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8
;   LENGTH: 328
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-172-399-8

  Query Match             85.2%;  Score 1502.5;  DB 9;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 2.3e-117;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| |||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||| ||||| |||||||| |||||||||| ||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:|||||||||:|||:|||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:|||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 14
US-09-828-825-4
; Sequence 4, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 526
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-4

  Query Match             85.2%;  Score 1502.5;  DB 10;  Length 526;
  Best Local Similarity   85.3%;  Pred. No. 4.4e-117;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

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Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
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Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
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Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
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Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
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Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
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; Sequence 2, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
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;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 527
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-09-828-825-2

  Query Match             85.2%;  Score 1502.5;  DB 10;  Length 527;
  Best Local Similarity   85.3%;  Pred. No. 4.4e-117;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
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Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
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Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
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Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
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Job time : 16.3606 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 06:24:59 ; Search time 88.1704 Seconds
(without alignments)
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Perfect score: 1599
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1219.4	76.3	1623	2	US-08-751-767A-9	Sequence 9, Appli
2	1219.4	76.3	6139	2	US-08-751-767A-7	Sequence 7, Appli
3	1172.4	73.3	1560	2	US-08-751-767A-11	Sequence 11, Appl
4	983.8	61.5	990	4	US-09-079-984A-11	Sequence 11, Appl
5	969.4	60.6	990	4	US-09-079-984A-1	Sequence 1, Appli
6	772.6	48.3	987	1	US-08-186-529-1	Sequence 1, Appli
7	772.6	48.3	987	1	US-08-640-386A-1	Sequence 1, Appli
8	772.6	48.3	1018	2	US-08-184-009-194	Sequence 194, App
9	772.6	48.3	1018	2	US-08-458-356-194	Sequence 194, App
10	772.6	48.3	1018	4	US-08-460-736-194	Sequence 194, App
11	772.6	48.3	1399	2	US-08-751-767A-3	Sequence 3, Appli
12	772.6	48.3	2362	1	US-08-265-087-1	Sequence 1, Appli
13	772.6	48.3	2362	1	US-08-621-493-1	Sequence 1, Appli
14	772.6	48.3	2362	2	US-08-965-688-1	Sequence 1, Appli
15	772.6	48.3	2362	4	US-09-260-173-1	Sequence 1, Appli
16	771	48.2	987	4	US-08-848-760B-24	Sequence 24, Appl
17	771	48.2	1870	4	US-09-310-842-4	Sequence 4, Appli
18	771	48.2	2318	4	US-09-851-062-3	Sequence 3, Appli
19	545	34.1	669	4	US-09-079-984A-12	Sequence 12, Appl
20	541.8	33.9	669	4	US-09-079-984A-2	Sequence 2, Appli
21	511.6	32.0	1061	2	US-08-385-335A-13	Sequence 13, Appl
22	510	31.9	6295	2	US-08-659-206A-4	Sequence 4, Appli
23	510	31.9	7287	2	US-08-659-206A-1	Sequence 1, Appli
24	471.4	29.5	660	1	US-08-186-529-3	Sequence 3, Appli
25	471.4	29.5	660	1	US-08-640-386A-3	Sequence 3, Appli
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28	471.4	29.5	1316	4	US-09-851-520-3	Sequence 3, Appli
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33	469.8	29.4	1645	4	US-09-310-842-2	Sequence 2, Appli
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36	468.2	29.3	721	4	US-08-460-736-199	Sequence 199, App
37	468.2	29.3	1026	2	US-08-751-767A-1	Sequence 1, Appli
38	297	18.6	713	2	US-08-385-335A-10	Sequence 10, Appl
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c 40	39.4	2.5	625	4	US-09-328-111-593	Sequence 593, App
41	34.2	2.1	2768	1	US-08-321-478-1	Sequence 1, Appli
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43	34.2	2.1	2768	1	US-08-321-478-5	Sequence 5, Appli
44	33.8	2.1	1921	3	US-08-482-677-3	Sequence 3, Appli
45	33.8	2.1	1926	1	US-08-152-019A-43	Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-08-751-767A-9
; Sequence 9, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, ROBERT J.
; APPLICANT: GRANT, HUGH
; APPLICANT: MACDONALD, IAN D.
; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,767A
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164091
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1623 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1620
US-08-751-767A-9

Query Match 76.3%; Score 1219.4; DB 2; Length 1623;
Best Local Similarity 85.6%; Pred. No. 0;
Matches 1390; Conservative 0; Mismatches 206; Indels 27; Gaps 2;

Qy 1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

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Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
Db        181 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
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Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
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Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
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Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Db       1198 ACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAAT 1257

Qy       1237 TCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTT 1296
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Db       1318 ATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTC 1377

Qy       1357 AAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAAC 1416
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RESULT 2
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; Sequence 7, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, ROBERT J.
; APPLICANT: GRANT, HUGH
; APPLICANT: MACDONALD, IAN D.
; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,767A
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164091
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 7:

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;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  6139 base pairs
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;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  3222..4841
US-08-751-767A-7

  Query Match            76.3%;  Score 1219.4;  DB 2;  Length 6139;
  Best Local Similarity  85.6%;  Pred. No. 0;
  Matches 1390;  Conservative    0;  Mismatches  206;  Indels   27;  Gaps    2;

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Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
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Db       3702 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 3761

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Db       3879 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 3938

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              ||| |||||||||||||| || |||||||||| ||||||||||||||||| |||||
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              |||||||||| || |||||||||||||||||||||||||| ||| | |||| |||||||
Db       3999 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 4058

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| |

Db       4059 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 4118

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| ||| |||||| || |||||| |||| |||||||||||||| ||||| |||
Db       4119 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 4178

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGT---------------------- 996
              ||||| |||||||||||| | ||||||||||||||
Db       4179 AGCGAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGC 4238

Qy        997 GGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTG 1056
              || |||||    |||||| | ||     | ||||||  ||| || ||||||| |||  |
Db       4239 GGTGGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTT 4298

Qy       1057 AACCACTCCCAAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACT 1116
              |||||||||||| | || |||| |||||||||||||| ||| ||||||||||||||||||
Db       4299 CACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACT 4358

Qy       1117 CTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAA 1176
              |||||||| ||  | |||||||| |||||||||||||||||||||||||||||| ||||||
Db       4359 CTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAA 4418

Qy       1177 ACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCT 1236
              |||||||||||||||||||| |||||| |||||||||||| ||||||||||||||   |
Db       4419 ACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAAT 4478

Qy       1237 TCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTT 1296
              |||||||||| |||||| |||||||| ||||||||||||||||  ||||| |||||||
Db       4479 TCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTT 4538

Qy       1297 ATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTC 1356
              |||| || |||||||||||| || || ||||| |||||||||||||||||| |||| |||
Db       4539 ATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTC 4598

Qy       1357 AAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAAC 1416
              ||| ||||||| |||||||| | |||||||| |||||||||||||||| |||||||||
Db       4599 AAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAAC 4658

Qy       1417 ATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCA 1476
              |||||| ||| ||| |||||||||| | ||||||||||||||||||||| ||||||||||
Db       4659 ATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCA 4718

Qy       1477 CAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 1536
              || |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db       4719 CAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTT 4778

Qy       1537 CTTCATGCTTTCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCT 1596
              |||||||||||||||||||| || ||||| ||  | ||| ||| |  |||  |||| ||
Db       4779 CTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCT 4838

Qy       1597 TCC 1599
              |||
Db       4839 TCC 4841


RESULT 3
US-08-751-767A-11
; Sequence 11, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
```

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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1560 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1557
US-08-751-767A-11

  Query Match             73.3%;  Score 1172.4;  DB 2;  Length 1560;
  Best Local Similarity   85.7%;  Pred. No. 0;
  Matches 1337;  Conservative    0;  Mismatches  196;  Indels   27;  Gaps    2;

Qy         64 GCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCC 123
              |||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || ||||||
Db          1 GCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGATGCC 60

Qy        124 CCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACC 183
              || ||||||||||||||||||||||  | ||||||||||||||  ||||| ||||||
Db         61 CCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGGACC 120

Qy        184 TCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAA 243
              |  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||||
Db        121 TTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAAGAG 180

Qy        244 TTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTC 303
              |||||||||||||||||||| ||||| || ||||||||| ||||||| |||| || |||
Db        181 TTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCGCTC 240

Qy        304 CTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAA 363
              ||| || |||||||||| ||||||||||||||||||||||||||||| ||||||| ||||||
Db        241 CTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAGAAA 300

Qy        364 GAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACA 423
              ||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||||||
Db        301 GAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTCACC 360

Qy        424 TGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGC 483
              |||||||||||||||| |||||||||||||||||| |||||||||||||| |||||||||
Db        361 TGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGAGGC 420

Qy        484 TTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGA 543
              |  |||||||||||||||||||| || ||||| |  ||||| || |||||||| ||||||
Db        421 TCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTCAGA 480

Qy        544 GTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCC 603
              | |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||||
Db        481 GGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGCCCA 537

Qy        604 TCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTAT 663
              |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||||||
Db        538 GCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAGTAT 597

Qy        664 GAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAAC 723
              |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||  |||

Db        598 GAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAGAAC 657

Qy        724 CTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGAC 783
              ||||||||||||||||| || |||||||||| |||||||||||||||| ||||| |||
Db        658 TTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCTGAC 717

Qy        784 ACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAG 843
              |||||||| || ||||||||||||||||||||||||||| ||| | |||| ||||||||||
Db        718 ACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGCAAG 777

Qy        844 AACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGC 903
              | ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| | |||
Db        778 AGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATCTGC 837

Qy        904 CACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGC 963
              | |||  |||||| ||  |||||| |||| |||||||||||||| ||||| ||||||
Db        838 CGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGGAGC 897

Qy        964 GACTGGGCATCTGTGTCATGCAGTGGTGGCGGT----------------------GGC 999
              || |||||||||||| | ||||||||||||||                      ||
Db        898 GAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGCGGTGGCGGAAGCGGCGGT 957

Qy       1000 GGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAAC 1059
              |||||    |||||| | ||     | ||||||  ||| || ||||||| |||  |  ||
Db        958 GGCGGCAGCAGAAACCTCCCCCTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCAC 1017

Qy       1060 CACTCCCAAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTA 1119
              |||||||||| | || |||| ||||||||||| ||| ||||||||||||||||||||
Db       1018 CACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTA 1077

Qy       1120 GAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACC 1179
              ||||| ||  | |||||||| ||||||||||||||||||||||||||||| |||||||||
Db       1078 GAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACC 1137

Qy       1180 AGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCC 1239
              |||||||||||||||| |||||| |||||||||||| ||||||||||||||   ||||
Db       1138 AGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCC 1197

Qy       1240 AGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATG 1299
              ||||||| |||||| |||||||| |||||||||||||||||  ||||| ||||||||||
Db       1198 AGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATG 1257

Qy       1300 ACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAG 1359
              | || |||||||||||| || || ||||| |||||||||||||||||| |||| ||||||
Db       1258 ATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAG 1317

Qy       1360 GCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATG 1419
              ||||||| ||||||||| | |||||||| |||||||||||||||| ||||||||||||
Db       1318 ACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATG 1377

Qy       1420 CTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAG 1479
              ||| ||| ||| |||||||||| | ||||||||||||||||||||| ||||||||||||
Db       1378 CTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAA 1437

Qy       1480 AAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTT 1539
              |||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db       1438 AAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTT 1497

Qy       1540 CATGCTTTCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
              |||||||||||||||| || ||||| ||  | ||| ||| |  |||  |||| |||||
Db       1498 CATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAATGCTTCC 1557


RESULT 4
US-09-079-984A-11
; Sequence 11, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
```

```
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-11

  Query Match             61.5%;  Score 983.8;  DB 4;  Length 990;
  Best Local Similarity   99.8%;  Pred. No. 6.8e-301;
  Matches  985;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||||||| |||||||
Db        961 AGCGACTGGGCATCTGTGTCCTGCAGT 987


RESULT 5
US-09-079-984A-1
; Sequence 1, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
```

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;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  990 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 987
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-1

  Query Match             60.6%;  Score 969.4;  DB 4;  Length 990;
  Best Local Similarity   98.9%;  Pred. No. 2.4e-296;
  Matches  976;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| ||||||||||||||||||||||||||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              |||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db        421 ACATGCTGGTGGCTGAGCGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        721 AACCTGCAGCTGAAGCCATTGGAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              |||||||||||||||||| | ||||||
Db        961 AGCGACTGGGCATCTGTGCCCTGCAGT 987


RESULT 6
US-08-186-529-1
; Sequence 1, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-186-529-1

  Query Match             48.3%;  Score 772.6;  DB 1;  Length 987;
  Best Local Similarity   87.1%;  Pred. No. 4e-234;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
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Db         61 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||||  ||| |||| ||||| ||||| ||||||||||||||||||
Db        181 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||||| ||||| || ||||||||| ||||||| ||||  ||
Db        241 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||||| |||||||| |||
Db        301 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        361 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        421 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        481 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        541 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 597

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| ||||||||||  ||||||||||||||
Db        598 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 657

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||||| ||||||||||||| ||||||||||
Db        658 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 717

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||| || |||||||||| |||||||||||||||||| |||||
Db        718 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 777

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || |||||||||||||||||||||||| ||| | |||| |||||||
Db        778 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 837

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        838 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 897

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  |||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db        898 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 957

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        958 AGCGAATGGGCATCTGTGCCCTGCAGT 984


RESULT 7
US-08-640-386A-1
; Sequence 1, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  G1 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  987 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..987
US-08-640-386A-1

  Query Match             48.3%;  Score 772.6;  DB 1;  Length 987;
  Best Local Similarity   87.1%;  Pred. No. 4e-234;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db          1 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| |||||||||||||| ||||| ||||| ||| | || |||
Db         61 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        121 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||||  ||| |||| ||||| ||||| ||||||||||||||||||
Db        181 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||||| ||||| || ||||||||| ||||||| ||||  ||
Db        241 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||||| |||||||| |||
Db        301 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        361 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
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Db        421 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| ||||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        481 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        541 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 597

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db        598 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 657

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||| ||||||||||||| |||||||||
Db        658 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 717

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||| || |||||||||| |||||||||||||||| |||||
Db        718 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 777

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || ||||||||||||||||||||||| ||| | |||| |||||||
Db        778 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 837

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  ||||||||||||||||| |||| |
Db        838 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 897

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  |||||| ||  |||||| ||||  |||||||||||||| |||| |||
Db        898 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 957

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        958 AGCGAATGGGCATCTGTGCCCTGCAGT 984


RESULT 8
US-08-184-009-194
; Sequence 194, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-194

  Query Match             48.3%;  Score 772.6;  DB 2;  Length 1018;
  Best Local Similarity   87.1%;  Pred. No. 4.1e-234;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         32 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 91

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| |||||||||||||| ||||| ||||| ||| | || |||
Db         92 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 151

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||  | ||||||||||||||  ||||| |||
Db        152 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 211

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  | |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        212 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 271

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| ||||| || |||||||| ||||||| |||| · ||
Db        272 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 331

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| |||||||||||||||||||||||| |||||||| |||
Db        332 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 391

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        392 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 451

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        452 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 511

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        512 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 571

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        572 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 628

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db        629 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 688

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        689 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 748

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||| || |||||||||| |||||||||||||||| |||||
Db        749 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 808

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || |||||||||||||||||||||||| ||| | |||| |||||||
Db        809 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 868

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        869 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 928
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  ||||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db        929 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 988

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        989 AGCGAATGGGCATCTGTGCCCTGCAGT 1015


RESULT 9
US-08-458-356-194
; Sequence 194, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-194

  Query Match             48.3%;  Score 772.6;  DB 2;  Length 1018;
  Best Local Similarity   87.1%;  Pred. No. 4.1e-234;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  ||||||||||||||||| ||||||||||| ||||| ||||| |||||||||
Db         32 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 91

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              ||||||||||||||||| ||||||||||||||| ||||| ||||| ||| | || |||
Db         92 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 151

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        152 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 211

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        212 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 271

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||||| ||||| || ||||||||| ||||||| ||||  ||
Db        272 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 331

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||||| |||||||| |||
Db        332 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 391

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        392 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 451

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        452 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 511

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        512 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 571

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||     ||||| |||||||||| ||||||| |||||||||
Db        572 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 628

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| ||||| |||||||||  ||||||||||||||
Db        629 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 688

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        689 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 748

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || |||||||||| ||||||||||||||||| |||||
Db        749 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 808

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || |||||||||||||||||||||||||| ||| | |||| |||||||
Db        809 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 868

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        869 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 928

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  ||||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db        929 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 988

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db        989 AGCGAATGGGCATCTGTGCCCTGCAGT 1015


RESULT 10
US-08-460-736-194
; Sequence 194, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
```

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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  194:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1018 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-194

  Query Match             48.3%;  Score 772.6;  DB 4;  Length 1018;
  Best Local Similarity   87.1%;  Pred. No. 4.1e-234;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  ||||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         32 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 91

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               |||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db         92 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 151

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||  | ||||||||||||||| ||||| |||
Db        152 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 211

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db        212 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 271

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| ||||| || ||||||||| ||||||| |||| ||
Db        272 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 331

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||| |||||||| |||
Db        332 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 391

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        392 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 451

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        452 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 511

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        512 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 571

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        572 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 628

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db        629 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 688

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||| |||||||||
Db        689 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 748

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||| || |||||||||| |||||||||||||||| |||||
Db        749 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 808

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||  || |||||||||||||||||||||||||| ||| | |||| |||||||
Db        809 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 868

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        869 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 928

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| ||| |||||| || |||||| |||| ||||||||||||| |||| |||
Db        929 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 988

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
              ||||| |||||||||||| | ||||||
Db        989 AGCGAATGGGCATCTGTGCCCTGCAGT 1015


RESULT 11
US-08-751-767A-3
; Sequence 3, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1399 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  43..1026
US-08-751-767A-3
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  Query Match             48.3%;  Score 772.6;  DB 2;  Length 1399;
  Best Local Similarity   87.1%;  Pred. No. 4.9e-234;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  ||||||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         43 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 102

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               ||||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db        103 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 162

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        163 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 222

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| |||| ||||| ||||||||||||||||||||
Db        223 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 282

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| |||| || |||||||| ||||||| |||| ||
Db        283 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 342

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||| |||||||| |||
Db        343 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 402

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| |||| ||||||||||||||||||||||
Db        403 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 462

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||| ||||||||||||| ||||||
Db        463 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 522

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||| || ||||| |  |||||| || |||||||| |||
Db        523 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 582

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    |||| |||||||||| ||||||| ||||||||||
Db        583 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 639

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| ||||||||||  ||||||||||||
Db        640 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 699

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        700 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 759

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||| || |||||||||| ||||||||||||||||| |||||
Db        760 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 819

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || ||||||||||||||||||||||||| ||| | |||| |||||||
Db        820 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 879

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        880 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 939

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  |||||| ||  |||||| ||||  |||||||||||||| ||||| |||
Db        940 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 999

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db       1000 AGCGAATGGGCATCTGTGCCCTGCAGT 1026
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RESULT 12
US-08-265-087-1
; Sequence 1, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-265-087-1

  Query Match             48.3%;  Score 772.6;  DB 1;  Length 2362;
  Best Local Similarity   87.1%;  Pred. No. 6.7e-234;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  ||||||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         33 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 92

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               ||||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db         93 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 152

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        153 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 212

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||||
Db        213 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 272

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
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Db        273 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 332
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Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||| |||||||| |||
Db        333 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 392

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        393 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 452

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        453 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 512

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        513 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 572

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        573 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 629

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db        630 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 689

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        690 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 749

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||  || |||||||||| ||||||||||||||||  |||||
Db        750 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 809

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || |||||||||||||||||||||||||| ||| | |||| |||||||
Db        810 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 869

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||| ||| |  |||||||||||||||| |||| |
Db        870 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 929

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  |||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db        930 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 989

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db        990 AGCGAATGGGCATCTGTGCCCTGCAGT 1016


RESULT 13
US-08-621-493-1
; Sequence 1, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-621-493-1

  Query Match           48.3%;  Score 772.6;  DB 1;  Length 2362;
  Best Local Similarity  87.1%;  Pred. No. 6.7e-234;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         33 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 92

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db         93 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 152

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||  | ||||||||||||||  |||||| |||
Db        153 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 212

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  | |||||||||| ||| |||| |||| |||| ||||||||||||||||||
Db        213 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 272

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| |||| || |||||||| ||||||| |||| ||
Db        273 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 332

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| |||||||||||||||||||||||||||| |||||||| |||
Db        333 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 392

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db        393 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 452

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        453 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 512

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        513 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 572

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        573 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 629

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db        630 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 689
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Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
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Db        690 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 749

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || |||||||||||| |||||||||||||||||| |||||
Db        750 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 809

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||| || |||||||||||||||||||||||||| ||| | |||| |||||||
Db        810 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 869

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        870 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 929

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Db        930 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 989

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db        990 AGCGAATGGGCATCTGTGCCCTGCAGT 1016


RESULT 14
US-08-965-688-1
; Sequence 1, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2362 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  33..1016
US-08-965-688-1

  Query Match             48.3%;  Score 772.6;  DB 2;  Length 2362;
  Best Local Similarity   87.1%;  Pred. No. 6.7e-234;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db         33 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 92

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               |||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db         93 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 152

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db        153 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 212

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        213 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 272

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| ||||| || |||||||| ||||||| ||||  ||
Db        273 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 332

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
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Db        333 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 392

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db        453 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 512

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
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Db        513 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 572

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||     |||| |||||||||| |||||| ||||||||||
Db        573 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 629

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db        630 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 689

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||| |||||||||||||| ||||||||||
Db        690 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 749

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||||| || |||||||||||| |||||||||||||||||| |||||
Db        750 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 809

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||| || |||||||||||||||||||||||||| ||| | |||| |||||||
Db        810 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 869

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Db        870 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 929

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Db        930 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 989
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Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db        990 AGCGAATGGGCATCTGTGCCCTGCAGT 1016


RESULT 15
US-09-260-173-1
; Sequence 1, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;        APPLICANT: Scott, Phillip
;                   Trinchieri, Giorgio
;        TITLE OF INVENTION: Compositions and Methods for Use of
;                            IL-12 as an Adjuvant
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Howson and Howson
;             STREET: Spring House Corporate Center, PO Box 457
;             CITY: Spring House
;             STATE: Pennsylvania
;             COUNTRY: USA
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/260,173
;             FILING DATE: 01-Mar-1999
;             CLASSIFICATION: <Unknown>
;                             17-JUN-1994
;                             18-APR-1994
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/965,688
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/265,087
;             FILING DATE: 17-JUN-1994
;             APPLICATION NUMBER: US 08/229,282
;             FILING DATE: 18-APR-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: WST51AUSA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 215-540-9206
;             TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2362 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: unknown
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  33..1016
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-260-173-1

  Query Match             48.3%;  Score 772.6;  DB 4;  Length 2362;
  Best Local Similarity   87.1%;  Pred. No. 6.7e-234;
  Matches  860;  Conservative    0;  Mismatches  124;  Indels    3;  Gaps    1;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
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Db         33 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 92

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               |||||||||||||||| |||||||||||||| ||||| |||| | || |||
Db         93 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 152

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
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Db        153 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 212

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db        213 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 272

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| ||||| || ||||||||| ||||||| |||| ||
Db        273 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 332

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| |||||||||||||||||||||||||| |||||||| |||
Db        333 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 392

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Db        393 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 452

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||||| |||||||||||||| ||||||
Db        453 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 512

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db        513 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 572

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db        573 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 629

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db        630 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 689

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db        690 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAG 749

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
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Db        750 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 809

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || |||||||||||||||||||||||| ||| | |||| |||||||
Db        810 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 869

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||| ||| |  ||||||||||||||||| |||| |
Db        870 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACGGACAAGACCTCAGCCACGGTCATC 929

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| ||| |||||| || |||||| |||| |||||||||||||| ||||| |||
Db        930 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 989

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGT 987
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Db        990 AGCGAATGGGCATCTGTGCCCTGCAGT 1016


Search completed: July 16, 2003, 13:21:10
Job time : 90.1704 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:38:23 ; Search time 312.905 Seconds
(without alignments)
8158.492 Million cell updates/sec

Title: US-09-917-265-61
Perfect score: 1599
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1114047 seqs, 798260406 residues

Total number of hits satisfying chosen parameters: 2228094

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
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	3	1533	95.9	1533	10	US-09-917-265-66	Sequence 66, Appl
c	4	1533	95.9	1533	10	US-09-917-265-68	Sequence 68, Appl
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	7	1373	85.9	1533	10	US-09-917-265-43	Sequence 43, Appl
c	8	1373	85.9	1533	10	US-09-917-265-45	Sequence 45, Appl
	9	1231.6	77.0	8608	10	US-09-828-825-7	Sequence 7, Appli
	10	1231.6	77.0	8629	10	US-09-828-825-15	Sequence 15, Appl
	11	1216.6	76.1	8578	10	US-09-828-825-1	Sequence 1, Appli
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	14	1216.6	76.1	8644	10	US-09-828-825-13	Sequence 13, Appl
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	34	772.6	48.3	2362	10	US-09-924-703-3	Sequence 3, Appli
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c	43	543.4	34.0	1455	10	US-09-917-265-106	Sequence 106, App
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ALIGNMENTS

RESULT 1
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC AC1D MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
; OTHER INFORMATION:
US-09-917-265-61

Query Match 100.0%; Score 1599; DB 10; Length 1599;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

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  Matches 1599;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
Db       1119 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 1060

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Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
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Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
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Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Qy       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140
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Qy       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320
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Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380
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RESULT 3
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match           95.9%;  Score 1533;  DB 10;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
Db          1 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy        127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
Db         61 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 120

Qy        187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
Db        121 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy        247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306
Db        181 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 240

Qy        307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366
Db        241 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 300

Qy        367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426
Db        301 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 360

Qy        427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
Db        361 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 420

Qy        487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546
Db        421 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 480

Qy        547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606
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Db        481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 540

Qy        607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 600

Qy        667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 660

Qy        727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 720

Qy        787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 780

Qy        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 900

Qy        967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy       1027 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1020

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1080

Qy       1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1081 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1200

Qy       1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1201 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1260

Qy       1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1261 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1320

Qy       1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1321 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1380

Qy       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1381 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1440

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1500

Qy       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
              ||||||||||||||||||||||||||||||||
Db       1501 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533

RESULT 4

US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT: Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match           95.9%;  Score 1533;  DB 10;  Length 1533;
  Best Local Similarity  100.0%;  Pred. No. 0;
  Matches 1533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1533 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 1414

Qy         187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1413 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1353 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 1294

Qy         307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1293 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 1234

Qy         367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1233 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 1174

Qy         427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1173 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 1114

Qy         487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1113 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 1054

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 994

Qy         607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         993 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 934

Qy         667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 874

Qy         727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         873 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 814

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846
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Db        813 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 754

Qy        847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        753 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy        907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        693 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 634

Qy        967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy       1027 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 514

Qy       1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 454

Qy       1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        453 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy       1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 334

Qy       1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        333 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 274

Qy       1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        273 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 214

Qy       1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 154

Qy       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        153 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 94

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 34

Qy       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
              ||||||||||||||||||||||||||||||||
Db          33 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 5
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-38

  Query Match             89.4%;  Score 1429.4;  DB 10;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||||||||||| ||||| ||||||| |||||||||||  ||||||||
Db          1 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 60

Qy         61 ATGGCCATATGGGAACTGGAGAAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||
Db         61 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              |||||||||||||||||||||||||||| |||| |||||||||||||||||||| |||
Db        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 180

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  |||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        181 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||  ||
Db        241 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||  |||| |||||||| ||||||||||||||||||||||||||||| |||||||
Db        301 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 360

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        361 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||||| |||||||||||| |||||||| ||||||
Db        421 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 480

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||||| |||||| ||||||||| |||||| |||||||||| ||||
Db        481 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 540

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        601 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 660

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              || |||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db        661 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 720

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||| |||||||||||| |||||||||||||| ||||| || ||||||||||||
Db        721 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 780

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 840

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||||| ||||||| ||||||||||||||||||||||||||||
Db        841 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
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Db        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 960

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db        961 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020

Qy       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080
              |||||||||||||||||||| |||||||| ||  | |||||||||||||| || || ||
Db       1021 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 1080

Qy       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140
              ||| ||||||||||||||||||||||||||||||||||||||||| || ||||||||||||
Db       1081 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 1140

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1141 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 1260

Qy       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320
              || |||||||||||||||  ||||| ||||||||||||  ||||||||||||||
Db       1261 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 1320

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380
              |||||||||||||||||||||||| |||| |||||||||||||| |||||||| |||
Db       1321 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 1380

Qy       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440
              |||||||| || ||||||||||||||||||||||||||||||||||||| |||||||||
Db       1381 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 1440

Qy       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500
              |||||||||||||||  |||||||||||||||||||||||||| |||||| | ||||| |||
Db       1441 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 1500

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 1560

Qy       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
              |||||||||||||||||||||  |||  ||||  |||||
Db       1561 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1599


RESULT 6
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-40

  Query Match             89.4%;  Score 1429.4;  DB 10;  Length 1599;
  Best Local Similarity   93.4%;  Pred. No. 0;
  Matches 1493;  Conservative    0;  Mismatches  106;  Indels    0;  Gaps    0;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              ||||| |||||||||||||||| |||| |||||| ||||||||||  |||||||
Db       1599 ATGCATCCTCAGCAGTTGGTCATCGCCTGGCTTTCCCTGGTTTTGCTGGCACCTCCCCTC 1540

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||||||||| | ||||||||||||||||||||||||||||||||||
Db       1539 ATGGCCATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 1480

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              |||||||||||||||||||||||||||||| |||| |||||||||||||||||| |||
Db       1479 GCCCCCGGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGG 1420

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||| |  ||||||||||||||||| ||||||||||||||||||||||||||||||||
Db       1419 ACCTCTGACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAA 1360

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              ||||||| |||||||||||||||||||| |||||||||||| ||||||||||||  ||
Db       1359 GAATTTGCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCG 1300

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              ||||  |||| |||||||| ||||||||||||||||||||||||||||||| |||||||
Db       1299 TTCCTCCTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAG 1240

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       1239 AAAGAATCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 1180

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||||||||||| |||||||||||| ||||||||| ||||||
Db       1179 ACCTGCTGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGA 1120

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              |||| |||||||||||| |||||| |||||||||| ||||| ||||||||||| ||||
Db       1119 GGCTCCTCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTC 1060

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1059 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 1000

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||||||||||||||||| || |||||||||| ||||||||||||||||||||
Db        999 CCGGCTGCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAG 940

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              || |||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db        939 TACGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAG 880

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              |||||||| |||||||||| |||||||||||||| ||||| || ||||||||||||||
Db        879 AACCTGCAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCT 820

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||||||||||||||||||||||| | |||||| || |||||| |||||||
Db        819 GACACCTGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGC 760

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||||||| |||||||||||| ||||||| ||||||||||||||||||||||||||||||
Db        759 AAGAACAACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTG 700

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||||||||||||||||||||||||||||||| |||||||||||||| ||||||||
Db        699 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGG 640

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||| |||||||||| ||||| ||||||||||||||||||||||||||||||||||||||||
Db        639 AGCAACTGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 580

Qy       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080
              |||||||||||||||||||| |||||||| ||  | |||||||||||||| || || ||
Db        579 ACCCCTACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGA 520

Qy       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140
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Db        519 GCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCC 460

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
Db        459 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTA 400

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260
Db        399 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACT 340

Qy       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320
Db        339 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGT 280

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380
Db        279 ATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTA 220

Qy       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440
Db        219 ATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTG 160

Qy       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500
Db        159 TTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCG 100

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560
Db         99 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCA 40

Qy       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
Db         39 GTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 1
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RESULT 7
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Felis catus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1533)
; OTHER INFORMATION:
US-09-917-265-43

Query Match 85.9%; Score 1373; DB 10; Length 1533;
Best Local Similarity 93.5%; Pred. No. 0;
Matches 1433; Conservative 0; Mismatches 100; Indels 0; Gaps 0;

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Qy          67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
Db           1 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 60

Qy         127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
Db          61 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 120

Qy         187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
Db         121 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 180

Qy         247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306
Db         181 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 240

Qy         307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366
Db         241 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 300

Qy         367 TCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426
Db         301 TCCAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 360

Qy         427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
Db         361 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 420

Qy         487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546
Db         421 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 480

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606
Db         481 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 540

Qy         607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666
Db         541 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 600

Qy         667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726
Db         601 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 660

Qy         727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786
Db         661 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 720

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846
Db         721 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 780

Qy         847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
Db         781 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 840

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966
Db         841 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 900

Qy         967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
Db         901 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 960

Qy        1027 ACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086
Db         961 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 1020

Qy        1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146
Db         1021 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 1080

Qy        1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
Db         1081 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1140

Qy        1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266
Db         1141 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 1200

Qy        1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326
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Db       1201 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 1260

Qy       1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386
             |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db       1261 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 1320

Qy       1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446
             || || ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db       1321 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 1380

Qy       1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506
             |||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db       1381 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 1440

Qy       1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db       1441 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 1500

Qy       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
             ||||||||||||||| ||| |||| |||||
Db       1501 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1533


RESULT 8
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-45

  Query Match             85.9%;  Score 1373;  DB 10;  Length 1533;
  Best Local Similarity   93.5%;  Pred. No. 0;
  Matches 1433;  Conservative    0;  Mismatches  100;  Indels    0;  Gaps    0;

Qy          67 ATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 126
               |||||||||||||||||| | ||||||||||||||||||||||||||||||||||||||
Db        1533 ATATGGGAACTGGAGAAAAACGTTTATGTTGTAGAGTTGGACTGGCACCCTGATGCCCCC 1474

Qy         127 GGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGGACCTCA 186
               |||||||||||||||||||||| |||| ||||||||||||||||||| ||||||||
Db        1473 GGAGAAATGGTGGTCCTCACCTGCAATACTCCTGAAGAAGATGACATCACCTGGACCTCT 1414

Qy         187 GCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 246
               |  |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        1413 GACCAGAGCAGTGAAGTCCTAGGCTCTGGTAAAACTCTGACCATCCAAGTCAAAGAATTT 1354

Qy         247 GGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCACTCCTG 306
               | |||||||||||||||||||| |||||||||||| ||||||||||||  ||  ||||
Db        1353 GCAGATGCTGGCCAGTATACCTGTCATAAAGGAGGCGAGGTTCTGAGCCATTCGTTCCTC 1294

Qy         307 TTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAGAAAGAA 366
               ||||  |||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db        1293 CTGATACACAAAAAGGAAGATGGAATTTGGTCCACTGATATCTTAAGGGAACAGAAAGAA 1234

Qy         367 TCCAAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACATGC 426
               |||||||||||||||||||| |||||||||||||||||||||||||||||||||| |||
Db        1233 TCCAAAAAATAAGATCTTTCTAAAATGTGAGGCAAAGAATTATTCTGGACGTTTCACCTGC 1174

Qy         427 TGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGAGGCTTC 486
               |||||||||||||||||||||||||||| |||||||||||||| ||||||||| |||||||||| |
Db        1173 TGGTGGCTGACGGCAATCAGTACCGATTTGAAATTCACTGTCAAAAGCAGCAGAGGCTCC 1114

Qy         487 TCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTCAGAGTG 546
               |||||||||||| |||||| |||||||||| |||||| |||||||||| ||||||||||
Db        1113 TCTGACCCCCAAGAGGTGACTTGTGGAGCAGCGACACTCTCAGCAGAGAAGGTCAGAGTG 1054

Qy         547 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCCTCT 606
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        1053 GACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGCCCGGCT 994

Qy         607 GCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAGTATGAA 666
               |||||||||||||||||||| || |||||||||| |||||||||||||||||||| |||
Db         993 GCCGAGGAGAGCCTACCCATTGAAGTCGTGGTGGACGCTATTCACAAGCTCAAGTACGAA 934

Qy         667 AACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACAAACCTG 726
               |||||||||||||||||||||||| |||||||||||||| |||||||||| ||||||
Db         933 AACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCGGACCCACCCAAGAACCTG 874

Qy         727 CAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCCGACACC 786
               || |||||||||||| |||||||||||||| ||||| || ||||||||||||||| ||||||
Db         873 CAACTGAAGCCATTAAAAAATTCTCGGCATGTGGAAGTGAGCTGGGAATACCCTGACACC 814

Qy         787 TGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGCAAGAAC 846
               |||||||||||||||||||||||||||| | |||||| || |||||| ||||||||||||
Db         813 TGGAGCACCCCACATTCCTACTTCTCCTTAACATTTGGCGTACAGGTCCAGGGCAAGAAC 754

Qy         847 AATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 906
               || |||||||||||||| ||||||| ||||||||||||||||||||||||||||||||||
Db         753 AACAGAGAAAAGAAAGACAGACTCTCCGTGGACAAGACCTCAGCCAAGGTCGTGTGCCAC 694

Qy         907 AAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGGAGCGAC 966
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db         693 AAGGATGCCAAGATCCGCGTGCAAGCCAGAGACCGCTACTATAGCTCATCCTGGAGCAAC 634

Qy         967 TGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 1026
               |||||||| ||||| |||||||||||||||||||||||||||||||||||||||||||||
Db         633 TGGGCATCCGTGTCCTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCT 574

Qy        1027 ACTCCATCCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTC 1086
               |||||||||||||| |||||||| ||  | ||||||||||||||| || || ||||| ||
Db         573 ACTCCATCCCCGGGGATGTTCCAGTGCCTCAACCACTCCCAAACCCTGCTGCGAGCCATC 514

Qy        1087 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAG 1146
               |||||||||||||||||||||||||||||||||||||||||||| || ||||||||||||||
Db         513 AGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTACTCCTGCACTTCCGAAGAG 454

Qy        1147 ATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 1206
               |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         453 ATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTG 394

Qy        1207 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGG 1266
               |||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |||
Db         393 GAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTCTGATAACTAATGGG 334

Qy        1267 AGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTAT 1326
               |||||||||||||| ||||| |||||||||||||| ||||||||||||||| ||||||
Db         333 AGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTGTGCCTTAGCAGTATCTAT 274

Qy        1327 GAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGAT 1386
               |||||||||||||||||||| |||| |||||||||||||| |||||||| |||||||||
Db         273 GAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAATGCAAAGCTGTTAATGGAT 214

Qy        1387 CCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAG 1446
               || || ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         213 CCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATTGATGAGCTGTTACAG 154

Qy        1447 GCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTT 1506
               |||||||| |||||||||||||||||||||||| |||||| | ||||| |||||||||
Db         153 GCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCCTTGGAAGAACCGGATTTT 94

Qy        1507 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACC 1566
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Db         93 TATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCAGTGACC 34

Qy       1567 ATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
Db         33 ATCAATAGAATGATGAGCTATCTGAATGCTTCC 1


RESULT 9
US-09-828-825-7
; Sequence 7, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 8608
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.2 sequence (2460-4253 is coding
;   OTHER INFORMATION: sequence, 13 amino acid flexible linker at
;   OTHER INFORMATION: 3606-3676)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4253)
;   OTHER INFORMATION: IL12.2 coding sequence (13 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4362)..(4383)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4393)..(4614)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4709)..(5164)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5228)..(6595)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7006)..(7866)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-7

  Query Match           77.0%;  Score 1231.6;  DB 10;  Length 8608;
  Best Local Similarity   86.2%;  Pred. No. 0;
  Matches 1392;  Conservative    0;  Mismatches  204;  Indels   18;  Gaps    2;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
Db       2640 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 2699

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
Db       2700 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 2759

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
Db       2760 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 2819

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
Db       2820 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 2879

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
Db       2880 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 2939

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
Db       2940 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 2999

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
Db       3000 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 3059

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
Db       3060 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 3119

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
Db       3120 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 3179

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
Db       3180 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 3236

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
Db       3237 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 3296

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
Db       3297 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAC 3356

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
Db       3357 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 3416

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
Db       3417 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 3476

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
Db       3477 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACCGACAAGACCTCAGCCACGGTCATC 3536

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
Db       3537 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 3596

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGG---------------A 1005
Db       3597 AGCGAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGTGGCGGTGGAAGCCCA 3656

Qy       1006 TCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCC 1065
Db       3657 TGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCC 3716

Qy       1066 CAAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTA 1125
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Db       3717 CAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTT 3776

Qy       1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Db       3777 TACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACA 3836

Qy       1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Db       3837 GTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAG 3896

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Db       4017 AATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCA 4076

Qy       1426 GCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCC 1485

Db       4077 GTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCC 4136

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RESULT 10
US-09-828-825-15
; Sequence 15, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 8629
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2726)
;   OTHER INFORMATION: Human IL12.2 (coding sequence is 1103-2716, 10
;   OTHER INFORMATION: amino acid linker at 2087-2116)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2716)
;   OTHER INFORMATION: Human IL12.2 (10 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2752)..(3332)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3369)..(4263)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4383)..(4404)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4414)..(4635)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4730)..(5185)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5249)..(6616)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7027)..(7887)
;   OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-15

  Query Match           77.0%;  Score 1231.6;  DB 10;  Length 8629;
  Best Local Similarity   86.2%;  Pred. No. 0;
  Matches 1392;  Conservative    0;  Mismatches  204;  Indels   18;  Gaps    2;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

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Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

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Db       1223 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 1282

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Db       1583 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 1642

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600

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Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660

Db       1700 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 1759

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720

Db       1760 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAC 1819

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
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Db       1820 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 1879

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Db       1880 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 1939

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900

Db       1940 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACCGACAAGACCTCAGCCACGGTCATC 1999

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960

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Qy        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGG---------------A 1005

Db       2060 AGCGAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGTGGCGGTGGAAGCCCA 2119

Qy       1006 TCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCC 1065

Db       2120 TGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCC 2179

Qy       1066 CAAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTA 1125

Db       2180 CAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTT 2239

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Qy       1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTC 1305

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Qy       1306 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATG 1365

Db       2420 CTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATG 2479

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Qy       1426 GCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCC 1485

Db       2540 GTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCC 2599

Qy       1486 TCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCT 1545

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RESULT 11
US-09-828-825-1
; Sequence 1, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 8578
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: enhancer
;   LOCATION: (1)..(659)
;   OTHER INFORMATION: CMV IE
;   NAME/KEY: promoter
;   LOCATION: (669)..(750)
;   OTHER INFORMATION: CMV  IE
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA Promoter
;   NAME/KEY: mRNA
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: mRNA
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.0 (2640-4223 coding sequence, flexible
;   OTHER INFORMATION: linker at 3624-3629)
;   NAME/KEY: promoter
;   LOCATION: (4352)..(4431)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4362)..(4583)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4678)..(5133)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5197)..(6564)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (6975)..(7835)
;   OTHER INFORMATION: Ampicillin resistance
;   OTHER INFORMATION: Description of Artificial Sequence: Plasmid
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4223)
;   OTHER INFORMATION: IL 12.0 coding sequence - 2 amino acid linker at
;   OTHER INFORMATION: 3624
US-09-828-825-1

  Query Match             76.1%;  Score 1216.6;  DB 10;  Length 8578;
  Best Local Similarity   86.1%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches  204;  Indels   18;  Gaps    2;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60

Db       2640 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 2699

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

Db       2700 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 2759

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

Db       2760 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 2819

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

Db       2820 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 2879

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300

Db       2880 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 2939

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
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Db       2940 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 2999

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420

Db       3000 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 3059

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480

Db       3060 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 3119

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540

Db       3120 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 3179

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Db       3237 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 3296

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Db       3357 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 3416

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840

Db       3417 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 3476

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Db       3762 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTA 3821

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Db       3822 CCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACT 3881

Qy       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320

Db       3882 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGT 3941

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380

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Qy       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440

Db       4002 ATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTG 4061

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Db       4182 GTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 4220
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RESULT 12
US-09-828-825-3
; Sequence 3, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 8578
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: enhancer
;   LOCATION: (1)..(659)
;   OTHER INFORMATION: CMV IE Enhancer
;   NAME/KEY: promoter
;   LOCATION: (669)..(750)
;   OTHER INFORMATION: CMV IE Promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: InTervening Sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.0 sequence (2640-4217 is coding
;   OTHER INFORMATION: sequence)
;   NAME/KEY: promoter
;   LOCATION: (4346)..(4425)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4356)..(4577)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4672)..(5127)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5191)..(6558)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (6969)..(7829)
;   OTHER INFORMATION: Ampicillin resistance
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;   NAME/KEY: CDS
;   LOCATION: (2640)..(4217)
;   OTHER INFORMATION: IL12.0 coding sequence - no linker
US-09-828-825-3

  Query Match             76.1%;  Score 1216.6;  DB 10;  Length 8578;
  Best Local Similarity   86.1%;  Pred. No. 0;
  Matches 1377;  Conservative    0;  Mismatches  204;  Indels   18;  Gaps    2;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  ||||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db       2640 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 2699

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               |||||||||||||||| |||||||||||||| ||||| ||||| ||| | || |||
Db       2700 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 2759

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db       2760 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 2819

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db       2820 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 2879

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| ||||| || ||||||||| ||||||| ||||  ||
Db       2880 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 2939

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| |||||||||||||||||||||||||| |||||||| |||
Db       2940 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 2999

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||||| |||||| | ||| |||| ||||||||||||||||||||||
Db       3000 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 3059

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db       3060 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 3119

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||| || ||||| |  ||||| || |||||||| |||
Db       3120 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 3179

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db       3180 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 3236

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db       3237 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 3296

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||| ||||||||||
Db       3297 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAC 3356

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||| || |||||||||| |||||||||||||||| |||||
Db       3357 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 3416

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||| || |||||||||||||||||||||||| ||| | |||| |||||||
Db       3417 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 3476

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |   ||||||||||||||| |||| |
Db       3477 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACCGACAAGACCTCAGCCACGGTCATC 3536

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| ||| |||||| || |||||| |||| ||||||||||||| ||||| |||
Db       3537 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 3596

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCA 1020
              ||||| |||||||||||| | ||||||                 ||  |||||| | ||
Db       3597 AGCGAATGGGCATCTGTGCCCTGCAGT--------------CCATGGAGAAACCTCCCC 3641

Qy       1021 ACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCCCAAACCTTGTTGAGA 1080
                | ||||||  ||| || ||||||| |||  |  |||||||||||| | || ||||
Db       3642 GTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAAAACCTGCTGAGG 3701

Qy       1081 GCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCC 1140
              |||||||||||||| ||| |||||||||||||||||||||||||| ||  | ||||||||
Db       3702 GCCGTCAGCAACATGCTCCAGAAGGCCAGACAAACTCTAGAATTTTACCCTTGCACTTCT 3761

Qy       1141 GAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTA 1200
              |||||||||||||||||||||||||||||||| |||||||||||||||||||||||| |||
Db       3762 GAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTGGAGGCCTGTTTA 3821

Qy       1201 CCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACT 1260
              ||| |||||||||||| |||||||||||||||   |||||||||| |||||| ||||||
Db       3822 CCATTGGAATTAACCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACCTCTTTCATAACT 3881

Qy       1261 AACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGC 1320
              || ||||||||||||||||  ||||| |||||||||||| || ||||||||||||| ||
Db       3882 AATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGATGGCCCTGTGCCTTAGTAGT 3941

Qy       1321 ATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTA 1380
              || ||||| |||||||||||||||||| |||| |||||| ||||||| |||||||| |
Db       3942 ATTTATGAAGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAATGCAAAGCTTCTG 4001

Qy       1381 ATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTG 1440
              |||||||| |||||||||||||||| |||||||||||||| ||| ||| |||||||||
Db       4002 ATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGCAGTTATTGATGAGCTG 4061

Qy       1441 TTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCG 1500
                | ||||||||||||||||||||| |||||||||||| ||||||||||||||| |||
Db       4062 ATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCCCTTGAAGAACCG 4121

Qy       1501 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCG 1560
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db       4122 GATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCA 4181

Qy       1561 GTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599
              ||||| ||  ||||| |||||  |||  ||||  |||||
Db       4182 GTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 4220


RESULT 13
US-09-828-825-5
; Sequence 5, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 8623
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
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;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4278)
;   OTHER INFORMATION: Human IL12.3 - 2640-4268 is coding sequence,
;   OTHER INFORMATION: flexible linker from 3606-3690
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4268)
;   OTHER INFORMATION: IL 12.3 coding sequence - has 28 amino acid linker
;   OTHER INFORMATION: sequence
;   NAME/KEY: promoter
;   LOCATION: (4398)..(4407)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4408)..(4629)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4724)..(5179)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5243)..(6610)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7021)..(7881)
;   OTHER INFORMATION: Ampicillin resistance
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-5

  Query Match             76.1%;  Score 1216.6;  DB 10;  Length 8623;
  Best Local Similarity   85.5%;  Pred. No. 0;
  Matches 1392;  Conservative    0;  Mismatches  204;  Indels   33;  Gaps    2;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||||| |||||||||| ||||| ||||| |||||||||
Db       2640 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 2699

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
               ||||||||||||||||| |||||||||||||||| ||||| ||||| ||| | || |||
Db       2700 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 2759

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
              ||||| |||||||||||||||||||||||  | ||||||||||||||||  ||||| |||
Db       2760 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 2819

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
              ||||  |  |||||||||| ||| |||| ||||| ||||| ||||||||||||||||||
Db       2820 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 2879

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
              || |||||||||||||||||| ||||| || ||||||||| ||||||| |||  ||
Db       2880 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 2939

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
              |||||| || |||||||||| ||||||||||||||||||||||||| |||||||| |||
Db       2940 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 2999

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
              |||||| |||||||||| |||||| | ||| ||||| ||||||||||||||||||||
Db       3000 AAAGAACCCAAAAATAAGACCTTTCTAAGATGCGAGGCCAAGAATTATTCTGGACGTTTC 3059

Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
              || |||||||||||||| |||||||||||||||| |||||||||||||| ||||||
Db       3060 ACCTGCTGGTGGCTGACGACAATCAGTACTGATTTGACATTCAGTGTCAAAAGCAGCAGA 3119

Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
              ||||  |||||||||||||||||||| || ||||| |  |||||| || |||||||| |||
Db       3120 GGCTCTTCTGACCCCCAAGGGGTGACGTGCGGAGCTGCTACACTCTCTGCAGAGAGAGTC 3179

Qy        541 AGAGTGGACAACAGGGATTATAAGAAGTACACAGTGGAGTGTCAGGAGGGCAGTGCCTGC 600
              |||| |||||||| ||| |||    ||||| |||||||||| ||||||| ||||||||||
Db       3180 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 3236

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
              ||  |||| |||||||| || ||||| |||||| |||||||||  ||||||||||||||
Db       3237 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 3296

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              |||||||||||||||||||||||||||||||| |||||||||||| |||||||||||
Db       3297 TATGAAAACTACACCAGCAGCTTCTTCATCAGGGACATCATCAAACCTGACCCACCCAAC 3356

Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
              ||| |||||||||||||| || |||||||||| |||||||||||||| |||||
Db       3357 AACTTGCAGCTGAAGCCATTAAAGAATTCTCGGCAGGTGGAGGTCAGCTGGGAGTACCCT 3416

Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
              |||||||||||  || |||||||||||||||||||||||||| ||| | |||| |||||||
Db       3417 GACACCTGGAGTACTCCACATTCCTACTTCTCCCTGACATTCTGCGTTCAGGTCCAGGGC 3476

Qy        841 AAGAACAATAGAGAAAAGAAAGATAGACTCTGCGTGGACAAGACCTCAGCCAAGGTCGTG 900
              |||| ||| |||||||||||||||||| ||| |   |||||||||||||||| |||| |
Db       3477 AAGAGCAAGAGAGAAAAGAAAGATAGAGTCTTCACCGACAAGACCTCAGCCACGGTCATC 3536

Qy        901 TGCCACAAGGATGCCAAGATCCGCGTGCAAGCCCGAGACCGCTACTATAGTTCATCCTGG 960
              |||| |||  |||||  ||  ||||||  ||||  |||||||||||||| ||||| |||
Db       3537 TGCCGCAAAAATGCCAGCATTAGCGTGCGGGCCCAGGACCGCTACTATAGCTCATCTTGG 3596

Qy        961 AGCGACTGGGCATCTGTGTCATGCAGTGGTGGCGGTGGCGGCGG---------------- 1004
              ||||| |||||||||||| | |||||||||||||||  ||||
Db       3597 AGCGAATGGGCATCTGTGCCCTGCAGTGGTGGCGGTGGAAGCGGTGGCGGTGGAAGCGGT 3656

Qy       1005 --------------ATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAA 1050
                           ||  |||||| | ||      | ||||||  ||| || ||||||| |
Db       3657 GGCGGTGGAAGCCCATGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCA 3716

Qy       1051 TGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGA 1110
              ||  |  |||||||||||| | || |||| |||||||||||| ||| ||||||||||||
Db       3717 TGCCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGA 3776

Qy       1111 CAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAG 1170
              |||||||||||||| ||  | |||||||| ||||||||||||||||||||||||||||
Db       3777 CAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAA 3836

Qy       1171 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 1230
              |||||||||||||||||||||||||||||||| |||||| |||||||||||| ||||||||||
Db       3837 GATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGC 3896

Qy       1231 CTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCC 1290
              ||  |||||||||| |||||| |||||||| ||||||||||||||||  ||||| ||
Db       3897 CTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACC 3956

Qy       1291 TCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATG 1350
              |||||||||| || |||||||||||| || || ||||| |||||||||||||||||| ||
Db       3957 TCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTG 4016

Qy       1351 GAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGAT 1410
              || |||||| |||||| |||||||| | |||||||| ||||||||||||||||| |||
Db       4017 GAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGAT 4076

Qy       1411 CAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACT 1470
              |||||||||||| ||| ||| ||||||||| | |||||||||||||||||||||| ||||
Db       4077 CAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACT 4136

Qy       1471 GTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGC 1530
              |||||||| |||||||||||||||| ||||||||||||||||||||||||||||||||||
Db       4137 GTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGC 4196

Qy       1531 ATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTG 1590
              |||||||||||||||||||||||||| || ||||| ||  |||||  |||  ||
Db       4197 ATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTG 4256

Qy       1591 AACTCTTCC 1599
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Db        4257 AATGCTTCC 4265


RESULT 14
US-09-828-825-13
; Sequence 13, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 8644
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2731)
;   OTHER INFORMATION: Human IL12.3 (1103-2731 is coding sequence, 15
;   OTHER INFORMATION: amino acid linker at 2087-2131)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2731)
;   OTHER INFORMATION: IL12.3 (15 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2767)..(3347)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3384)..(4278)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4398)..(4419)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4429)..(4650)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4745)..(5200)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5264)..(5681)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7042)..(7902)
;   OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-13

  Query Match           76.1%;  Score 1216.6;  DB 10;  Length 8644;
  Best Local Similarity  85.5%;  Pred. No. 0;
  Matches 1392;  Conservative    0;  Mismatches  204;  Indels   33;  Gaps    2;

Qy          1 ATGCACCCTCAGCAGTTGGTCATCTCCTGGTTTTCCCTCGTTTTGCTGGCGTCTCCCCTC 60
              |||   |  |||||||||||||||| ||||||||||| ||||| ||||| |||||||||
Db       1103 ATGTGTCACCAGCAGTTGGTCATCTCTTGGTTTTCCCTGGTTTTTCTGGCATCTCCCCTC 1162

Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120
              |||||||||||||||| ||||||||||||||| ||||| ||||| ||| | || |||
Db       1163 GTGGCCATATGGGAACTGAAGAAAGATGTTTATGTCGTAGAATTGGATTGGTATCCGGAT 1222

Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180
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Db       1223 GCCCCTGGAGAAATGGTGGTCCTCACCTGTGACACCCCTGAAGAAGATGGTATCACCTGG 1282

Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240
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Db       1283 ACCTTGGACCAGAGCAGTGAGGTCTTAGGCTCTGGCAAAACCCTGACCATCCAAGTCAAA 1342

Qy        241 GAATTTGGAGATGCTGGCCAGTATACCTGCCATAAAGGAGGCAAGGTTCTGAGCCGCTCA 300
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Db       1343 GAGTTTGGAGATGCTGGCCAGTACACCTGTCACAAAGGAGGCGAGGTTCTAAGCCATTCG 1402

Qy        301 CTCCTGTTGATTCACAAAAAAGAAGATGGAATTTGGTCCACTGATATCTTAAAGGAACAG 360
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Db       1403 CTCCTGCTGCTTCACAAAAAGGAAGATGGAATTTGGTCCACTGATATTTTAAAGGACCAG 1462

Qy        361 AAAGAATCCAAAAATAAGATCTTTCTGAAATGTGAGGCAAAGAATTATTCTGGACGTTTC 420
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Qy        421 ACATGCTGGTGGCTGACGGCAATCAGTACTGATTTGAAATTCAGTGTCAAAAGTAGCAGA 480
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Qy        481 GGCTTCTCTGACCCCCAAGGGGTGACATGTGGAGCAGTGACACTTTCAGCAGAGAGGGTC 540
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Db       1643 AGAGGGGACAACAAGGAGTAT---GAGTACTCAGTGGAGTGCCAGGAGGACAGTGCCTGC 1699

Qy        601 CCCTCTGCCGAGGAGAGCCTACCCATCGAGGTCGTGGTGGATGCTATTCACAAGCTCAAG 660
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Db       1700 CCAGCTGCTGAGGAGAGTCTGCCCATTGAGGTCATGGTGGATGCCGTTCACAAGCTCAAG 1759

Qy        661 TATGAAAACTACACCAGCAGCTTCTTCATCAGAGACATCATCAAACCAGACCCACCCACA 720
              ||||||||||||||||||||||||||||||||| ||||||||||| ||||||||||
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Qy        721 AACCTGCAGCTGAAGCCATTGAAAAATTCTCGGCACGTGGAGGTCAGCTGGGAATACCCC 780
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Qy        781 GACACCTGGAGCACCCCACATTCCTACTTCTCCCTGACATTTTGCATACAGGCCCAGGGC 840
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              ||||| |||||||||||| | |||||||||||||||||  ||||
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Qy       1005 --------------ATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAA 1050
                           ||  |||||| | ||     | ||||||  ||| || |||||||
Db       2120 GGCGGTGGAAGCCCATGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCA 2179

Qy       1051 TGTTTGAACCACTCCCAAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGA 1110
              ||  |  |||||||||||| | || |||| |||||||||||||| ||| ||||||||||||
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Qy       1111 CAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAG 1170
              |||||||||||||| ||  | |||||||| |||||||||||||||||||||||||||||
Db       2240 CAAACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAA 2299

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Db       2300 GATAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGC 2359

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Db       2360 CTAAATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACC 2419

Qy       1291 TCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATG 1350

Db       2420 TCTTTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTG 2479

Qy       1351 GAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGAT 1410

Db       2480 GAGTTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGAT 2539

Qy       1411 CAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACT 1470

Db       2540 CAAAACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACT 2599

Qy       1471 GTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGC 1530

Db       2600 GTGCCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGC 2659

Qy       1531 ATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTG 1590

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Qy       1591 AACTCTTCC 1599

Db       2720 AATGCTTCC 2728


RESULT 15
US-09-828-825-9
; Sequence 9, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 8638
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1954 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4293)
;   OTHER INFORMATION: Human IL12.4 (coding sequence is 2640-4283, 33
;   OTHER INFORMATION: amino acid linker at 3606-3706)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4283)
;   OTHER INFORMATION: IL12.4 coding sequence (33 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4392)..(4413)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4423)..(4644)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4739)..(5194)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5258)..(6625)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7036)..(7896)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-9

  Query Match            75.1%;  Score 1201.6;  DB 10;  Length 8638;
  Best Local Similarity  84.7%;  Pred. No. 0;
  Matches 1392;  Conservative    0;  Mismatches  204;  Indels   48;  Gaps    2;

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Qy         61 ATGGCCATATGGGAACTGGAGAAAGATGTTTATGTTGTAGAGTTGGACTGGCACCCTGAT 120

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Qy        121 GCCCCCGGAGAAATGGTGGTCCTCACCTGCCATACCCCTGAAGAAGATGACATCACTTGG 180

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Qy        181 ACCTCAGCGCAGAGCAGTGAAGTCCTAGGTTCTGGTAAAACTCTGACCATCCAAGTCAAA 240

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Qy       1005 ----------------------------ATCTAGAAACTTGCCAACCCCTACTCCATCC 1035
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Qy       1096 CTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCAT 1155
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Qy       1156 GAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACC 1215
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Qy       1396 CAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAAT 1455
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Qy       1516 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCAATAGA 1575
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Db       4197 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGA 4256

Qy       1576 ATGATGTCCTACTTGAACTCTTCC 1599
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Db       4257 GTGATGAGCTATCTGAATGCTTCC 4280


Search completed: July 16, 2003, 13:16:31
Job time : 315.905 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:54:38 ; Search time 53.5793 Seconds
(without alignments)
1325.559 Million cell updates/sec

Title: US-09-917-265-62
Perfect score: 2804
Sequence: 1 MHPQQLVISWFSLVLLASPL.....HAFRIRAVTINRMMSYLNSS 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2393.5	85.4	540	21	AAY54921	Interleukin-12 fus
2	2392	85.3	537	23	AAE19820	Human IL-12.2 prot
3	2389.5	85.2	542	23	AAE19819	Human IL-12.3 prot
4	2387	85.1	547	23	AAE19821	Human IL-12.4 prot
5	2358	84.1	527	23	AAE19817	Human IL-12.1 prot
6	2354	84.0	526	23	AAE19818	Human IL-12.0 prot
7	1764	62.9	329	19	AAW41791	Canine IL-12 P40 s
8	1764	62.9	329	20	AAY02342	Canine Interleukin
9	1764	62.9	329	20	AAW84373	Canine interleukin
10	1764	62.9	329	22	AAG66482	Canine protein #3.
11	1735	61.9	329	19	AAW41790	Canine IL-12 P40 s
12	1735	61.9	329	20	AAY02339	Canine Interleukin
13	1735	61.9	329	20	AAW84371	Canine interleukin
14	1735	61.9	329	22	AAG66480	Canine protein #1.
15	1729.5	61.7	330	20	AAW74322	Canine full length
16	1651	58.9	329	19	AAW76173	Feline FLAFp40 pro
17	1618.5	57.7	308	20	AAW74323	Canine mature CLAF
18	1567	55.9	329	22	AAE08602	Modified human cyt
19	1557	55.5	327	22	AAE08599	Modified human cyt
20	1554	55.4	307	19	AAW76174	Feline FLAFp40 mat
21	1515	54.0	327	21	AAB15391	Bovine interleukin
22	1512	53.9	327	22	AAE08598	Modified human cyt
23	1504	53.6	327	22	AAE08597	Modified human cyt
24	1502.5	53.6	328	23	AAU75579	Human interleukin
25	1501.5	53.5	328	13	AAR22769	Natural killer cel
26	1501.5	53.5	328	16	AAR79186	Human interleukin-
27	1501.5	53.5	328	17	AAW07398	Human interleukin-
28	1501.5	53.5	328	18	AAW24235	40 kDa subunit of
29	1501.5	53.5	328	18	AAW36941	40 kDa subunit of
30	1501.5	53.5	328	18	AAW36939	40 kDa subunit of
31	1501.5	53.5	328	19	AAW62992	Human interleukin-
32	1501.5	53.5	328	19	AAW58725	Cytotoxic lymphocy
33	1501.5	53.5	328	19	AAW51311	Human Interleukin-
34	1501.5	53.5	328	19	AAW57482	Human interleukin-
35	1501.5	53.5	328	19	AAW51221	Human interleukin-
36	1501.5	53.5	328	19	AAW44324	Heterodimeric huma
37	1501.5	53.5	328	20	AAY42487	Human interleukin
38	1501.5	53.5	328	21	AAB23796	Human interleukin
39	1501.5	53.5	328	21	AAY54919	Human p40 protein
40	1501.5	53.5	328	21	AAY44181	Human interleukin-
41	1501.5	53.5	328	22	AAE11198	Human interleukin-
42	1501.5	53.5	328	22	AAE08603	Human cytokine p40
43	1501.5	53.5	328	22	AAB67262	IL-12 vaccine adju
44	1501.5	53.5	328	22	AAB36649	Human cytokine rec
45	1495.5	53.3	328	22	AAE11193	Human interleukin

ALIGNMENTS

RESULT 1
AAY54921
ID AAY54921 standard; Protein; 540 AA.
XX
AC AAY54921;
XX
DT 14-FEB-2000 (first entry)
XX
DE Interleukin-12 fusion protein, Flexi-12.
XX
KW Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
KW IL-12 p40 subunit; gene therapy; tumour; leukaemia; Flexi-12.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5994104-A.
XX
PD 30-NOV-1999.
XX
PF 08-NOV-1996; 96US-0751767.
XX
PR 08-NOV-1996; 96US-0751767.
XX
PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI Anderson RJ, Prentice HG, MacDonald ID;
XX
DR WPI; 2000-038261/03.
DR N-PSDB; AAZ40023.
XX
PT Nucleic acid constructs encoding interleukin-12 fusion proteins useful
PT for treating leukemia and other cancers -

```
XX
PS   Example; Fig 11; 73pp; English.
XX
CC   This sequence is the human interleukin-12 fusion protein sequence,
CC   designated Flexi-12. The invention relates to an isolated nucleic acid
CC   construct (I) comprising a region encoding an interleukin-12 (IL-12)
CC   fusion protein (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and
CC   a linker peptide (joining the subunits)) and a region encoding a B7
CC   protein. (I) may be used to produce IL-12 fusion proteins according to
CC   standard recombinant DNA methodologies. The fusion proteins may be
CC   produced either in vitro in a fermentation culture or in vivo as part of
CC   a gene therapy protocol (in this case (I) is used to transform a patients
CC   cells, which then secrete the functional polypeptide to supplement the
CC   patients own production of IL-12 or to rectify mutations which lead to
CC   the expression of inactive polypeptides). The fusion proteins produced in
CC   this way may be used to treat any disease which responds to IL-12 such as
CC   tumours (both solid and dispersed of the kidney, breast, colon, ovarian
CC   and cervical tumours and melanomas) and in particular, tumours of the
CC   blood such as leukaemia. Alternatively, the polypeptides may be used as
CC   antigens in the production of antibodies to IL-12 and to assay for
CC   agonists and antagonists of its activity. The antibodies and antagonists
CC   may be used to inhibit the activity of IL-12. (I) may also be used
CC   diagnostically as a probe which hybridizes to sequences encoding IL-12
CC   and the antibodies may be used to detect the presence of IL-12
CC   polypeptides in samples. They may be used diagnostically to quantitate
CC   the expression of the polypeptide by patients and hence which subjects
CC   may be in need of restorative therapy.
XX
SQ   Sequence   540 AA;

  Query Match             85.4%;  Score 2393.5;  DB 21;  Length 540;
  Best Local Similarity   84.3%;  Pred. No. 1.8e-192;
  Matches  456;  Conservative   28;  Mismatches   48;  Indels    9;  Gaps    2;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              |  |||||||||||  |||||:|||||:||||||||||:||||||||||||  ||||| |||
Db          1 MGHQQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              |  ||||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|
Db         61 TLDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              || ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||
Db        121 KEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              | ||::| :|:||||| ||||:|||||||||:|||:|||||||||||||||||||||||
Db        181 RGDNKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPK 239

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||||||||| ||||||||||||||||||||||:| |||: |||||:  ||||| |:
Db        240 NLQLKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVI 299

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCSGG--------GGGGSRNLPTPTPSPGMFQCL 352
              | |:| | |:|:|||||||||:|||| ||||        |||||||||  || |||| ||
Db        300 CRKNASISVRAQDRYYSSSWSEWASVPCSGGGGSGGGGSGGGGSRNLPLATPDPGMFPCL 359

Qy        353 NHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLA 412
              :||| ||||||| |||||||| | ||||||||||||||||||||||||||| |||||
Db        360 HHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLN 419

Qy        413 SREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQN 472
              ||| | |||||||| | |||  |||||||||||||:||| ||||||||||||||||||
Db        420 SRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQN 479

Qy        473 MLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNS 532
              ||  ||||:|||||| ||||||||||||||||||||||||||||||:|: ||||:
Db        480 MLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNA 539

Qy        533 S 533
              |
Db        540 S 540
```

```
RESULT 2
AAE19820
ID   AAE19820 standard; Protein; 537 AA.
XX
AC   AAE19820;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human IL-12.2 protein.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12.2; human.
XX
OS   Homo sapiens.
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
DR   N-PSDB; AAD31548.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
PT   operably linked to promoter that directs the expression of DNA molecule
PT   -
XX
PS   Example 1; Fig 9; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is a protein encoded by human IL-12.2
CC   DNA present in pIRES-hB7-1-IL12.2 vector.
XX
SQ   Sequence   537 AA;

  Query Match             85.3%;  Score 2392;  DB 23;  Length 537;
  Best Local Similarity   85.2%;  Pred. No. 2.4e-192;
  Matches  456;  Conservative   28;  Mismatches   45;  Indels    6;  Gaps    3;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||| ||||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| ||||:|||||||||:|||:|||||||||||||||||||||| |||
```

```
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303

Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGG---GGGGS--RNLPTPTPSPGMFQCLNHSQTL 358

Db        303 NASISVRAQDRYYSSSWSEWASVPCSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNL 362

Qy        359 LRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISL 418

Db        363 LRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSF 422

Qy        419 ITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAID 478

Db        423 ITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVID 482

Qy        479 ELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533

Db        483 ELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 537


RESULT 3
AAE19819
ID   AAE19819 standard; Protein; 542 AA.
XX
AC   AAE19819;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human IL-12.3 protein.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12.3; human.
XX
OS   Homo sapiens.
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
DR   N-PSDB; AAD31547.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
PT   operably linked to promoter that directs the expression of DNA molecule
PT   .
XX
PS   Example 1; Fig 8; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is a protein encoded by human IL-12.3
CC   DNA present in pIRES-hB7-1-IL12.3 vector.
XX
SQ   Sequence   542 AA;

  Query Match           85.2%;  Score 2389.5;  DB 23;  Length 542;
  Best Local Similarity   84.4%;  Pred. No. 4e-192;
  Matches  456;  Conservative   28;  Mismatches   45;  Indels   11;  Gaps    3;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63

Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123

Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183

Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243

Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303

Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGG--------GGGGS--RNLPTPTPSPGMFQCLN 353

Db        303 NASISVRAQDRYYSSSWSEWASVPCSGGGGSGGGGSGGGGSPWRNLPVATPDPGMFPCLH 362

Qy        354 HSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS 413

Db        363 HSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNS 422

Qy        414 REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNM 473

Db        423 RETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNM 482

Qy        474 LTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533

Db        483 LAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 542


RESULT 4
AAE19821
ID   AAE19821 standard; Protein; 547 AA.
XX
AC   AAE19821;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human IL-12.4 protein.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12.4; human.
XX
OS   Homo sapiens.
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
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```
DR   N-PSDB; AAD31549.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
PT   operably linked to promoter that directs the expression of DNA molecule
PT    -
XX
PS   Example 1; Fig 10; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is a protein encoded by human IL-12.4
CC   DNA present in pIRES-hB7-1-IL12.4 vector.
XX
SQ   Sequence   547 AA;

  Query Match             85.1%;  Score 2387;  DB 23;  Length 547;
  Best Local Similarity   83.7%;  Pred. No. 6.6e-192;
  Matches  456;  Conservative   28;  Mismatches   45;  Indels   16;  Gaps    3;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| ||||||||||||||||||||||||||||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||||||||||||||||||||||||||||||:||| ||||:||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| ||||:|||||||||:|||:|||||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGG------------GGGGS--RNLPTPTPSPGM 348
              :| | |:|:|||||||||:|||| ||||             |||||  ||||  || |||
Db        303 NASISVRAQDRYYSSSWSEWASVPCSGGGGSGGGGSGGGGSGGGGSPWRNLPVATPDPGM 362

Qy        349 FQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNE 408
              | ||:||| ||||||| |||||||| | ||||||||||||||||||||||||||| ||
Db        363 FPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNE 422

Qy        409 SCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIF 468
              ||| ||| | |||||||| | |||  ||||||||||||||:||| ||||||||||||||
Db        423 SCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIF 482

Qy        469 LDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMS 528
              |||||| ||||:||||||| ||||||||||||||||||||||||||||||:|:||
Db        483 LDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMS 542

Qy        529 YLNSS 533
              |||:|
Db        543 YLNAS 547


RESULT 5
AAE19817
ID   AAE19817 standard; Protein; 527 AA.
XX
AC   AAE19817;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human IL-12.1 protein.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12.1; human.
XX
OS   Homo sapiens.
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
DR   N-PSDB; AAD31545.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
PT   operably linked to promoter that directs the expression of DNA molecule
PT    -
XX
PS   Example 1; Fig 6; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is a protein encoded by human IL-12.1
CC   DNA present in pIRES-hB7-1-IL12.1 vector.
XX
SQ   Sequence   527 AA;

  Query Match             84.1%;  Score 2358;  DB 23;  Length 527;
  Best Local Similarity   84.7%;  Pred. No. 1.7e-189;
  Matches  449;  Conservative   28;  Mismatches   47;  Indels    6;  Gaps    2;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| ||||||||||||||||||||||||||||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||||||||||||||||||||||||||||||:||| ||||:||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| ||||:|||||||||:|||:|||||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302
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Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVS 363
              :| | |:|:||||||||||:|||| ||       ||||  || |||| ||:||| ||||||
Db        303 NASISVRAQDRYYSSSWSEWASVPCSPW-----RNLPVATPDPGMFPCLHHSQNLLRAVS 357

Qy        364 NTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGS 423
              | ||||||||| | ||||||||||||||||||||||||||||| ||||| ||| | |||||
Db        358 NMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGS 417

Qy        424 CLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQA 483
              |||| | |||  |||||||||||||||:||| ||||||||||||||||||  ||||:||
Db        418 CLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQA 477

Qy        484 LNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533
              ||||| |||||||||||||||||||||||||||||||:|:||||||:|
Db        478 LNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 527
```

RESULT 6
AAE19818
ID AAE19818 standard; Protein; 526 AA.
XX
AC AAE19818;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human IL-12.0 protein.
XX
KW Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW immunotherapeutic response; IL-12; human.
XX
OS Homo sapiens.
XX
PN US2002018767-A1.
XX
PD 14-FEB-2002.
XX
PF 10-APR-2001; 2001US-0828825.
XX
PR 27-JUL-2000; 2000KR-0043498.
XX
PA (LEES/) LEE S.
PA (KIMH/) KIM H.
XX
PI Lee S, Kim H;
XX
DR WPI; 2002-239247/29.
DR N-PSDB; AAD31546.
XX
PT New expression system, useful as vaccine for treating cancer, comprises
PT DNA molecule encoding interleukin-12 and costimulatory molecule,
PT operably linked to promoter that directs the expression of DNA molecule
PT -
XX
PS Example 1; Fig 7; 76pp; English.
XX
CC The invention relates to an expression system which comprises a DNA
CC molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC operably linked to a promoter that directs the expression of the DNA
CC molecule. Expression vectors of the invention are useful for in vitro
CC generation of genetically modified human cancer cells for cancer
CC therapy. These cells share phenotypes of both antigen presenting cells
CC and cancer cells and are suitable as a cellular vaccine for certain
CC types of cancer. Expression vectors are useful for eliciting an anti
CC tumour immune response in a individual. They are useful for activating
CC T cells for immunotherapeutic responses against primary or metastatic
CC cancers. The present sequence is a protein encoded by human IL-12.0
CC DNA present in pIRES-hB7-1-IL12.0 vector.
XX
SQ Sequence 526 AA;

Query Match 84.0%; Score 2354; DB 23; Length 526;
Best Local Similarity 84.7%; Pred. No. 3.7e-189;
Matches 448; Conservative 28; Mismatches 47; Indels 6; Gaps 2;

```
Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| ||||:|||||:|||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:||||||||:|||:|||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVS 363
              :| | |:|:||||||||||:|||| ||       ||||  || |||| ||:||| ||||||
Db        303 NASISVRAQDRYYSSSWSEWASVPCSPW-----RNLPVATPDPGMFPCLHHSQNLLRAVS 357

Qy        364 NTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGS 423
              | ||||||||| | ||||||||||||||||||||||||||||| ||||| ||| | |||||
Db        358 NMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGS 417

Qy        424 CLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQA 483
              |||| | |||  |||||||||||||||:||| ||||||||||||||||||  ||||:||
Db        418 CLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQA 477

Qy        484 LNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNS 532
              ||||| ||||||||||||||||||||||||||||||||||:|:|||||:
Db        478 LNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNA 526
```

RESULT 7
AAW41791
ID AAW41791 standard; peptide; 329 AA.
XX
AC AAW41791;
XX
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P40 subunit.
XX
KW Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW antiviral; vaccine adjuvant.
XX
OS Canis sp.
XX
PN JP10036397-A.
XX
PD 10-FEB-1998.
XX
PF 08-NOV-1996; 96JP-0296789.
XX
PR 23-MAY-1996; 96JP-0128104.
PR 08-NOV-1995; 95JP-0289729.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1998-174914/16.
DR N-PSDB; AAV13817.
XX
PT Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT activities are expected
XX
PS Claim 2; Pages 10-11; 12pp; Japanese.
XX

```
CC   The present sequence is a canine interleukin-12 (IL-12) P40
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence   329 AA;

  Query Match            62.9%;  Score 1764;  DB 19;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-140;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||||||||
Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 8
AAY02342
ID   AAY02342 standard; Protein; 329 AA.
XX
AC   AAY02342;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Canine Interleukin-12 (IL-12) protein sequence.
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease.
XX
OS   Canis sp.
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   N-PSDB; AAX35625.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 14-15; 16pp; Japanese.
XX
CC   The present sequence represents canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence   329 AA;

  Query Match            62.9%;  Score 1764;  DB 20;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-140;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||||||||
Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 9
AAW84373
ID   AAW84373 standard; Protein; 329 AA.
XX
AC   AAW84373;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Canine interleukin 12 protein.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis.
XX
OS   Canis sp.
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
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DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03162.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 30-32; 45pp; Japanese.
XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   329 AA;

  Query Match             62.9%;  Score 1764;  DB 20;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-140;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||||||||
Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 10
AAG66482
ID   AAG66482 standard; Protein; 329 AA.
XX
AC   AAG66482;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #3.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Signal_peptide
FT   Protein         23..329
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64388.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Disclosure; Page 17; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence   329 AA;

  Query Match             62.9%;  Score 1764;  DB 22;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-140;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||||||||
Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 11
AAW41790
ID   AAW41790 standard; peptide; 329 AA.
XX
AC   AAW41790;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant.
XX
OS   Canis sp.
XX
PN   JP10036397-A.
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XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   N-PSDB; AAV13816.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 2; Page 8; 12pp; Japanese.
XX
CC   The present sequence is a canine interleukin-12 (IL-12) P40
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence   329 AA;

  Query Match             61.9%;  Score 1735;  DB 19;  Length 329;
  Best Local Similarity   99.4%;  Pred. No. 2.2e-137;
  Matches  324;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 LKPLENSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||| ||
Db        304 DAKIRVQARDRYYSSSWSDWASVPCS 329


RESULT 12
AAY02339
ID   AAY02339 standard; Protein; 329 AA.
XX
AC   AAY02339;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Canine Interleukin-12 (IL-12) protein sequence.
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease.
XX
OS   Canis sp.
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   N-PSDB; AAX35615.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 12; 16pp; Japanese.
XX
CC   The present sequence represents canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence   329 AA;

  Query Match             61.9%;  Score 1735;  DB 20;  Length 329;
  Best Local Similarity   99.4%;  Pred. No. 2.2e-137;
  Matches  324;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 LKPLENSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||| ||
Db        304 DAKIRVQARDRYYSSSWSDWASVPCS 329


RESULT 13
AAW84371
ID   AAW84371 standard; Protein; 329 AA.
XX
AC   AAW84371;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Canine interleukin 12 protein.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
```

```
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis.
XX
OS   Canis sp.
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03152.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 23-25; 45pp; Japanese.
XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   329 AA;

  Query Match             61.9%;  Score 1735;  DB 20;  Length 329;
  Best Local Similarity   99.4%;  Pred. No. 2.2e-137;
  Matches  324;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 LKPLENSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||| ||
Db        304 DAKIRVQARDRYYSSSWSDWASVPCS 329

RESULT 14
AAG66480
ID   AAG66480 standard; Protein; 329 AA.
XX
AC   AAG66480;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #1.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Signal_peptide
FT   Protein         23..329
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64378.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Disclosure; Page 14; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence   329 AA;

  Query Match             61.9%;  Score 1735;  DB 22;  Length 329;
  Best Local Similarity   99.4%;  Pred. No. 2.2e-137;
  Matches  324;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              ||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        244 LKPLENSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||| ||
```

```
Db        304 DAKIRVQARDRYYSSSWSDWASVPCS 329


RESULT 15
AAW74322
ID   AAW74322 standard; Protein; 330 AA.
XX
AC   AAW74322;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p40 subunit.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   N-PSDB; AAX18176.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 1; Page 22-24; 51pp; Japanese.
XX
CC   This sequence is the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence   330 AA;

  Query Match            61.7%;  Score 1729.5;  DB 20;  Length 330;
  Best Local Similarity  98.5%;  Pred. No. 6.3e-137;
  Matches  325;  Conservative    1;  Mismatches    3;  Indels    1;  Gaps    1;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLL-IHKKEDGIWSTDILKE 119
              ||||||||||||||||||||||||||||||||||||||||||    ||:||||||||||||
Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLFDSTKKKDGIWSTDILKE 120

Qy        120 QKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAER 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAER 180

Qy        180 VRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPP 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPP 240

Qy        240 TNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKV 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TNLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKV 300

Qy        300 VCHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              ||||||||||||||||||||||||||||||
Db        301 VCHKDAKIRVQARDRYYSSSWSDWASVSCS 330


Search completed: July 15, 2003, 11:02:55
Job time : 54.5793 secs
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:49 ; Search time 23.3616 Seconds
(without alignments)
2193.328 Million cell updates/sec

Title: US-09-917-265-62
Perfect score: 2804
Sequence: 1 MHPQQLVISWFSLVLLASPL.....HAFRIRAVTINRMMSYLNSS 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1501.5	53.5	328	2	A38957	interleukin 12B pr
2	1141.5	40.7	335	2	I72789	interleukin 12 p40
3	873	31.1	253	2	B38957	interleukin 12A pr
4	549	19.6	215	2	I56135	interleukin 12 p35
5	211.5	7.5	468	1	A41242	interleukin-6 rece
6	195	7.0	440	2	JL0144	interleukin-6 rece
7	191	6.8	460	2	JL0145	interleukin-6 rece
8	181.5	6.5	372	2	I58141	ciliary neurotroph
9	178	6.3	362	2	S60614	growth promoting a
10	170	6.1	372	1	UHHUCN	ciliary neurotroph
11	159.5	5.7	422	2	I37891	interleukin-11 rec
12	157	5.6	432	2	I48343	interleukin-11 rec
13	143	5.1	812	2	H96544	hypothetical prote
14	123.5	4.4	739	2	JS0675	vascular cell adhe
15	123	4.4	462	1	A37986	interleukin-6 rece
16	122.5	4.4	1277	2	T30532	neural cell adhesi
17	120	4.3	831	2	JQ1655	prolactin receptor
18	120	4.3	1197	2	T30581	neural cell adhesi
19	119.5	4.3	977	2	I45877	protein-tyrosine k
20	114.5	4.1	3678	2	S28916	dystrophin - mouse
21	112.5	4.0	1323	2	PN0568	connectin 3B - chi
22	111.5	4.0	310	2	A29884	prolactin receptor
23	111.5	4.0	412	2	A41070	prolactin receptor
24	111.5	4.0	610	2	A34631	lactogen receptor
25	111.5	4.0	610	2	A36116	prolactin receptor
26	111.5	4.0	1323	2	E88257	protein let-23 [im
27	111.5	4.0	1374	2	S70712	protein-tyrosine k
28	111	4.0	279	2	B32985	somatotropin-bindi
29	111	4.0	638	2	A33505	somatotropin recep
30	111	4.0	2670	2	A46719	inositol 1,4,5-tri
31	110.5	3.9	718	2	T26646	hypothetical prote
32	109.5	3.9	1181	2	T19736	hypothetical prote
33	108	3.9	581	2	I45971	prolactin receptor
34	108	3.9	635	2	A45266	MPL-P protein prec
35	107.5	3.8	615	2	T20187	hypothetical prote
36	107.5	3.8	638	2	S12136	somatotropin recep
37	106	3.8	288	2	B59405	prolactin receptor
38	106	3.8	376	2	A59405	prolactin receptor
39	106	3.8	622	2	A40144	prolactin receptor
40	106	3.8	739	2	JN0581	vascular cell adhe
41	106	3.8	978	1	A49814	protein-tyrosine k
42	105.5	3.8	1232	2	T43027	neural cell adhesi
43	105.5	3.8	1601	2	AE2011	hypothetical prote
44	104.5	3.7	638	2	B28176	somatotropin recep
45	104.5	3.7	677	2	S33608	somatotropin-bindi

ALIGNMENTS

RESULT 1
A38957
interleukin 12B precursor [validated] - human
N;Alternate names: cytotoxic lymphocyte maturation factor 40K chain; natural killer c
C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Nov-2000
C;Accession: A38957; B39359; S21688; B36055
R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.
i, G.; Perussia, B.
J. Immunol. 146, 3074-3081, 1991
A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric
A;Reference number: A38957; MUID:91201875; PMID:1673147
A;Accession: A38957
A;Molecule type: mRNA
A;Residues: 1-328 <WOL>
A;Cross-references: GB:M65290
R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nab
Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
A;Title: Coexpression of two distinct genes is required to generate secreted bioactiv
A;Reference number: A39359; MUID:91239523; PMID:1674604
A;Accession: B39359
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-328 <GUB>
A;Cross-references: GB:M65272; GB:M38444; NID:g180625; PIDN:AAA35695.1; PID:g180626
R;Podlaski, F.J.; Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Levin, W.; Danho, W.; Chi
Arch. Biochem. Biophys. 294, 230-237, 1992
A;Title: Molecular characterization of interleukin 12.
A;Reference number: S21688; MUID:92198015; PMID:1347984
A;Accession: S21688
A;Molecule type: protein
A;Residues: 23-28;46-59;74-80,'X',94-130;161-169,'X',171-180;213-235;240-250;289-299,
A;Experimental source: lymphoblastoid cell line NC-37
R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A;Title: Purification to homogeneity and partial characterization of cytotoxic lympho
A;Reference number: A36055; MUID:90370873; PMID:2204066
A;Accession: B36055
A;Molecule type: protein
A;Residues: 23-45 <STE>
A;Experimental source: lymphoblastoid cell line NC-37
C;Genetics:
A;Gene: GDB:IL12B; NKSF2
A;Cross-references: GDB:127870; OMIM:161561
A;Map position: 5q31.1-5q33.1
C;Keywords: cytokine; glycoprotein; heparin binding; heterodimer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-328/Product: interleukin 12B #status predicted <MAT>
F;27-30/Region: heparin binding #status predicted
F;125/Binding site: carbohydrate (Asn) (covalent) #status absent
F;135,303/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;222/Binding site: carbohydrate (Asn) (covalent) #status experimental

```
F;319/Modified site: 2'-mannosyl-tryptophan (Trp) (partial) #status experimental

  Query Match             53.5%;  Score 1501.5;  DB 2;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 6.7e-108;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||  |||||:|||||:||||||||||:||||||||||||  |||||  ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||||||||||||||||||||||||:|||  ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              |||  ||:|||||||||||||||  |||||  ||||||||  |||||||||  ||||||||  |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::|  :|:|||||  ||||:|||||||||:|||:|||||||||||||||||||||||  |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              ||||||||  |||||||||||||||||||||||:|  |||:  ||||||:  |||||  |:|  |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :|  |  |:|:|||||||||:||||  ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 2
I72789
interleukin 12 p40 subunit - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I72789
R;Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K.;
J. Immunol. 148, 3433-3440, 1992
A;Title: Cloning and Expression of Murine IL-12.
A;Reference number: I56135; MUID:92268481; PMID:1350290
A;Accession: I72789
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-335 <RES>
A;Cross-references: GB:M86671; NID:g293663; PIDN:AAA39296.1; PID:g293664

  Query Match             40.7%;  Score 1141.5;  DB 2;  Length 335;
  Best Local Similarity   65.5%;  Pred. No. 3.5e-80;
  Matches  220;  Conservative   38;  Mismatches   65;  Indels   13;  Gaps    4;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              | ||:| ||||::||| |||||:||||||||||:|| |||||| | ||| |||||||||
Db          1 MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |   |:||||||||  |||| ||||||||||: || | ||:||||:|||||:||
Db         61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              |  ||| |||||| ||||||||  ||    : ||||::|||    | : ||||  :||||:|
Db        118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKV 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
               :| |||:||:| |||   ||:|||:||||: ::|  : |||||::||||||||||||
Db        178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
              |||:||||||: |||||||||:|||||||||| | :: | |  : |         |    |
Db        238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLV 296

Qy        293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
              :||| :| | |   : |||:||||:|| | || | |
Db        297 EKTSTEVQC-KGGNVCVQAQDRYYNSSCSKWACVPC 331


RESULT 3
B38957
interleukin 12A precursor [validated] - human
N;Alternate names: cytotoxic lymphocyte maturation factor 35K chain; natural killer c
C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 01-Dec-2000
C;Accession: B38957; A39359; A36055
R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.
i, G.; Perussia, B.
J. Immunol. 146, 3074-3081, 1991
A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric
A;Reference number: A38957; MUID:91201875; PMID:1673147
A;Accession: B38957
A;Molecule type: mRNA
A;Residues: 1-253 <WOL>
A;Cross-references: GB:M65290
A;Note: it is uncertain whether Met-1 or Met-35 is the initiator
R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nab
Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
A;Title: Coexpression of two distinct genes is required to generate secreted bioactiv
A;Reference number: A39359; MUID:91239523; PMID:1674604
A;Accession: A39359
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 35-246,'T',248-253 <GUB>
A;Cross-references: GB:M65271; GB:M38443; NID:g180623; PIDN:AAA35694.1; PID:g180624
R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A;Title: Purification to homogeneity and partial characterization of cytotoxic lympho
A;Reference number: A36055; MUID:90370873; PMID:2204066
A;Accession: A36055
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'X',58-70,'X',72-82 <STE>
C;Genetics:
A;Gene: GDB:IL12A; NKSF1
A;Cross-references: GDB:127869; OMIM:161560
A;Map position: 3p12-3q13.2
C;Keywords: cytokine; glycoprotein; heterodimer
F;57-253/Product: interleukin 12A #status predicted <MAT>
F;127,141,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             31.1%;  Score 873;  DB 2;  Length 253;
  Best Local Similarity   86.4%;  Pred. No. 1.1e-59;
  Matches  171;  Conservative    7;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        336 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 395
              :||||  || |||| ||:||| ||||||| ||||||||| | ||||||||||||||||||
Db         56 ARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTST 115

Qy        396 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 455
              |||||||||| ||||| ||| | ||||||||| | |||  ||||||||||||:||| |
Db        116 VEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM 175

Qy        456 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 515
              ||||||||||||||||||  ||||:|||||| ||||||||||||||||||||||||||||
Db        176 NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHA 235

Qy        516 FRIRAVTINRMMSYLNSS 533
              ||||||||:|:|||||:|
Db        236 FRIRAVTIDRVMSYLNAS 253


RESULT 4
I56135
interleukin 12 p35 subunit - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I56135
R;Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K
```

J. Immunol. 148, 3433-3440, 1992
A;Title: Cloning and Expression of Murine IL-12.
A;Reference number: I56135; MUID:92268481; PMID:1350290
A;Accession: I56135
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: GB:M86672; NID:g198336; PIDN:AAA39292.1; PID:g198337

Query Match 19.6%; Score 549; DB 2; Length 215;
Best Local Similarity 57.4%; Pred. No. 7.7e-35;
Matches 109; Conservative 29; Mismatches 52; Indels 0; Gaps 0;

```
Qy        344 PSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLE 403
Db         26 PVSGPARCLSQSRNLLKTTDDMVKTAREKLKHYSCTAEDIDHEDITRDQTSTLKTCLPLE 85

Qy        404 LTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDP 463
Db         86 LHKNESCLATRETSSTTRGSCLPPQKTSLMMTLCLGSIYEDLKMYQTEFQAINAALQNHN 145

Qy        464 KRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTI 523
Db        146 HQQIILDKGMLVAIDELMQSLNHNGETLRQKPPVGEADPYRVKMKLCILLHAFSTRVVTI 205

Qy        524 NRMMSYLNSS 533
Db        206 NRVMGYLSSA 215
```

RESULT 5
A41242
interleukin-6 receptor precursor - human
N;Contains: interleukin-6 receptor, soluble form
C;Species: Homo sapiens (man)
C;Date: 27-Mar-1992 #sequence_revision 02-Dec-1994 #text_change 21-Jul-2000
C;Accession: A41242; JU0080; S17468; A61459; S14621
R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.
Science 241, 825-828, 1988
A;Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor.
A;Reference number: A41242; MUID:88305347; PMID:3136546
A;Accession: A41242
A;Molecule type: mRNA
A;Residues: 1-468 <YAM>
A;Cross-references: GB:M20566; NID:g33845; PIDN:CAA31312.1; PID:g33846
R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.
Proc. Jpn. Acad. 64, 209-211, 1988
A;Title: Molecular structure of interleukin 6 receptor.
A;Reference number: JU0080
A;Accession: JU0080
A;Molecule type: mRNA
A;Residues: 1-468 <YA2>
R;Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich
Biochem. J. 277, 659-664, 1991
A;Title: Structural and functional studies on the human hepatic interleukin-6 receptor.
A;Reference number: S17468; MUID:91336983; PMID:1872801
A;Accession: S17468
A;Molecule type: mRNA
A;Residues: 1-468 <SCH>
A;Cross-references: EMBL:X58298; NID:g32580; PIDN:CAA41231.1; PID:g32581
A;Experimental source: hepatoma cell line HepG2
R;Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.
J. Exp. Med. 170, 1409-1414, 1989
A;Title: Soluble cytokine receptors are present in normal human urine.
A;Reference number: A61459; MUID:90010793; PMID:2529343
A;Accession: A61459
A;Molecule type: protein
A;Residues: 20-49 <NOV>
C;Comment: Through this receptor, interleukin-6 induces proliferation, activation, and d
C;Comment: This growth factor receptor does not have a tyrosine kinase domain.
C;Genetics:
A;Gene: GDB:IL6R
A;Cross-references: GDB:127966; OMIM:147880
A;Map position: 1q21-1q21
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-468/Product: interleukin-6 receptor #status predicted <MAT>
F;20-363/Domain: extracellular #status predicted <EXT>
F;40-98/Domain: immunoglobulin homology <IMM2>
F;121-309/Domain: cytokine receptor homology <CRS>
F;364-386/Domain: transmembrane #status predicted <TMM>
F;387-468/Domain: intracellular #status predicted <INT>
F;47-96/Disulfide bonds: #status predicted
F;55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.5%; Score 211.5; DB 1; Length 468;
Best Local Similarity 21.1%; Pred. No. 2.2e-08;
Matches 92; Conservative 79; Mismatches 157; Indels 109; Gaps 19;

```
Qy         42 PGEMVVLTCHTPEEDD---ITW------TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK 92
Db         39 PGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYR 98

Qy         93 GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW-------L 145
Db         99 AGRPAGTVHLLV----------DVPPEEPQ------LSCFRKSPLSNVVCEWGPRSTPSL 142

Qy        146 T--AISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS---AC 200
Db        143 TTKAVLLVRKFQNSPAEDFQEP----C-----------------QYSQESQKFSCQLAV 180

Qy        201 PSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEY 259
Db        181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240

Qy        260 PDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDA------KIRVQARD 313
Db        241 PHSWNS--SFYRLRFELRYRAERSKTFTTWMVKDLQHHCVI--HDAWSGLRHVVQLRAQE 296

Qy        314 RYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTL 373
Db        297 EFGQGEWSEW-SPEAMGTPWTESRSPPAE----------NEVSTPMQAL---------- 334

Qy        374 ELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFM 433
Db        335 -----TTNKDDDNILFRDSANATS--LPVQ--------DSSSVPLPT--FLVAGGSLAFG 377

Qy        434 TVLCLSSIYEDLKMYQM 450
Db        378 TLLCIAIVLRFKKTWKL 394
```

RESULT 6
JL0144
interleukin-6 receptor precursor (clone lambda P1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C;Accession: JL0144
R;Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto,
J. Exp. Med. 171, 2001-2009, 1990
A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle
A;Reference number: JL0144; MUID:90278354; PMID:2112585
A;Accession: JL0144
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-440 <SUG>
A;Cross-references: GB:X51976; NID:g53548; PIDN:CAA36238.1; PID:g53549
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-440/Product: interleukin-6 receptor #status predicted <MAT>
F;40-94/Domain: immunoglobulin homology <IMM>
F;117-306/Domain: cytokine receptor homology <CRS>
F;358-385/Domain: transmembrane #status predicted <TRA>

```
  Query Match             7.0%;  Score 195;  DB 2;  Length 440;
  Best Local Similarity   20.7%;  Pred. No. 3.8e-07;
  Matches  100;  Conservative   74;  Mismatches  184;  Indels  126;  Gaps   20;

Qy         13 LVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPE-EDDIT----WTSAQSSE 67
              : |||:| :|:          |         ||  | | |    |   ::|    :: :|: |
Db         10 VALLAAPAVALVLGSCRALEVANGTVTSLPGATVTLICPGKEAAGNVTIHWVYSGSQNRE 69

Qy         68 VLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKI 127
                :| || ::   :  | | | |      ::    ||:          |:  |: :
Db         70 WTTTGNTLVLRDVQLSDTGDYLCSLNDHLVGTVPLLV----------DVPPEEPK----- 114

Qy        128 FLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDY 187
               | |  ||      | |              |  | |   |     | |:::   |
Db        115 -LSCFRKNPLVNAICEW--------------RPSSTPSPTT--KAVLFAKKINTTN-GK 155

Qy        188 KKYTVECQEGSACPSAEESLPIEVVV-DAIHKL----------KYENYTSSFFIRDIIKP 236
               : | ||      |   |  :|::  | :: :            ::  :|    :::|
Db        156 SDFQVPCQYSQQLKSF--SCQVEILEGDKVYHIVSLCVANSVGSKSSHNEAFHSLKMVQP 213

Qy        237 DPPTNLQLKPLK-NSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRL----- 290
              ||| || :  :    | ::|||::|:||    ||: | | :: :   ::|    |
Db        214 DPPANLVVSAIPGRPRWLKVSWQHPETWDP--SYYLLQFQLRYRPVWSKEFTVLLLPVAQ 271

Qy        291 --CVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGM 348
                ||   : : | |    ::|: ::      ||:|:*             |  | :| :
Db        272 YQCVIHDALRGVKH---VVQVRGKEELDLGQWSEWS--------------PEVTGTPWI 313

Qy        349 FQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNE 408
               :      |    : |  | :           :  :|||  :  |       |:: : :
Db        314 AE---PRTTPAGILWNPTQVS---------VEDSANHEDQYESSTEATSVLAPVQESSSM 361

Qy        409 S----------------------CLASREISLITNG--SCLASGK---------ASFMT 434
              |                      |   |  | : :|  ||: |||          | :
Db        362 SLPTFLVAGGSLAFGLLLCVFIILCWEPRPHSPLQDGADSCVLSGKQIICACAEGGSPLH 421

Qy        435 VLCL 438
              ||||
Db        422 VLCL 425
```

RESULT 7
JL0145
interleukin-6 receptor precursor (clone lambda 301) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C;Accession: JL0145; S14543
R;Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle gen
A;Reference number: JL0144; MUID:90278354; PMID:2112585
A;Accession: JL0145
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-460 <SUG>
A;Cross-references: GB:X51975; NID:g49725; PIDN:CAA36237.1; PID:g49726
A;Experimental source: clone lambda 301
R;Fiorillo, M.T.; Ciliberto, G.; Dente, L.
submitted to the EMBL Data Library, July 1990
A;Description: Cloning and expression of murine IL-6 receptor.
A;Reference number: S14543
A;Accession: S14543
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373,'R',375-460 <FIO>
A;Cross-references: EMBL:X53802; NID:g52692; PIDN:CAA37810.1; PID:g52693
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C;Keywords: cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-460/Product: interleukin-6 receptor #status predicted <MAT>
F;40-94/Domain: immunoglobulin homology <IMM>
F;117-306/Domain: cytokine receptor homology <CRS>
F;358-385/Domain: transmembrane #status predicted <TRA>

```
  Query Match             6.8%;  Score 191;  DB 2;  Length 460;
  Best Local Similarity   20.9%;  Pred. No. 8.1e-07;
  Matches   94;  Conservative   73;  Mismatches  181;  Indels  102;  Gaps   19;

Qy         13 LVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPE-EDDIT----WTSAQSSE 67
              : |||:| :|:          |         ||  | | |    |   ::|    :: :|: |
Db         10 VALLAAPAVALVLGSCRALEVANGTVTSLPGATVTLICPGKEAAGNVTIHWVYSGSQNRE 69

Qy         68 VLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKI 127
                :| || ::   :  | | | |      ::    ||:          |:  |: :
Db         70 WTTTGNTLVLRDVQLSDTGDYLCSLNDHLVGTVPLLV----------DVPPEEPK----- 114

Qy        128 FLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDY 187
               | |  ||      | |                |  | |   |     | |:::   |
Db        115 -LSCFRKNPLVNAICEW--------------RPSSTPSPTT--KAVLFAKKINTTN-GK 155

Qy        188 KKYTVECQEGSACPSAEESLPIEVVV-DAIHKL----------KYENYTSSFFIRDIIKP 236
               : | ||      |   |  :|::  | :: :            ::  :|    :::|
Db        156 SDFQVPCQYSQQLKSF--SCQVEILEGDKVYHIVSLCVANSVGSKSSHNEAFHSLKMVQP 213

Qy        237 DPPTNLQLKPLK-NSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRL----- 290
              ||| || :  :    | ::|||::|:||    ||: | | :: :   ::|    |
Db        214 DPPANLVVSAIPGRPRWLKVSWQHPETWDP--SYYLLQFQLRYRPVWSKEFTVLLLPVAQ 271

Qy        291 --CVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGM 348
                ||   : : | |    ::|: ::      ||:|:              |  | :| :
Db        272 YQCVIHDALRGVKH---VVQVRGKEELDLGQWSEWS--------------PEVTGTPWI 313

Qy        349 FQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNE 408
               :      |    : |  | :           :  :|||  :  |       |::
Db        314 AE---PRTTPAGILWNPTQVS---------VEDSANHEDQYESSTEATSVLAPVQ----- 356

Qy        409 SCLASREISLITNGSCLASGKASFMTVLCL 438
                   |  :|| |    :| |  :|  :|||:
Db        357 ---ESSSMSLPT--FLVAGGSLAFGLLLCV 381
```

RESULT 8
I58141
ciliary neurotrophic factor receptor alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C;Accession: I58141; A47387
R;Ip, N.Y.; McClain, J.; Barrezueta, N.X.; Aldrich, T.H.; Pan, L.; Li, Y.; Wiegand, S
Neuron 10, 89-102, 1993
A;Title: The alpha component of the CNTF receptor is required for signaling and defin
A;Reference number: I58141; MUID:93152175; PMID:8381290
A;Accession: I58141
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-372 <IPN>
A;Cross-references: GB:S54212; NID:g265055; PIDN:AAB25290.1; PID:g265056
R;Clatterbuck, R.E.; Price, D.L.; Koliatsos, V.E.
Proc. Natl. Acad. Sci. U.S.A. 90, 2222-2226, 1993
A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult
A;Reference number: A47387; MUID:93211934; PMID:8460125
A;Accession: A47387
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 185-260,'D',262-277 <CLA>
A;Cross-references: GB:S57711; NID:g299331; PIDN:AAB25918.1; PID:g299332
A;Experimental source: Sprague-Dawley, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:128471, NCBIP:128472)
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: growth factor receptor
F;39-91/Domain: immunoglobulin homology <IMM>
F;116-296/Domain: cytokine receptor homology <CRS>

```
  Query Match             6.5%;  Score 181.5;  DB 2;  Length 372;
  Best Local Similarity   22.2%;  Pred. No. 3.2e-06;
  Matches   81;  Conservative   55;  Mismatches  150;  Indels   79;  Gaps   15;
```

```
Qy          8 ISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAP-------GEMVVLTCHTPEED-DIT 59
              : |    :||:   |::  :            :||       |  | | | |   |  :|
Db          5 VPWACCAVLAAAAAAVYTQKHS--------PQEAPHVQYERLGTDVTLPCGTASWDAAVT 56

Qy         60 W--TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDIL 117
              |       :  | :|  | ::  | | :| | |        |  :|:|    |:
Db         57 WRVNGTDLAPDLLNGSQLILRSLELGHSGLYACFHRDSWHLRHQVLLHV---GL------ 107

Qy        118 KEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL--KFSVKSSRGFSDPQGVTCGAVTL 175
                :  | | :  |   | | | :  | :   |:|             |  |:  :
Db        108 -----PPREPVLSCRSNTYPKGFYCSWHLSAPTYIPNTFNVT----------VLHGSKMM 152

Qy        176 SAER-VRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDII 234
              |:   : || : :|               ::  :| :   : | :     :|    |:
Db        153 VCEKDPALKNRCHIRYM----------HLFSTIKYKVSISVSNALGHNTTAITFDEFTIV 202

Qy        235 KPDPPTNLQLKPL-KNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVD 293
              ||||| |:   :|:  | | :||:|: | ||  | | | | | :: :          | :|
Db        203 KPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPES-FPLKFFLRYR---------PLILD 252

Qy        294 K------------TSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCSGGGGGGSRNLPT 341
              :            |       |:  |:| |:|     :||||:  : :       |:| |
Db        253 QWQHVELSNGTAHTITDAYAGKEYIIQVAAKDNEI-GTWSDWSVAAHATPWTEEPRHLTT 311

Qy        342 PTPSP 346
                :|
Db        312 EAQAP 316


RESULT 9
S60614
growth promoting activity receptor alpha precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C;Accession: S60614
R;Heller, S.; Finn, T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pueschel, A.W.; Rohrer, H.
Development 121, 2681-2693, 1995
A;Title: Analysis of function and expression of the chick GPA receptor (GPARalpha) sugge
A;Reference number: S60614; MUID:95401882; PMID:7671828
A;Accession: S60614
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-362 <HEL>
A;Cross-references: EMBL:Z48168; NID:g971417; PIDN:CAA88184.1; PID:g3063774
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C;Keywords: growth factor receptor
F;2-89/Domain: immunoglobulin homology <IMM>
F;114-294/Domain: cytokine receptor homology <CRS>

  Query Match             6.3%;  Score 178;  DB 2;  Length 362;
  Best Local Similarity   23.9%;  Pred. No. 5.8e-06;
  Matches   73;  Conservative   48;  Mismatches  112;  Indels   72;  Gaps   14;

Qy         43 GEMVVLTCHTPEED-DITWTSAQSSEVLGS---GKTLTIQVKEFGDAGQYTCHKGGKVLS 98
              |  | : | : : |  :||| |  :::  |   |  | ::  :   :|||:|:::|
Db         37 GADVTMKCGSMDWDAAVTWT-ANGTDIDDSHLNGSYLILKNVDLTQSGQYSCYEGSS--- 92

Qy         99 RSLLLIHKKEDGIWSTDILKEQKESK-----NKIFLKCEAKNYSGRFTCWWLTAISTDLK 153
                        |    || |   :       :  | | : ||   | | |     | :
Db         93 ------------WH---LKYQTYLRVGVPPKEPVLMCRSNNYPKGFYCSWHLPSPTYIP 136

Qy        154 FSVKSSRGFSDPQGVTCGAVTLSAER-VRVDNRDYKKYTVECQEGSACPSAEESLPIEVV 212
              |   |        |  |   :  |: :   || : :|               ::  :|
Db        137 NSFNIS--------VIHGTREMVCEKDIFPKNRCHIRYL----------QLFSTVKYKVT 178

Qy        213 VDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNS-RHVEVSWEYPDTWSTPHSYFS 271
              :   : |   : | :|    |:|||| ::  ||: |: | :||||: | :|  | | |
Db        179 LTVTNALGKNSTTLTFDEFAIVKPDPPESVVAKPVPNNPRRLEVSWQNPSSWPDPES-FP 237

Qy        272 LTFCIQAQGKNNREKKDRLCVDK------------TSAKVVCHKDAKIRVQARDRYYSSS 319
              | | :: :          | :|:           |       |:  |:| |:|     :
Db        238 LKFFLRYR---------PLILDQWQHVELSDGTSHTITDAYAGKEYIIQVAAKDNDI-GT 287

Qy        320 WSDWA 324
              ||||:
Db        288 WSDWS 292


RESULT 10
UHHUCN
ciliary neurotrophic factor receptor alpha precursor - human
N;Alternate names: CNTF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: A40854; A56526
R;Davis, S.; Aldrich, T.H.; Valenzuela, D.M.; Wong, V.; Furth, M.E.; Squinto, S.P.; Y
Science 253, 59-63, 1991
A;Title: The receptor for ciliary neurotrophic factor.
A;Reference number: A40854; MUID:91289158; PMID:1648265
A;Accession: A40854
A;Molecule type: mRNA
A;Residues: 1-372 <DAV>
A;Cross-references: GB:M73238
R;Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Brannan, C.I.; McClai
Genomics 25, 157-163, 1995
A;Title: Genomic organization and chromosomal localization of the human and mouse gen
A;Reference number: A56526; MUID:95293367; PMID:7774913
A;Accession: A56526
A;Molecule type: DNA
A;Residues: 1-346,'S',348-372 <VAL>
A;Cross-references: GB:L38025; NID:g608654; PIDN:AAA91337.1; PID:g608656
C;Comment: The CNTF receptor is attached to the membrane by a glycosylphosphatidylino
C;Comment: The CNTF receptor sequence appears to contain several PEST regions.
C;Genetics:
A;Gene: GDB:CNTFR
A;Cross-references: GDB:134652; OMIM:118946
A;Map position: 9p13-9p13
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: glycoprotein; growth factor receptor; membrane protein; phosphatidylinosi
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-372/Product: ciliary neurotrophic factor receptor #status predicted <MAT>
F;39-91/Domain: immunoglobulin homology <IMM>
F;116-296/Domain: cytokine receptor homology <CRS>
F;46-89/Disulfide bonds: #status predicted
F;60,70,142,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             6.1%;  Score 170;  DB 1;  Length 372;
  Best Local Similarity   23.0%;  Pred. No. 2.5e-05;
  Matches   69;  Conservative   42;  Mismatches  127;  Indels   62;  Gaps   12;

Qy         43 GEMVVLTCHTPEED-DITW--TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSR 99
              |  | | | |   |  :||       :  | :|  | :   | | :| | |        |
Db         39 GSDVTLPCGTANWDAAVTWRVNGTDLAPDLLNGSQLVLHGLELGHSGLYACFHRDSWHLR 98

Qy        100 SLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL--KFSVK 157
                :|:|    |:             :  | | :  |   | | |     | :   |:|
Db         99 HQVLLHV---GL----------PPREPVLSCRSNTYPKGFYCSWHLPTPTYIPNTFNVT 144

Qy        158 SSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIH 217
                |           : :  :   : || : :|                 ::  :| :   :
Db        145 VLHG---------SKIMVCEKDPALKNRCHIRYM----------HLFSTIKYKVSISVSN 185

Qy        218 KLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEYPDTWSTPHSYFSLTFCI 276
              | :     :|    |:|||||| |:  :|:  | | :||:|: | ||  | | | | | :
Db        186 ALGHNATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPES-FPLKFFL 244

Qy        277 QAQGKNNREKKDRLCVDK------------TSAKVVCHKDAKIRVQARDRYYSSSWSDWA 324
              : :           | :|:            |       |:  |:| |:|     :||||:
Db        245 RYR---------PLILDQWQHVELSDGTAHTITDAYAGKEYIIQVAAKDNEI-GTWSDWS 294


RESULT 11
I37891
interleukin-11 receptor alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Dec-1999
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C;Accession: I37891; G01970; G01971
R;Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minvielle,
Blood 86, 2534-2540, 1995
A;Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic cyt
A;Reference number: I37891; MUID:95399754; PMID:7670098
A;Accession: I37891
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-422 <RES>
A;Cross-references: EMBL:Z38102; NID:g995653; PIDN:CAA86224.1; PID:g995654
R;Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A;Reference number: G08959
A;Accession: G01970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-422 <VAN>
A;Cross-references: EMBL:U32323; NID:g975334; PIDN:AAB36491.1; PID:g975335
R;Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A;Reference number: G08961
A;Accession: G01971
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-422 <VA2>
A;Cross-references: EMBL:U32324; NID:g975336; PIDN:AAB36492.1; PID:g975337
C;Genetics:
A;Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 390/2; 418/1
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
F;120-310/Domain: cytokine receptor homology <CRS>

  Query Match             5.7%;  Score 159.5;  DB 2;  Length 422;
  Best Local Similarity   20.1%;  Pred. No. 0.00019;
  Matches   76;  Conservative   54;  Mismatches  174;  Indels   75;  Gaps   15;

Qy         37 WHPDA-----PGEMVVLTC-HTPEEDDITWTSAQSSEVL-----GSGKTLTIQVKEFGDA 85
              | |        ||  | | |       | ::|      ::|     | |  | :   :  |
Db         30 WGPPGVQYGQPGRSVKLCCPGVTAGDPVSWFRDGEPKLLQGPDSGLGHELVLAQADSTDE 89

Qy         86 GQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW- 144
              | | |               :  ||     :  :      :  : |:| :|   |:| |
Db         90 GTYIC--------------QTLDGALGGTVTLQLGYPPARPVVSCQAADYE-NFSCTWS 133

Qy        145 -----------LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDY-KKYTV 192
                        ||:          | |         |    | | |  |   ::  :| :
Db        134 PSQISGLPTRYLTSYRKKTVLGADSQRRSPSTGPWPCPQDPLGAARCVVHGAEFWSQYRI 193

Qy        193 ECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKN-SR 251
                 | :   ::   | :                     :: |::|||| |::: :    |
Db        194 NVTEVNPLGASTRLLDVS------------------LQSILRPDPPQGLRVESVPGYPR 234

Qy        252 HVEVSWEYPDTW-STPHSYFSLTFCIQAQGKNNR--EKKDRLCVDKTSAKVVCHKDAKIR 308
               :  || || :|   ||  | | | :| :   :      :   :::     |      :|
Db        235 RLRASWTYPASWPCQPH--FLLKFRLQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVR 292

Qy        309 VQARDRYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQK 368
              | |||   : :|| |   |    |   :  :|   |: |      |:|  :    ::
Db        293 VSARDFLDAGTWSTW---SPEAWGTPSTGTIPKEIPAWGQL----HTQPEVEPQVDSPAP 345

Qy        369 ARQTLELYSCTSEEIDHED 387
               | :|: :      :|| |
Db        346 PRPSLQPH---PRLLDHRD 361


RESULT 12
I48343
interleukin-11 receptor alpha-chain precursor - mouse
N;Alternate names: cytokine type 1 receptor
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Jan-2000
C;Accession: I48343; S51619
R;Neuhaus, H.; Bettenhausen, B.; Bilinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gossle
Dev. Biol. 166, 521-542, 1994
A;Title: etl2, a novel putative type-1 cytokine receptor expressed during mouse embry
A;Reference number: I48343
A;Accession: I48343
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-432 <RES>
A;Cross-references: EMBL:X74953; NID:g673437; PIDN:CAA52908.1; PID:g673438
R;Hilton, D.J.; Hilton, A.A.; Raicevic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M
EMBO J. 13, 4765-4775, 1994
A;Title: Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for hi
A;Reference number: S51619; MUID:95045367; PMID:7957045
A;Accession: S51619
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-432 <HIL>
A;Cross-references: EMBL:U14412; NID:g576454; PIDN:AAA53248.1; PID:g576455
C;Genetics:
A;Gene: Etl2/IL11
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: cytokine receptor
F;120-310/Domain: cytokine receptor homology <CRS>

  Query Match             5.6%;  Score 157;  DB 2;  Length 432;
  Best Local Similarity   21.4%;  Pred. No. 0.00031;
  Matches   94;  Conservative   52;  Mismatches  154;  Indels  140;  Gaps   22;

Qy         37 WHPDA-----PGEMVVLTC-----HTPEEDDITWTSAQSSEVL-----GSGKTLTIQVKE 81
              | |        ||  |:| |       ||    ::|     | :|     | |  | :   :
Db         30 WGPPGVQYGQPGRPVMLCCPGVSAGTP----VSWFRDGDSRLLQGPDSGLGHRLVLAQVD 85

Qy         82 FGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLK---------- 130
               | | |                :  ||:          |   : ||
Db         86 SPDEGTYVC--------------QTLDGV----------SGGMVTLKLGFPPARPEVS 119

Qy        131 CEAKNYSGRFTCWW-----------LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAE 178
              |:| :|   |:| |             ||:          :| |         |    | |
Db        120 CQAVDYE-NFSCTWSPGQVSGLPTRYLTSYRKKTLPGAESQRESPSTGPWPCPQDPLEAS 178

Qy        179 RVRVDNRDY-KKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPD 237
              | |   ::  :| :   | :   ::   | :                      :: |::||
Db        179 RCVVHGAEFWSEYRINVTEVNPLGASTCLLDVR------------------LQSILRPD 219

Qy        238 PPTNLQLKPLKN-SRHVEVSWEYPDTW-STPHSYFSLTFCIQAQGKNNR--EKKDRLCVD 293
              ||  |::: :    | :  || || :|   ||  | | | :| :   :      : : ::
Db        220 PPQGLRVESVPGYPRRLHASWTYPASWRRQPH--FLLKFRLQYRPAQHPAWSTVEPIGLE 277

Qy        294 KTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQ--- 350
              :     |      :|| |||   : :|| |:  :                |||  |  |
Db        278 EVITDAVAGLPHAVRVSARDFLDAGTWSAWSPEAWG------------TPSTGPLQDEI 324

Qy        351 ---CLNHSQTLLRAVS--NTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELT 405
                  | |  |  |:  ::   || :|:        :|| |             |||
Db        325 PDWSQGHGQQLEAVVAQEDSPAPARPSLQ---PDPRPLDHRD------------PLE-- 366

Qy        406 MNESCLASREISLITNGSCL 425
              : |||  |      |||
Db        367 -QVAVLASLGIF-----SCL 380


RESULT 13
H96544
hypothetical protein F8A12.4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96544
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
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ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-812 <STO>
A;Cross-references: GB:AE005173; NID:g11094686; PIDN:AAG29622.1; GSPDB:GN00141
C;Genetics:
A;Gene: F8A12.4
A;Map position: 1

  Query Match             5.1%;  Score 143;  DB 2;  Length 812;
  Best Local Similarity   22.1%;  Pred. No. 0.009;
  Matches   97;  Conservative   57;  Mismatches  174;  Indels  110;  Gaps   23;

Qy         48 LTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKK 107
              ::| ||   | :|       |:|| |||   :   ||   :    | |:  ||
Db        426 ISCDTPMFCD-SW----RKRVVGSAKTLRTSI---GDDTSFV-PSGSKMNRRS------- 469

Qy        108 EDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL--------------- 152
              |||      : |    |   |:|   ||     |       || |
Db        470 EDG----RKIAEDSTKKRLKFMKSARKNDGS--TMGQKQVISDDADDDDSLTVAQITTLY 523

Qy        153 --KFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP-SAEESLPI 209
                |:|  |    |:| |           |:  ||   :     ||: |:     :|::|
Db        524 KKKYSENSGGNASEPLG--------KKIRLEADNNGLE----PCQKLSSIRYDGDETVPP 571

Qy        210 EVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSY 269
                :    | : |   |   :| :: |   :|    |:   | :::    |:|
Db        572 PEI-----KKRNEETGSKSGMRVVLSPFDESNSSKPPVDFGRAIDIVVSAPET------- 619

Qy        270 FSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKI-RVQAR-DRYYSSSWSDWASVS 327
              :|||    | || |||  :  |    | : |:|  | |  || |:   |     |
Db        620 --MTFCDDVYG-NNAEKKTMIDDDSEELKCLLHEDGTITREMARSDKKCCSE----AEKE 672

Qy        328 CSGGG---------GGGSRNLPTPTPSPGMFQCLNHSQT--------LLRAVSN------ 364
              : ||           :::|    : |   | |  :|        | |:  |
Db        673 DADGGISDKVLASKADNKKSIPYQKLASG---CANGDETSKAYKPKVLKRSDGNQAHACL 729

Qy        365 ---------TLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACL-PLELTMNESCL-AS 413
                      |: : |:::   : ::   |:  | |       |  | |:: |  | |
Db        730 LPDDGIRSEETMKSNEQLKVFEKRNNDLGEGDVDNDTTEKRSQKLNVLALSIEERVLKAE 789

Qy        414 REISLITNGSCLASGKAS 431
              | :: :     :   | :
Db        790 RTVAWLNQRRAIKQRKVA 807


RESULT 14
JS0675
vascular cell adhesion molecule-1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Nov-1999
C;Accession: JS0675; S19872; S23136
R;Hession, C.; Moy, P.; Tizard, R.; Chisholm, P.; Williams, C.; Wysk, M.; Burkly, L.; Mi
Biochem. Biophys. Res. Commun. 183, 163-169, 1992
A;Title: Cloning of murine and rat vascular cell adhesion molecule-1.
A;Reference number: JS0674; MUID:92181437; PMID:1371918
A;Accession: JS0675
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-739 <HES>
A;Cross-references: GB:M84488; NID:g207642; PIDN:AAA42332.1; PID:g207643
R;Williams, A.; Atkins, R.; Fries, J.; Gimbrone, M.A.; Cybulsky, M.I.; Collins, T.
submitted to the EMBL Data Library, February 1992
A;Description: Nucleotide sequence of rat vascular cell adhesion molecule-1.
A;Reference number: S19872
A;Accession: S19872
A;Molecule type: mRNA
A;Residues: 1-2,'G',4-121,'HL',124-165,'N',167-738,'G' <WIL>
A;Cross-references: EMBL:X63722; NID:g57471; PIDN:CAA45254.1; PID:g57472
R;Williams, A.J.; Atkins, R.C.; Fries, J.W.U.; Gimbrone Jr., M.A.; Cybulsky, M.I.; Colli
Biochim. Biophys. Acta 1131, 214-216, 1992
A;Title: Nucleotide sequence of rat vascular cell adhesion molecule-1 cDNA.
A;Reference number: S23136; MUID:92305064; PMID:1377031
A;Accession: S23136
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2,'G',4-165,'N',167-738,'G' <WI2>
C;Comment: This protein interacts with the beta-1 integrin very late antigen 4 on leu
C;Genetics:
A;Gene: VCAM-1
C;Superfamily: immunoglobulin homology
C;Keywords: cell adhesion; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-739/Product: vascular cell adhesion molecule 1 #status predicted <VAS>
F;239-293/Domain: immunoglobulin homology <IMM1>
F;328-385/Domain: immunoglobulin homology <IMM2>
F;526-581/Domain: immunoglobulin homology <IMM3>
F;676-696/Domain: transmembrane #status predicted <TRA>
F;697-715/Domain: intracellular #status predicted <INT>

  Query Match             4.4%;  Score 123.5;  DB 2;  Length 739;
  Best Local Similarity   20.0%;  Pred. No. 0.25;
  Matches  113;  Conservative   85;  Mismatches  204;  Indels  163;  Gaps   31;

Qy         27 EKDVYV----VELDWHPDA---PGEMVVLTCHT-----PEEDDITWTSAQSS---EVLGS 71
              |  ||       |:  ||       |  | :|| :     ||   | |:    :   ::|
Db        216 ELQVYTSPKNTEISVHPSTRLHEGAAVTMTCASEGLPAPE---IFWSKKLDNGVLQLLSG 272

Qy         72 GKTLTIQVKEFGDAGQYTCHKGGKVLSRSL----LLIHKKEDGIWSTDILKEQK---ESK 124
                ||:       |:| | | :|  :: |       |:: :|    :: ||    :   :
Db        273 NATLTLIAMRMEDSGIYVC-EGVNLVGRDKTEVELIVQEKP---FTVDISPGSQVAAQVG 328

Qy        125 NKIFLKCEAKNY-SGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              : : | | |    |  |:  | |   : |   |:          :| |    ||:   | |:
Db        329 DSVVLTCAAVGCDSPSFS--WRTQTDSPLNGEVRD-------EGATS---TLTLSPVGVE 376

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              :       || ||        |::: :||               ||       |: |
Db        377 DEHSYLCTVTCQR----RKLEKTIQVEVY-------------SF-------PEDPEIEI 411

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSL---------TFCIQAQGKNNREKKDR----- 289
                || : | | |:   |: :   |    |           |  :  |  : | |
Db        412 SGPLVHGRPVTVNCTVPNVYPFDHLEIELLKGETTLLNKFLREEIGTKSLETKSLEMTFI 471

Qy        290 LCVDKTSAKVVC---------HKDAKIRVQARDRYYSSSWSD---WAS------------ 325
                : |   :||          : | |   :  | : :  :    | |
Db        472 PTAEDTGKALVCLAKLHSSQMESEPKQRQSTQTLYVNVAPKEPTIWVSPSPVPEEGSPVN 531

Qy        326 VSCSGGGGGGSRNLPTP------TPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCT 379
              ::||  |       |||          |  | |: : ||     : :    :   :| |
Db        532 LTCSSDG------FPTPKILWSRQLKNGELQPLSQNTTL-----SFMATKMEDSGIYVCE 580

Qy        380 SEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLS 439
                                    :||: :: : : ||  |    | |   :||
Db        581 G------------------------INEAGISKKSVELIIQG----SSKDIQLTVFPSK 611

Qy        440 SIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEE 499
              |: |       :   ::      |:  | | :   |  | :|:::|  | |: :|: |::
Db        612 SVKEG------DTVIISCTCGSVPEIWIILKKKAKTG-DMVLKSVN-GSYTI-RKAQLQD 662

Qy        500 PDFYKTKIKLCILLHAFRIRAVTIN 524
                |: : |  :     ::|::|::
Db        663 AGVYECESKTEV---GSQLRSLTLD 684


RESULT 15
A37986
interleukin-6 receptor precursor - rat
N;Alternate names: IL-6 receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A37986
R;Baumann, M.; Baumann, H.; Fey, G.H.
```

J. Biol. Chem. 265, 19853-19862, 1990
A;Title: Molecular cloning, characterization and functional expression of the rat liver
A;Reference number: A37986; MUID:91060602; PMID:2174054
A;Accession: A37986
A;Molecule type: mRNA
A;Residues: 1-462 <BAU>
A;Cross-references: GB:M58587; GB:J05668; NID:g204921; PIDN:AAA41431.1; PID:g204922
C;Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is es
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C;Keywords: acute phase; cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-462/Product: interleukin-6 receptor #status predicted <MAT>
F;20-362/Domain: extracellular #status predicted <EXT>
F;40-94/Domain: immunoglobulin homology <IMM>
F;117-306/Domain: cytokine receptor homology <CRS>
F;363-385/Domain: transmembrane #status predicted <TMM>
F;386-462/Domain: intracellular #status predicted <INT>
F;47-92/Disulfide bonds: #status predicted

Query Match 4.4%; Score 123; DB 1; Length 462;
Best Local Similarity 21.0%; Pred. No. 0.14;
Matches 98; Conservative 54; Mismatches 205; Indels 110; Gaps 20;

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Qy          13 LVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPE---EDDITW--TSAQSSE 67
               : |||:| :|:         |         ||  | | |   |      | |  : :|| |
Db          10 VALLAAPAVALVLGSCRALEVANGTVTSLPGATVTLICPGKEAAGNATIHWVYSGSQSRE 69

Qy          68 VLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKI 127
                 :| || ::  :  | | | |     ::   ||:          |:  |: :
Db          70 WTTTGNTLVLRAVQVNDTGHYLCFLDDHLVGTVPLLV----------DVPPEEPK----- 114

Qy         128 FLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDY 187
                | |  ||      | |  :               | |   |     : |:::   |
Db         115 -LSCFRKNPLVNAFCEWHPS--------------STPSPTT--KAVMFAKKINTTN-GK 155

Qy         188 KKYTVECQEGSACPSAEESLPIEVV----VDAIHKLKYENYTSS-------FFIRDIIKP 236
                 : | ||      |   |  :|::    |  |  |   |  |       |    :::|
Db         156 SDFQVPCQYSQQLKSF--SCEVEILEGDKVYHIVSLCVANSVGSRSSHNVVFQSLKMVQP 213

Qy         237 DPPTNLQLK----PLKNSRHVEVSWEYPDTWST--------PHSYFSLTFCIQAQGKNNR 284
               ||| || :      |  |: |  :   | |  |           |   || :
Db         214 DPPANLVVSAIPGSLVGSKSVGKTLS-PGTQVTTCCNSSFDTDLYGQRTFTVWP-----L 267

Qy         285 EKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCSGGGGGGSRNLPTPTP 344
               :     ||   : : | |    ::|: :: :    || |:      |    :    ||
Db         268 QVAQHQCVIHDALRGVKH---VVQVRGKEEFDIGQWSKWSPEVT--GTPWLAEPRTTPAG 322

Qy         345 SPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLEL 404
                ||      | :|  :    |                    |||     |       |::
Db         323 IPG-----NPTQVSVEDYDN-------------------HEDQYGSSTEATSVLAPVQ- 356

Qy         405 TMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQME 451
                   | | | |    :| |  :|  :||:  |    | :: :
Db         357 -------GSSPIPLPT--FLVAGGSLAFGLLLCVFIILRLKKKWKSQ 394
```

Search completed: July 15, 2003, 11:08:46
Job time : 25.3616 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:28 ; Search time 11.6808 Seconds
(without alignments)
1892.583 Million cell updates/sec

Title: US-09-917-265-62
Perfect score: 2804
Sequence: 1 MHPQQLVISWFSLVLLASPL.....HAFRIRAVTINRMMSYLNSS 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1751	62.4	329	1	I12B_CANFA	Q28268 canis famil
2	1643	58.6	329	1	I12B_FELCA	O02744 felis silve
3	1551	55.3	329	1	I12B_HORSE	Q9xsq5 equus cabal
4	1527	54.5	327	1	I12B_CEREL	Q28234 cervus elap
5	1515	54.0	327	1	I12B_BOVIN	P46282 bos taurus
6	1511	53.9	327	1	I12B_SHEEP	O02815 ovis aries
7	1501.5	53.5	328	1	I12B_HUMAN	P29460 homo sapien
8	1493.5	53.3	328	1	I12B_MACMU	P48095 macaca mula
9	1477.5	52.7	324	1	I12B_PIG	Q28938 sus scrofa
10	1455.5	51.9	328	1	I12B_CERTO	P46658 cercocebus
11	1330	47.4	327	1	I12B_MARMO	Q61729 marmota mon
12	1141.5	40.7	335	1	I12B_MOUSE	P43432 mus musculu
13	961	34.3	222	1	I12A_FELCA	O02743 felis silve
14	949	33.8	222	1	I12A_CANFA	Q28267 canis famil
15	873	31.1	219	1	I12A_HUMAN	P29459 homo sapien
16	869	31.0	222	1	I12A_PIG	Q29053 sus scrofa
17	866	30.9	222	1	I12A_HORSE	Q9xsq6 equus cabal
18	829.5	29.6	221	1	I12A_CEREL	Q28233 cervus elap
19	827	29.5	219	1	I12A_MACMU	P48091 macaca mula
20	824.5	29.4	221	1	I12A_BOVIN	P54349 bos taurus
21	824.5	29.4	221	1	I12A_SHEEP	Q9tu27 ovis aries
22	822	29.3	219	1	I12A_CERTO	P46661 cercocebus
23	809.5	28.9	221	1	I12A_CAPHI	O02814 capra hircu
24	614.5	21.9	223	1	I12A_MARMO	Q61728 marmota mon
25	549	19.6	215	1	I12A_MOUSE	P43431 mus musculu
26	217.5	7.8	467	1	IL6A_PIG	O18796 sus scrofa
27	211.5	7.5	468	1	IL6A_HUMAN	P08887 homo sapien
28	191	6.8	460	1	IL6A_MOUSE	P22272 mus musculu
29	181.5	6.5	372	1	CNTR_RAT	Q08406 rattus norv
30	178	6.3	362	1	CNTR_CHICK	P51641 gallus gall
31	171	6.1	462	1	IL6A_RAT	P22273 rattus norv
32	170	6.1	372	1	CNTR_HUMAN	P26992 homo sapien
33	123.5	4.4	739	1	VCA1_RAT	P29534 rattus norv
34	122.5	4.4	978	1	KIT_FELCA	Q28889 felis silve
35	120	4.3	831	1	PRLR_CHICK	Q04594 gallus gall
36	119.5	4.3	977	1	KIT_BOVIN	P43481 bos taurus
37	116.5	4.2	978	1	KIT_CAPHI	Q28317 capra hircu
38	114.5	4.1	3678	1	DMD_MOUSE	P11531 mus musculu
39	114	4.1	611	1	GHR_COLLI	Q90375 columba liv
40	111.5	4.0	610	1	PRLR_RAT	P05710 rattus norv
41	111.5	4.0	1323	1	LT23_CAEEL	P24348 caenorhabdi
42	111	4.0	638	1	GHR_RAT	P16310 rattus norv
43	111	4.0	2670	1	IP3T_RAT	Q63269 rattus norv
44	108.5	3.9	1093	1	SM5B_MOUSE	Q60519 mus musculu
45	108	3.9	581	1	PRLR_BOVIN	Q28172 bos taurus

ALIGNMENTS

RESULT 1
I12B_CANFA
ID I12B_CANFA STANDARD; PRT; 329 AA.
AC Q28268;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE maturation factor 40 kDa subunit) (CLMF p40).
GN IL12B.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98280561; PubMed=9617567;
RA Buettner M., Belke-Louis G.F., Rziha H.J., McInnes C., Kaaden O.R.;
RT "Detection, cDNA cloning and sequencing of canine interleukin 12.";
RL Cytokine 10:241-248(1998).
CC -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC BY RESTING PBMC (BY SIMILARITY).
CC -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC
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CC ----------
DR EMBL; U49100; AAA92059.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 329 INTERLEUKIN-12 BETA CHAIN.
FT DOMAIN 43 97 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 236 321 FIBRONECTIN TYPE-III.
FT DISULFID 50 90 POTENTIAL.
FT DISULFID 200 200 INTERCHAIN (PROBABLE).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

```
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   329 AA;  37410 MW;  79F83ED02B5DA93C CRC64;

  Query Match           62.4%;  Score 1751;  DB 1;  Length 329;
  Best Local Similarity   99.1%;  Pred. No. 4e-128;
  Matches  326;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              |||||||||||||||||| || ||||||||||||||||||||||||||||||||||||||
Db          1 MHPQQLVISWFSLVLLASSLMTIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCVQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||||||||||||
Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 2
I12B_FELCA
ID   I12B_FELCA     STANDARD;      PRT;   329 AA.
AC   O02744; O46671;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=97246745; PubMed=9089110;
RA   Schijns V.E.C.J., Wierda C.M.H., Vahlenkamp T.W., Horzinek M.C.;
RT   "Molecular cloning of cat interleukin-12.";
RL   Immunogenetics 45:462-463(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98182592; PubMed=9522125;
RA   Fehr D., Dean G.A., Huder J., Fan Z., Huettner S., Higgins J.W.,
RA   Pedersen N.C., Lutz H.;
RT   "Nucleotide and predicted peptide sequence of feline interleukin-12
RT   (IL-12).";
RL   DNA Seq. 8:77-82(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y07762; CAA69068.1; -.
DR   EMBL; U83184; AAB93835.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    329       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    321       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    11     11       L -> F (IN REF. 2).
FT   CONFLICT    51     51       N -> D (IN REF. 2).
FT   CONFLICT   167    167       E -> G (IN REF. 2).
SQ   SEQUENCE   329 AA;  37374 MW;  12A069BC6322AE08 CRC64;

  Query Match           58.6%;  Score 1643;  DB 1;  Length 329;
  Best Local Similarity   93.0%;  Pred. No. 8.9e-120;
  Matches  306;  Conservative   10;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              |||||||:| |||||| ||||||||||:|||||||||||||||||||:|||||||||
Db          1 MHPQQLVIAWLSLVLLAPPLMAIWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||||||||||||| ||||||||||:||| | |||||||||||||||:||
Db         61 TSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              ||||||||||||||||||||||||||||||:|||||| |||| ||||| |||||:|
Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              |||||||||||||||||||||||||||||| :| |||||||||||| |||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              |||||||||||||||||||:|||||||
Db        301 CHKDAKIRVQARDRYYSSSWSNWASVSCS 329


RESULT 3
I12B_HORSE
ID   I12B_HORSE     STANDARD;      PRT;   329 AA.
AC   Q9XSQ5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20009534; PubMed=10541814;
RA   Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA   Argyle D.J., Onions D.E.;
RT   "Cloning and sequencing of horse interleukin-12 and interleukin-18
RT   cDNAs.";
RL   Immunogenetics 50:94-97(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y11129; CAA72011.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    329       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   329 AA;  37442 MW;  7104BB0DFF8FA73C CRC64;

  Query Match             55.3%;  Score 1551;  DB 1;  Length 329;
  Best Local Similarity   87.7%;  Pred. No. 1.2e-112;
  Matches  286;  Conservative   21;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              | ||:|||||||||||||||||||||||||||||:|||||||||||:||||: ||||||
Db          4 QWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGEMVVLTCNTPEEEGITWTSA 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||:|||||||||||||||||||| |||||||:||| | ||:|||||||||||||:|||| 
Db         64 QSNEVLGSGKTLTIQVKEFGDAGWYTCHKGGEVLSHSHLLLHKKEDGIWSTDILKDQKES 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| |||||||||||||||||||||||||||||||||||||| |||:|||||| |||||| ||
Db        124 KNKTFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGSSDPRGVTCGAATLSAERVSVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              :|:|||||||||||||:||||||||:||||:|||||||||| |||||||||||| ||| 
Db        184 DREYKKYTVECQEGSACPAAEESLPIEIVVDAVHKLKYENYTSGFFIRDIIKPDPPKNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||:||||||||||||| || |||| :|:|||| :|:||| | |||
Db        244 LKPLKNSRQVEVSWEYPETWSTPHSYFSLTFSIQVQGKNKKERKDRLFMDETSATVTCHK 303

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
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              | :|||||||||||||||:|||||||
Db        304 DGQIRVQARDRYYSSSWSEWASVSCS 329


RESULT 4
I12B_CEREL
ID   I12B_CEREL     STANDARD;      PRT;   327 AA.
AC   Q28234;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99304506; PubMed=10376218;
RA   Lockhart E., Slobbe L., Buchan G.;
RT   "The characterisation of a cervine immunoregulatory cytokine,
RT   interleukin 12.";
RL   DNA Seq. 10:139-148(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U57752; AAB02258.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37145 MW;  53AF5BB288907F06 CRC64;

  Query Match             54.5%;  Score 1527;  DB 1;  Length 327;
  Best Local Similarity   85.4%;  Pred. No. 8.3e-111;
  Matches  281;  Conservative   24;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              |||||||:|||||||| ||::||||||||:||||||||:|||||| ||| | ||||| |||
Db          1 MHPQQLVVSWFSLVLLTSPIVAIWELEKNVYVVELDWYPDAPGETVVLRCDTPEEDGITW 60
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Qy          61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
               || ||||||||||||:|||||||||||||||||:||||||||:|||||||||||||||:|
Db          61 TSDQSSEVLGSGKTLTVQVKEFGDAGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQ 120

Qy         121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
               || | | ||||||:||| ||||||||||||||||||||| |||:|||||| :|| |:|
Db         121 KEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSRGSSDPRGVTCGAASLSTEKV 180

Qy         181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
                ||:|:|||||||||||||:|||||||||:|:|||||||||||||||||||||||||||
Db         181 IVDHREYKKYTVECQEGSACPAAEESLPIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPK 240

Qy         241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
               ||||:|||||| ||||||||||||||||||||:| |||| |||| | :|:|||||
Db         241 NLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVT 298

Qy         301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
               ||||| |||||||||||:| ||:|||||||
Db         299 CHKDASIRVQARDRYYNSFWSEWASVSCS 327


RESULT 5
I12B_BOVIN
ID   I12B_BOVIN     STANDARD;      PRT;   327 AA.
AC   P46282;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Holstein; TISSUE=Lymphoid;
RX   MEDLINE=95244628; PubMed=7727547;
RA   Zarlenga D.S., Canals A., Aschenbrenner R.A., Gasbarre L.C.;
RT   "Enzymatic amplification and molecular cloning of cDNA encoding the
RT   small and large subunits of bovine interleukin 12.";
RL   Biochim. Biophys. Acta 1270:215-217(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U11815; AAA85792.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      236    319       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37050 MW;  D484DA36EF6F3D9F CRC64;

  Query Match             54.0%;  Score 1515;  DB 1;  Length 327;
  Best Local Similarity   84.8%;  Pred. No. 7e-110;
  Matches  279;  Conservative   25;  Mismatches   23;  Indels    2;  Gaps    1;

Qy           1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
               |||||||:||||||||||::|:|||||:||||||||:|||||| |||| ||||| |||
Db           1 MHPQQLVVSWFSLVLLASPIVAMWELEKNVYVVELDWYPDAPGETVVLTCDTPEEDGITW 60

Qy          61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
               || |||||||||||||||||||||||||||||||: |||||||:|||||||||||||:|
Db          61 TSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSRSLLLLHKKEDGIWSTDILKDQ 120

Qy         121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
               || | | ||||||:||| ||||||||||||||||||||| |||:|||||| ||||:|
Db         121 KEPKAKSFLKCEAKDYSGHFTCWWLTAISTDLKFSVKSSRGSSDPRGVTCGAALLSAEKV 180

Qy         181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
                :::|:| ||||||||||||:||||| ||||:|:|||||||||||||||||||||||||
Db         181 SLEHREYNKYTVECQEGSACPAAEESLLIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPK 240

Qy         241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
               ||||:|||||| |||||||||||||||||||||:| |||| |||| | :|:|||||
Db         241 NLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVT 298

Qy         301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
               ||||| :|||||||||||| ||:|||||||
Db         299 CHKDANVRVQARDRYYSSFWSEWASVSCS 327


RESULT 6
I12B_SHEEP
ID   I12B_SHEEP     STANDARD;      PRT;   327 AA.
AC   O02815; O18989; Q9TT18;
DT   01-NOV-1997 (Rel. 35, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Ovis aries (Sheep), and
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940, 9925;
RN   [1]
RP   SEQUENCE FROM N.A., AND SUBUNIT.
RC   SPECIES=Sheep; TISSUE=Peripheral blood;
RX   MEDLINE=20480126; PubMed=11023671;
RA   Swinburne S.J., Russ G.R., Krishnan R.;
RT   "Ovine interleukin 12 has biological activity on ovine and human
RT   activated peripheral blood mononuclear cells.";
RL   Cytokine 12:1546-1552(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=Sheep; STRAIN=Merino; TISSUE=Peripheral blood;
RX   MEDLINE=20344025; PubMed=10888112;
RA   De Rose R., Scheerlinck J.-P.Y., Casey G., Wood P.R., Tennent J.M.,
RA   Chaplin P.J.;
RT   "Ovine interleukin-12: analysis of biologic function and species
RT   comparison.";
RL   J. Interferon Cytokine Res. 20:557-564(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
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RC   SPECIES=C.hircus;
RA   Beyer J.C., Cheevers W.P., Kumpula-Mcwhirter N.M.;
RT   "Cloning of caprine IL-12 40 kDa subunit.";
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF004024; AAB61368.2; -.
DR   EMBL; AF209435; AAF20151.1; -.
DR   EMBL; AF007576; AAB62945.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       POTENTIAL.
FT   CHAIN       23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT   290    290       T -> A (IN REF. 2).
SQ   SEQUENCE   327 AA;  36936 MW;  DDCD983A10143A96 CRC64;

  Query Match             53.9%;  Score 1511;  DB 1;  Length 327;
  Best Local Similarity   85.1%;  Pred. No. 1.4e-109;
  Matches  280;  Conservative   25;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              |||||||:|||||||||||::|||||||:|||||||:|:|||| ||||| ||||| |||
Db          1 MHPQQLVVSWFSLVLLASPIVAIWELEKNVYVVELDWYPNAPGETVVLTCDTPEEDGITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||||||||||||||||||||||||:||||||||:|||||||||||||:|
Db         61 TSDQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              || | | ||||||||:||| ||| |||||||:|||||||||| |||:|||||| :||||:|
Db        121 KEPKAKSFLKCEAKDYSGHFTCSWLTAISTNLKFSVKSSRGSSDPRGVTCGAASLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
               :|:|:| ||||||||||||:|||||||||::|:|||||||||||||||||||||||||
Db        181 SMDHREYNKYTVECQEGSACPAAEESLPIEVVMEAVHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              ||||:|||||| ||||||||||||||||||||||:| |||| |||| | |:|||||
Db        241 NLQLRPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKNKREKK--LFTDQTSAKVT 298

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              ||||| |||||||||||| ||:|||||||
Db        299 CHKDANIRVQARDRYYSSFWSEWASVSCS 327


RESULT 7
I12B_HUMAN
ID   I12B_HUMAN     STANDARD;      PRT;   328 AA.
AC   P29460;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40) (NK cell stimulatory
DE   factor chain 2) (NKSF2).
GN   IL12B OR NKSF2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91239523; PubMed=1674604;
RA   Gubler U., Chua A.O., Schoenhaut D.S., Dwyer C.M., McComas W.,
RA   Motyka R., Nabavi N., Wolitzky A.G., Quinn P.M., Familletti P.C.,
RA   Gately M.K.;
RT   "Coexpression of two distinct genes is required to generate secreted
RT   bioactive cytotoxic lymphocyte maturation factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:4143-4147(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91201875; PubMed=1673147;
RA   Wolf S.F., Temple P.A., Kobayashi M., Young D., Dicig M., Lowe L.,
RA   Dzialo R., Fitz L., Ferenz C., Hewick R.M., Kelleher K.,
RA   Herrmann S.H., Clark S.C., Azzoni L., Chan S.H., Trinchieri G.,
RA   Perussia B.;
RT   "Cloning of cDNA for natural killer cell stimulatory factor, a
RT   heterodimeric cytokine with multiple biologic effects on T and
RT   natural killer cells.";
RL   J. Immunol. 146:3074-3081(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   PubMed=11197695;
RA   Huang D., Cancilla M.R., Morahan G.;
RT   "Complete primary structure, chromosomal localization, and definition
RT   of polymorphisms of the gene encoding the human interleukin 12 p40
RT   subunit.";
RL   Genes Immun. 1:515-520(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Hongyuan J., Meiyun Z.;
RT   "Cloning and sequence analysis of IL-12 cDNA from Chinese.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 23-45.
RX   MEDLINE=90370873; PubMed=2204066;
RA   Stern A.S., Podlaski F.J., Hulmes J.D., Pan Y.C.E., Quinn P.M.,
RA   Wolitzky A.G., Familletti P.C., Stremlo D.L., Truitt T.,
RA   Chizzonite R., Gately M.K.;
RT   "Purification to homogeneity and partial characterization of
RT   cytotoxic lymphocyte maturation factor from human B-lymphoblastoid
RT   cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6808-6812(1990).
RN   [6]
RP   SIMILARITY TO IL-6 RECEPTOR.
RX   MEDLINE=91300556; PubMed=2070420;
RA   Gearing D.P., Cosman D.;
RT   "Homology of the p40 subunit of natural killer cell stimulatory
RT   factor (NKSF) with the extracellular domain of the interleukin-6
RT   receptor.";
RL   Cell 66:9-10(1991).
RN   [7]
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RP   CARBOHYDRATE-LINKAGE SITE TRP-319.
RX   MEDLINE=99225373; PubMed=10207176;
RA   Doucey M.A., Hess D., Blommers M.J., Hofsteenge J.;
RT   "Recombinant human interleukin-12 is the second example of a
RT   C-mannosylated protein.";
RL   Glycobiology 9:435-441(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED
CC       T AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC.
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS. NKSF IS ESSENTIALLY A COMPLEX OF CYTOKINE AND SOLUBLE
CC       RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: KNOWN TO BE C-MANNOSYLATED IN THE RECOMBINANT PROTEIN; IT IS
CC       NOT YET KNOWN FOR SURE IF THE WILD-TYPE PROTEIN IS ALSO MODIFIED.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M65272; AAA35695.1; -.
DR   EMBL; M65290; AAA59938.1; -.
DR   EMBL; AY008847; AAG32620.1; -.
DR   EMBL; AF180563; AAD56386.1; -.
DR   PIR; B39359; B39359.
DR   PIR; B36055; B36055.
DR   GlycoSuiteDB; P29460; -.
DR   Genew; HGNC:5970; IL12B.
DR   MIM; 161561; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22
FT   CHAIN       23    328       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     235    320       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   222    222       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   319    319       C-LINKED (MAN).
FT                               /FTId=CAR_000187.
FT   CONFLICT   239    239       K -> N (IN REF. 2).
SQ   SEQUENCE   328 AA;  37169 MW;  118FA801B8F5BB2F CRC64;

  Query Match             53.5%;  Score 1501.5;  DB 1;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 7.8e-109;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| |||||:|||||:|||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| |||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| ||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:||||||||:|||:|||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:||||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 8
I12B_MACMU
ID   I12B_MACMU     STANDARD;      PRT;   328 AA.
AC   P48095;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19841; AAB60397.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    328       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     235    320       FIBRONECTIN TYPE-III.
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FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD    125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     106    106       K -> I.
FT   VARIANT     206    206       L -> P.
FT   VARIANT     218    218       L -> P.
FT   VARIANT     289    289       I -> T.
FT   VARIANT     295    295       S -> P.
SQ   SEQUENCE   328 AA;  37273 MW;  A46198AAC6D2746B CRC64;

  Query Match             53.3%;  Score 1493.5;  DB 1;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 3.2e-108;
  Matches  277;  Conservative   20;  Mismatches   28;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||  |||||||||||:||||||||||:|||||||||||  |||||  ||||
Db          4 QQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              || |||||||||||||||||||||||||||: || ||||:|||||||||||:|||:|||
Db         64 QSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLLLLHKKEDGIWSTDVLKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |:|||||||||||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSNPQGVTCGAVTLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:||| |||||:|||||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEERLPIEVMVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||||| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQVQGKSKREKKDRIFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :|   |||:|||||||||:|||| ||
Db        303 NASFSVQAQDRYYSSSWSEWASVPCS 328


RESULT 9
I12B_PIG
ID   I12B_PIG       STANDARD;      PRT;   324 AA.
AC   Q28938;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=97383978; PubMed=9239844;
RA   Foss D.L., Murtaugh M.P.;
RT   "Molecular cloning and mRNA expression of porcine interleukin-12.";
RL   Vet. Immunol. Immunopathol. 57:121-134(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U08317; AAA75356.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    324       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      231    316       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    195    195       INTERCHAIN (PROBABLE).
FT   CARBOHYD    125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    218    218       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   324 AA;  36828 MW;  F0E48B72F700086C CRC64;

  Query Match             52.7%;  Score 1477.5;  DB 1;  Length 324;
  Best Local Similarity   83.0%;  Pred. No. 5.5e-107;
  Matches  273;  Conservative   24;  Mismatches   27;  Indels    5;  Gaps    1;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              || ||||:|||||| |||||::|||||||:||||||||:|:|||||||||||:||||| |||
Db          1 MHLQQLVVSWFSLVWLASPIVAIWELEKNVYVVELDWYPNAPGEMVVLTCNTPEEDGITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||:|||||| |||||||||||| ||| |||:||||:|||||||||||||:|
Db         61 TSDQSSEVLGTGKTLTIHVKEFGDAGQYTCRKGGAVLSQSLLLLHKKEDGIWSTDILKDQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              || ||| |||||||||||||||||||||||||||||||| :|||:|||||  |||
Db        121 KEPKNKSFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGSTDPRGVTCGTATLSE--- 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
                |  :|||| ||||||||||:|||||||||::|:|||||||||||||||||||||||
Db        178 --DLGEYKKYRVECQEGSACPAAEESLPIEVVLEAVHKLKYENYTSSFFIRDIIKPDPPK 235

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              |||| |||||||||:|||||||||||||||| | :| |||| |||||:|  |: ||||
Db        236 NLQLNPLKNSRHVEISWEYPDTWSTPHSYFSLMFGVQVQGKNKREKKDKLFTDQISAKVT 295

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
              ||||| ||||||||||||||:||||||:
Db        296 CHKDANIRVQARDRYYSSSWSEWASVSCN 324


RESULT 10
I12B_CERTO
ID   I12B_CERTO     STANDARD;      PRT;   328 AA.
AC   P46658;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
```

```
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19834; AAA86701.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    328       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     235    320       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD   125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   303    303       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   328 AA;  37252 MW;  A2DE98E844435B14 CRC64;

  Query Match             51.9%;  Score 1455.5;  DB 1;  Length 328;
  Best Local Similarity   82.8%;  Pred. No. 2.8e-105;
  Matches  270;  Conservative   22;  Mismatches   33;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| |||||||||||:|||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLMAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              || |||||||||||||||||||||||||||: || |||| |||||||||||||:|||
Db         64 QSGEVLGSGKTLTIQVKEFGDAGQYTCHKGGEALSHSLLLPHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||: ||:||||||||| |||||: ||||| ||: |||| |:||||||| |||||||| |
Db        124 KNETFLRCEAKNYSGRITCWWLSTISTDLTFSIISSRGSSNPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||:||| |||||:||||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEERLPIEVMVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||||| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCIQVQGKSKREKKDRIFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
                :|   |||:||||||||::| || ||
Db        303 NASFSVQAQDRYYSSSWNEWTSVPCS 328


RESULT 11
I12B_MARMO
ID   I12B_MARMO     STANDARD;      PRT;   327 AA.
AC   Q61729;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RA   Laxton C.D., Foster G.R., Shanmuganathan S., Mills J.S.,
RA   Ackrill A.M.;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X97019; CAA65747.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     235    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD   134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37172 MW;  9A15445915AB90E6 CRC64;

  Query Match             47.4%;  Score 1330;  DB 1;  Length 327;
  Best Local Similarity   75.4%;  Pred. No. 1.4e-95;
  Matches  245;  Conservative   35;  Mismatches   43;  Indels    2;  Gaps    2;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||| ||| |||||:|||||||:|||||||||| ||| ||||| ||||| |||||
Db          4 QQLVISWVSLVWLASPLLAIWELEKNVYVVELDWHPDTPGEKVVLTCDTPEEDGITWTSE 63
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Qy          64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
               ||||||||||||||| |||| ||| ||| :|||:|||: |||:|| ||||||||||| :||
Db          64 QSSEVLGSGKTLTILVKEFEDAGHYTCRRGGEVLSQMLLLLHKNEDGIWSTDILK-KKEP 122

Qy         124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
               :||  : |||||||||||||||||||: ||||| || |||||||||  |||||||:::
Db         123 ENKNLVTCEAKNYSGRFTCWWLTAISTDVNFSVKSHRGSSDPQGVTCGEATLSAERVKIE 182

Qy         184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
               |:|||||:|:||| :|||:|||:||| |||||:|||||||| ||||||||||||| ||:
Db         183 QREYKKYSVQCQEDNACPTAEETLPITVVVDAVHKLKYENYISSFFIRDIIKPDPPKNLK 242

Qy         244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
               :|| |  : |||:|||||:||||||||||| :| |||  ::: : | |||||  | | |
Db         243 MKPSKTPQQVEVTWEYPDSWSTPHSYFSLTFSVQVQGK-KKKRSNTLHVDKTSVTVTCQK 301

Qy         304 DAKIRVQARDRYYSSSWSDWASVSC 328
                ||: ||||||||:||||:||::||
Db         302 GAKVSVQARDRYYNSSWSEWATMSC 326


RESULT 12
I12B_MOUSE
ID   I12B_MOUSE     STANDARD;      PRT;   335 AA.
AC   P43432;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Spleen;
RX   MEDLINE=92268481; PubMed=1350290;
RA   Schoenhaut D.S., Chua A.O., Wolitzky A.G., Quinn P.M., Dwyer C.M.,
RA   Gately M.K., Gubler U.;
RT   "Cloning and expression of murine IL-12.";
RL   J. Immunol. 148:3433-3440(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96257799; PubMed=8647196;
RA   Tone Y., Thompson S.A., Babik J.M., Nolan K.F., Tone M., Raven C.,
RA   Waldmann H.;
RT   "Structure and chromosomal location of the mouse interleukin-12 p35
RT   and p40 subunit genes.";
RL   Eur. J. Immunol. 26:1222-1227(1996).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M86671; AAA39296.1; -.
DR   EMBL; S82426; AAB37383.1; -.
DR   EMBL; S82421; AAB37383.1; JOINED.
DR   EMBL; S82422; AAB37383.1; JOINED.
DR   EMBL; S82424; AAB37383.1; JOINED.
DR   EMBL; S82425; AAB37383.1; JOINED.
DR   MGD; MGI:96540; Il12b.
DR   InterPro; IPR002996; CRlA.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    335       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      233    324       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    197    197       INTERCHAIN (PROBABLE).
FT   CARBOHYD     47     47       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    122    122       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    132    132       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    220    220       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DOMAIN      155    159       POLY-SER.
SQ   SEQUENCE   335 AA;  38235 MW;  19E4FA5EF0CFC82A CRC64;

  Query Match             40.7%;  Score 1141.5;  DB 1;  Length 335;
  Best Local Similarity   65.5%;  Pred. No. 5.5e-81;
  Matches  220;  Conservative   38;  Mismatches   65;  Indels   13;  Gaps    4;

Qy           1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
               | ||:| ||||::||| |||||:||||||||||||:|| |||||| | ||| |||||||||
Db           1 MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy          61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
               || |   |:||||||| |||| |||||||||||: || | ||:||||:|||||:||
Db          61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy         121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
               |  ||| |||||| |||||||| ||   : ||||::|||    | : |||| :||||:|
Db         118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKV 177

Qy         181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
                :| |||:||:| |||   ||:|||:||||: ::|  : |||||::||||||||||||
Db         178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237

Qy         241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
               |||:|||||: |||||||||:|||||||| | :: | |  : |        |    |
Db         238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLV 296

Qy         293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
               :||| :| | |   : |||:||||:|| | || | |
Db         297 EKTSTEVQC-KGGNVCVQAQDRYYNSSCSKWACVPC 331


RESULT 13
I12A_FELCA
ID   I12A_FELCA     STANDARD;      PRT;   222 AA.
AC   O02743; O46672;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=97246745; PubMed=9089110;
RA   Schijns V.E.C.J., Wierda C.M.H., Vahlenkamp T.W., Horzinek M.C.;
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RT   "Molecular cloning of cat interleukin-12.";
RL   Immunogenetics 45:462-463(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98182592; PubMed=9522125;
RA   Fehr D., Dean G.A., Huder J., Fan Z., Huettner S., Higgins J.W.,
RA   Pedersen N.C., Lutz H.;
RT   "Nucleotide and predicted peptide sequence of feline interleukin-12
RT   (IL-12).";
RL   DNA Seq. 8:77-82(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y07761; CAA69067.1; -.
DR   EMBL; U83185; AAB93836.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    222       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID     99     99       INTERCHAIN (PROBABLE).
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    183    183       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT     66     66       S -> P (IN REF. 2).
FT   CONFLICT    221    221       A -> S (IN REF. 2).
SQ   SEQUENCE   222 AA;  25076 MW;  223CF8FE0D30BF17 CRC64;

  Query Match             34.3%;  Score 961;  DB 1;  Length 222;
  Best Local Similarity   94.9%;  Pred. No. 2.8e-67;
  Matches  188;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        336 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 395
              :|||||||||||||||||||||||||:|||||||||||| ||||||||||||||||||||
Db         25 ARNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTST 84

Qy        396 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 455
              |||||||||||||||||||||||||||||| | |||| ||||||||||||:|||||
Db         85 VEACLPLELTMNESCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAM 144

Qy        456 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 515
              |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db        145 NAKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHA 204

Qy        516 FRIRAVTINRMMSYLNSS 533
              ||||||||||||||:|
Db        205 FRIRAVTINRMMSYLNAS 222


RESULT 14
I12A_CANFA
ID   I12A_CANFA     STANDARD;      PRT;   222 AA.
AC   Q28267;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98280561; PubMed=9617567;
RA   Buettner M., Belke-Louis G.F., Rziha H.J., McInnes C., Kaaden O.R.;
RT   "Detection, cDNA cloning and sequencing of canine interleukin 12.";
RL   Cytokine 10:241-248(1998).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U49085; AAA92058.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL        1     25       BY SIMILARITY.
FT   CHAIN        26    222       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID     99     99       INTERCHAIN (PROBABLE).
FT   CARBOHYD     42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD     96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   222 AA;  24992 MW;  48C7E53ECFD6ACE5 CRC64;

  Query Match             33.8%;  Score 949;  DB 1;  Length 222;
  Best Local Similarity   94.4%;  Pred. No. 2.4e-66;
  Matches  187;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        336 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 395
              :|:||| :||||:||||||| |||||||||||||||:   ||||||||||||||||||
Db         25 ARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTST 84

Qy        396 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 144

Qy        456 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 515
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 204

Qy        516 FRIRAVTINRMMSYLNSS 533
              ||||||||:|||||||||
Db        205 FRIRAVTIDRMMSYLNSS 222


RESULT 15
I12A_HUMAN
ID   I12A_HUMAN     STANDARD;      PRT;   219 AA.
AC   P29459; Q96QZ1;
DT   01-APR-1993 (Rel. 25, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35) (NK cell stimulatory
DE   factor chain 1) (NKSF1).
GN   IL12A OR NKSF1.
OS   Homo sapiens (Human).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91239523; PubMed=1674604;
RA   Gubler U., Chua A.O., Schoenhaut D.S., Dwyer C.M., McComas W.,
RA   Motyka R., Nabavi N., Wolitzky A.G., Quinn P.M., Familletti P.C.,
RA   Gately M.K.;
RT   "Coexpression of two distinct genes is required to generate secreted
RT   bioactive cytotoxic lymphocyte maturation factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:4143-4147(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91201875; PubMed=1673147;
RA   Wolf S.F., Temple P.A., Kobayashi M., Young D., Dicig M., Lowe L.,
RA   Dzialo R., Fitz L., Ferenz C., Hewick R.M., Kelleher K.,
RA   Herrmann S.H., Clark S.C., Azzoni L., Chan S.H., Trinchieri G.,
RA   Perussia B.;
RT   "Cloning of cDNA for natural killer cell stimulatory factor, a
RT   heterodimeric cytokine with multiple biologic effects on T and
RT   natural killer cells.";
RL   J. Immunol. 146:3074-3081(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 23-48.
RX   MEDLINE=90370873; PubMed=2204066;
RA   Stern A.S., Podlaski F.J., Hulmes J.D., Pan Y.C.E., Quinn P.M.,
RA   Wolitzky A.G., Familletti P.C., Stremlo D.L., Truitt T.,
RA   Chizzonite R., Gately M.K.;
RT   "Purification to homogeneity and partial characterization of
RT   cytotoxic lymphocyte maturation factor from human B-lymphoblastoid
RT   cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6808-6812(1990).
RN   [5]
RP   SIMILARITY TO IL-6.
RX   MEDLINE=92247293; PubMed=1374259;
RA   Merberg D.M., Wolf S.F., Clark S.C.;
RT   "Sequence similarity between NKSF and the IL-6/G-CSF family.";
RL   Immunol. Today 13:77-78(1992).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED
CC       T AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC.
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS. NKSF IS ESSENTIALLY A COMPLEX OF CYTOKINE AND SOLUBLE
CC       RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M65271; AAA35694.1; -.
DR   EMBL; M65291; AAA59937.1; ALT_INIT.
DR   EMBL; AF404773; AAK84425.1; -.
DR   PIR; A39359; A39359.
DR   PIR; A36055; A36055.
DR   Genew; HGNC:5969; IL12A.
DR   MIM; 161560; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    219       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID     96     96       INTERCHAIN (PROBABLE).
FT   CARBOHYD     93     93       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    213    213       M -> T (IN REF. 1).
SQ   SEQUENCE   219 AA;  24874 MW;  7C658AB7716112B2 CRC64;

  Query Match             31.1%;  Score 873;  DB 1;  Length 219;
  Best Local Similarity   86.4%;  Pred. No. 1.8e-60;
  Matches  171;  Conservative    7;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        336 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 395
              :||||  || |||| ||:||| |||||||| ||||||||| | ||||||||||||||||||
Db         22 ARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTST 81

Qy        396 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 455
              |||||||||| |||| ||| | ||||||||| | ||| ||||||||||||||:||| |
Db         82 VEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM 141

Qy        456 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 515
              ||||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||||
Db        142 NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHA 201

Qy        516 FRIRAVTINRMMSYLNSS 533
              ||||||||:|:|||||:|
Db        202 FRIRAVTIDRVMSYLNAS 219


Search completed: July 15, 2003, 11:07:03
Job time : 12.6808 secs
```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:57:19 ; Search time 47.2311 Seconds
(without alignments)
2325.231 Million cell updates/sec

Title: US-09-917-265-62
Perfect score: 2804
Sequence: 1 MHPQQLVISWFSLVLLASPL.....HAFRIRAVTINRMMSYLNSS 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1343.5	47.9	332	11	Q924V5	Q924v5 cavia porce
2	1343	47.9	327	11	Q9ET05	Q9et05 marmota mon
3	1282	45.7	327	11	Q91ZK7	Q91zk7 sigmodon hi
4	1146.5	40.9	335	11	Q9QUM1	Q9qum1 mus musculu
5	1135.5	40.5	335	11	Q9R278	Q9r278 rattus norv
6	1035	36.9	195	6	Q95N82	Q95n82 canis famil
7	1010	36.0	268	11	Q62712	Q62712 rattus norv
8	1004.5	35.8	344	11	Q924K7	Q924k7 meriones un
9	873	31.1	253	4	O60595	O60595 homo sapien
10	818	29.2	174	6	Q28232	Q28232 cervus elap
11	799	28.5	150	6	Q9BG70	Q9bg70 canis famil
12	770.5	27.5	221	11	Q924V6	Q924v6 cavia porce
13	768	27.4	149	6	Q9TV09	Q9tv09 canis famil
14	727.5	25.9	169	11	Q9Z1Y8	Q9z1y8 cavia porce
15	695	24.8	143	6	O62779	O62779 felis silve
16	643	22.9	215	11	Q91ZK6	Q91zk6 sigmodon hi
17	610.5	21.8	223	11	Q9ET04	Q9et04 marmota mon
18	558	19.9	215	11	Q9R103	Q9r103 rattus norv
19	525	18.7	210	11	Q924K6	Q924k6 meriones un
20	507	18.1	132	11	O70328	O70328 mesocricetu
21	441	15.7	94	6	O62777	O62777 felis silve
22	438.5	15.6	111	11	P97731	P97731 rattus sp.
23	272	9.7	61	6	Q9MYW1	Q9myw1 bos taurus
24	223	8.0	116	11	Q9QUT1	Q9qut1 mus musculu
25	180.5	6.4	372	11	O88507	O88507 mus musculu
26	170	6.1	432	11	P70225	P70225 mus musculu
27	159.5	5.7	422	4	Q16542	Q16542 homo sapien
28	157	5.6	432	11	Q64385	Q64385 mus musculu
29	156	5.6	431	11	Q99MF4	Q99mf4 rattus norv
30	143	5.1	812	10	Q9C6J9	Q9c6j9 arabidopsis
31	129.5	4.6	229	4	Q14213	Q14213 homo sapien
32	127.5	4.5	622	6	Q9N0J7	Q9n0j7 callithrix
33	123.5	4.4	739	11	Q63669	Q63669 rattus norv
34	122.5	4.4	1277	13	Q98902	Q98902 fugu rubrip
35	120	4.3	1197	13	Q90478	Q90478 brachydanio
36	118.5	4.2	229	4	O75269	O75269 homo sapien
37	116.5	4.2	978	6	Q9XS93	Q9xs93 canis famil
38	116	4.1	455	4	Q9UIR0	Q9uir0 homo sapien
39	116	4.1	626	5	Q22040	Q22040 caenorhabdi
40	115.5	4.1	1148	13	Q9IBA7	Q9iba7 gallus gall
41	115	4.1	628	11	Q9JKG1	Q9jkg1 cavia porce
42	114	4.1	838	13	Q90YM1	Q90ym1 brachydanio
43	113	4.0	428	5	Q8WPM7	Q8wpm7 oikopleura
44	113	4.0	731	6	Q8SPI6	Q8spi6 macropus eu
45	113	4.0	1146	13	Q9I8V6	Q9i8v6 gallus gall

ALIGNMENTS

RESULT 1
Q924V5
ID Q924V5 PRELIMINARY; PRT; 332 AA.
AC Q924V5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Interleukin-12 p40 subunit (IL-12 p40).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARTLEY;
RA Shiratori I., Matsumoto M., Tsuji S., Nomura M., Toyoshima K.,
RA Seya T.;
RT "Molecular cloning and functional characterization of guinea pig
RT Interleukin -12.";
RL Int. Immunol. 0:0-0(2001).
DR EMBL; AB025724; BAB63963.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ SEQUENCE 332 AA; 37632 MW; B75D16B23DE8B9B4 CRC64;

Query Match 47.9%; Score 1343.5; DB 11; Length 332;
Best Local Similarity 77.4%; Pred. No. 5.5e-106;
Matches 254; Conservative 25; Mismatches 42; Indels 7; Gaps 3;

```
Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              :||: || |||||||||:|:|||:||||||||||| ||||| |||||:| ||| |||||
Db          4 RQLISSWLSLVLLASPLLAMWELKKDVYVVELDWHTDAPGETVVLTCNTAEEDGITWTSD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
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                : |::|||||||||||||||| ||| |||||||:||||| ||:||||| ||||||||||| |
Db         64 RKSDILGSGKTLTIQVKEFEDAGGYTCHKGGEVLSRSQLLLHKKEDEIWSTDILKEQKGS 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
                | ||||||::|||||||||||||  ||:||||| ||| ||| |||||     ||||  |
Db        124 NGKTFLKCEARSYSGRFTCWWLTAFGTDVKFSVKGSRGSSDPSGVTCG----EAERVSGD 179

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
                |::| ||:||||| ||||:|||||||||||||||| |||||||||:|||||||||| |||
Db        180 NQEY-KYSVECQEDSACPTAEESLPIEVVVDAIHKFKYENYTSSFYIRDIIKPDPPKNLQ 238

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQG--KNNREKKDRLCVDKTSAKVVC 301
                |||  ||: |||||||||||||||||||||| :|  |  || ||||  |  ||||| | |
Db        239 LKPSVNSQQVEVSWEYPDTWSTPHSYFSLTFLVQTHGKNKNRREKKYELFTDKTSATVSC 298

Qy        302 HKDAKIRVQARDRYYSSSWSDWASVSCS 329
                || :|: |:|||||||||||:||||||
Db        299 HKISKVEVRARDRYYSSSWSEWASVSCS 326


RESULT 2
Q9ET05
ID   Q9ET05      PRELIMINARY;      PRT;   327 AA.
AC   Q9ET05;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p40 subunit.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21424491; PubMed=11533170;
RA   Garcia-Navarro R., Blanco-Urgoiti B., Berraondo P.,
RA   Sanchez De La Rosa R., Vales A., Hervas-Stubbs S., Lasarte J.J.,
RA   Borras F., Ruiz J., Prieto J.;
RT   "Protection against Woodchuck Hepatitis Virus (WHV) Infection by Gene
RT   Gun Coimmunization with WHV Core and Interleukin-12.";
RL   J. Virol. 75:9068-9076(2001).
DR   EMBL; AF288519; AAG01023.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   327 AA;  37140 MW;  42782B3559C224DD CRC64;

  Query Match           47.9%;  Score 1343;  DB 11;  Length 327;
  Best Local Similarity   76.0%;  Pred. No. 5.9e-106;
  Matches  247;  Conservative   35;  Mismatches   41;  Indels    2;  Gaps    2;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||| ||| |||||:|||||||:|||||||||| ||| ||||| ||||| |||||
Db          4 QQLVISWVSLVWLASPLLAIWELEKNVYVVELDWHPDTPGETVVLTCDTPEEDGITWTSE 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||||||||| |||| ||| ||||:||:|||: |||:|| |||||||||| :||
Db         64 QSSEVLGSGKTLTILVKEFEDAGHYTCHRGGEVLSQMLLLLHKNEDGIWSTDILK-KKEP 122

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              :||  : |||||||||||||||||:|||||| || |||||||||  |||||||::::
Db        123 ENKNLVTCEAKNYSGRFTCWWLTAISTDVKFSVKSHRGSSDPQGVTCGEATLSAERVKIE 182

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
                |:||||:|:||| :|||:|||:||| |||||:|||||||| ||||||||||||| ||:
Db        183 QREYKKYSVQCQEDNACPTAEETLPITVVVDAVHKLKYENYISSFFIRDIIKPDPPKNLK 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              :|| |  : |||:|||||:|||||||||||| :| |||  ::: : | |||||  | | |
Db        243 MKPSKTPQQVEVTWEYPDSWSTPHSYFSLTFSVQVQGK-KKKRSNTLHVDKTSVTVTCQK 301

Qy        304 DAKIRVQARDRYYSSSWSDWASVSC 328
                ||: ||||||||:||||:||::||
Db        302 GAKVSVQARDRYYNSSWSEWATMSC 326


RESULT 3
Q91ZK7
ID   Q91ZK7      PRELIMINARY;      PRT;   327 AA.
AC   Q91ZK7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 12 p40 subunit.
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pletneva L.M., Bacot S., Blanco J.C., Langley R.J., Prince G.A.;
RT   "Sigmodon hispidus cytokines, chemokines and interferons.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF421395; AAL16936.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ   SEQUENCE   327 AA;  37119 MW;  F096702CC950FD56 CRC64;

  Query Match           45.7%;  Score 1282;  DB 11;  Length 327;
  Best Local Similarity   72.8%;  Pred. No. 9.1e-101;
  Matches  238;  Conservative   37;  Mismatches   48;  Indels    4;  Gaps    3;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |:| |||||:||| |||||||||||||||:|| | |||| ||||| | ||||| |||
Db          4 QKLTISWFAMVLLVSPLMAIWELEKDVYVVEVDWSPGAPGERVVLTCDTSEEDDIIWTSD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||:|||||| :|||| |||||||||||: || | ||:||||||||||||:||:
Db         64 QSSEVVGSGKTLIVQVKEFSDAGQYTCHKGGETLSHSRLLLHKKEDGIWSTDILKDQKDP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| |||||| ||||||||||||:|||||||:|||   || : ||||| :|| |:| ||
Db        124 KNKTFLKCEAANYSGRFTCWWLTAVSTDLKFSLKSSSSSSDSRSVTCGAASLSTEKVTVD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
                ||| ||:| |||   ||:|||:||||:|::| || |||||:: |||||||||||| |||
Db        184 QRDYNKYSVACQEDITCPTAEETLPIELVMEAQHKYKYENYSTGFFIRDIIKPDPPKNLQ 243

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKK-DRLCVDKTSAKVVCH 302
              |||||:|: |||||||||:|||||||||| | :|   |  :||| : | ||| |||: |
Db        244 LKPLKSSQ-VEVSWEYPDSWSTPHSYFSLKFFVQVYRK--KEKKGESLLVDKPSAKIRCS 300

Qy        303 KDAKIRVQARDRYYSSSWSDWASVSCS 329
              |  ::||:|:| ||:|||||||||||:
Db        301 KGGEVRVRAQDHYYNSSWSEWASVSCN 327


RESULT 4
Q9QUM1
ID   Q9QUM1      PRELIMINARY;      PRT;   335 AA.
AC   Q9QUM1;
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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 12B P40 subunit.
GN   IL12B OR LL12B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SJL/J, AND B10.S/J; TISSUE=SPLEEN;
RA   Ma R.Z., Teuscher C.;
RT   "Screening for candidate genes of mouse autoimmnue diseases.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF128215; AAF22556.1; -.
DR   EMBL; AF128214; AAF22555.1; -.
DR   MGD; MGI:96540; Il12b.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   335 AA;  38171 MW;  7D061E116C00FC4A CRC64;

  Query Match             40.9%;  Score 1146.5;  DB 11;  Length 335;
  Best Local Similarity   65.8%;  Pred. No. 3.1e-89;
  Matches  221;  Conservative   38;  Mismatches   64;  Indels   13;  Gaps    4;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              | ||:| ||||::||| ||||||:|||||||||||||:|| |||||| | ||| ||||||||
Db          1 MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |   |:||||||| |||| ||||||||||: || | ||:||||:|||||:||
Db         61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              |  ||| |||||| |||||||| ||   : ||||::|||    | : |||| :||||:|
Db        118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGTASLSAEKV 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
               :| |||:||:| |||   ||:|||:|||| ::|  : ||||||:|||||||||||||
Db        178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
              |||:|||||: |||||||||:|||||||||| | :: | |  : |        |  | |
Db        238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGALLV 296

Qy        293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
              :||| :| | |   : |||:||||:|| | || | |
Db        297 EKTSTEVQC-KGGNVCVQAQDRYYNSSCSKWACVPC 331


RESULT 5
Q9R278
ID   Q9R278      PRELIMINARY;      PRT;   335 AA.
AC   Q9R278;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p40.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER;
RX   MEDLINE=98273736; PubMed=9613680;
RA   Khalife J., Pierrot C., Cocude C., Cetre C., Godin C., Capron A.;
RT   "Molecular cloning and sequencing of the rat interleukin-12 p40
RT   gene.";
RL   Eur. Cytokine Netw. 9:69-73(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER;
RA   Khalife J., Pierrot C., Cocude C., Cetre C., Godin C., Capron A.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF133197; AAD24190.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   335 AA;  38413 MW;  39BF5B49AF191007 CRC64;

  Query Match             40.5%;  Score 1135.5;  DB 11;  Length 335;
  Best Local Similarity   65.1%;  Pred. No. 2.7e-88;
  Matches  218;  Conservative   41;  Mismatches   63;  Indels   13;  Gaps    4;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |:|  |||::||| |||||:||||||||||:|| |||||| | ||| :||||||||||
Db          4 QKLTFSWFAMVLLVSPLMAMWELEKDVYVVEVDWRPDAPGETVTLTCDSPEEDDITWTSD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |   |:|||||||| |:|| ||||||||:||: || | ||:||||:|||||:||   |
Db         64 QRRGVIGSGKTLTITVREFLDAGQYTCHRGGETLSHSHLLLHKKENGIWSTEIL---KNF 120

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| |||||| ||||||||  ||   :|||||::|||    : : |||| :||||:| ::
Db        121 KNKTFLKCEAPNYSGRFTCSWLVHRNTDLKFNIKSSSSSPESRAVTCGRASLSAEKVTLN 180

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
               |||:||:| |||   ||:|||:||||:||:|  : |||||::||||||||||| |||
Db        181 QRDYEKYSVACQEDVTCPTAEETLPIELVVEAQQQNKYENYSTSFFIRDIIKPDPPKNLQ 240

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKT 295
              :||||||: |||||||||:|||||||||| | :: | |  : |        |    |:||
Db        241 VKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKTKETEEECNQKGAFLVEKT 299

Qy        296 SAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCSG 330
              ||:| | | | | |||:||||:|| | |  | | |
Db        300 SAEVQC-KGANICVQAQDRYYNSSCSKWTCVPCRG 333


RESULT 6
Q95N82
ID   Q95N82      PRELIMINARY;      PRT;   195 AA.
AC   Q95N82;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 subunit p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Fonfara S., Groene A., Koenig M., Baumgaertner W.;
RT   "Sequence of canine interleukin-12-p40 mRNA in DH82-cells.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF349536; AAK54070.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER       1      1
FT   NON_TER     195    195
SQ   SEQUENCE   195 AA;  21943 MW;  46D77A1570B2F8B9 CRC64;
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  Query Match             36.9%;  Score 1035;  DB 6;  Length 195;
  Best Local Similarity   100.0%;  Pred. No. 4.5e-80;
  Matches  195;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 60

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 120

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 180

Qy        184 NRDYKKYTVECQEGS 198
              |||||||||||||||
Db        181 NRDYKKYTVECQEGS 195


RESULT 7
Q62712
ID   Q62712      PRELIMINARY;      PRT;   268 AA.
AC   Q62712;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin-12p40 (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER; TISSUE=CULTURED SPLENOCYTES;
RA   Goodman R.E., Toews G.B.;
RT   "A partial cDNA of the coding region of rat IL-12p40, cloned by RT/PCR
RT   from Staphlococcal endotoxin stimulated splenocytes.";
RL   Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U16674; AAA52229.1; -.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
KW   Immunoglobulin domain.
FT   NON_TER     268    268
SQ   SEQUENCE   268 AA;  30644 MW;  9370D4CD28D9C73F CRC64;

  Query Match             36.0%;  Score 1010;  DB 11;  Length 268;
  Best Local Similarity   70.3%;  Pred. No. 9.4e-78;
  Matches  189;  Conservative   34;  Mismatches   42;  Indels    4;  Gaps    2;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |:|  |||::||| |||||:||||||||||||:|| ||||||  | ||| :||||||||||
Db          4 QKLTFSWFAMVLLVSPLMAMWELEKDVYVVEVDWRPDAPGETVTLTCDSPEEDDITWTSD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |   |:||||||||  |:|| ||||||||:||: || | ||:||||:|||||:||   |
Db         64 QRRGVIGSGKTLTITVREFLDAGQYTCHRGGETLSHSHLLLHKKENGIWSTEIL---KNF 120

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||| || ||||||||  ||   :|||||::|||    : : |||||  :||||:| ::
Db        121 KNKTFLKREAPNYSGRFTCSWLVHRNTDLKFNIKSSSSSPESRAVTCGAASLSAEKVTLN 180

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
               |||:||:| |||   ||:|||:||||:||:|  : |||||::||||||||||| |||
Db        181 QRDYEKYSVACQEDVTCPTAEETLPIELVVEAQQQNKYENYSTSFFIRDIIKPDPPKNLQ 240

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSL 272
              :||||||: ||||||||||:||||||||||
Db        241 VKPLKNSQ-VEVSWEYPDSWSTPHSYFSL 268


RESULT 8
Q924K7
ID   Q924K7      PRELIMINARY;      PRT;   344 AA.
AC   Q924K7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin-12 p40 subunit.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gaucher D., Chadee K.;
RT   "Molecular cloning of gerbil interleukin-12, and its expression as a
RT   bioactive single-chain protein.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288612; AAK83061.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ   SEQUENCE   344 AA;  39375 MW;  21B513448D73E8CB CRC64;

  Query Match             35.8%;  Score 1004.5;  DB 11;  Length 344;
  Best Local Similarity   57.8%;  Pred. No. 3.9e-77;
  Matches  199;  Conservative   54;  Mismatches   68;  Indels   23;  Gaps    8;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |:| ||||::|||||||||||||||:|||||:||   |  | ||||| | || |||||
Db          4 QKLTISWFAVVLLASPLMAIWELEKNVYVVEMDWRSGA-NESVVLTCDTSEEGDITWTKD 62

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |:::|  ||||:||:||:| :|||||||| : ||   ||:|||::| || :|||: | |
Db         63 QTTKVEQSGKTVTIEVKDFNEAGQYTCHKGDQTLSHFRLLLHKKKNGYWSNEILKQDKNS 122

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              :|: ||||||  |||||||| ||    ||||||:|:|    | : ||||||:|:||:|: |
Db        123 ENQTFLKCEAANYSGRFTCSWLVE-RTDLKFSIKNSSSSPDSRAVTCGAVSLTAEKVKGD 181

Qy        184 NRD--YKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTN 241
               :|   |:|:| |||   ||:|||::|| :|:::|  : |||||::|||||||| |||| |
Db        182 EKDGKLKQYSVTCQEDITCPTAEETVPIGLVLEAQEQNKYENYSTSFFIRDIITPDPPKN 241

Qy        242 LQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQG---------KNNREKKDR-LC 291
              |::||||| : |||||||||:||||||||:| | :  :           :|:| | |  |
Db        242 LKVKPLKNDK-VEVSWEYPDSWSTPHSYFALKFYVWTESNKENKMRNTNSNKENKMRNAC 300

Qy        292 -------VDKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
                    || || || | || :: |:|:||||:| :|  | | |
Db        301 IQNGTWLVDTTSTKVRC-KDGRVCVEAQDRYYNSLYSKHACVPC 343


RESULT 9
O60595
ID   O60595         PRELIMINARY;   PRT;   253 AA.
AC   O60595;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin 12 (Interleukin-12 P35 subunit).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liu Y., Guo Y., Wu M.;
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RT   "Human Interleukin-12 (or Natural Killer Cell Stimulatory Factor, or
RT   Cytotoxic Lymphocyte Maturation Factor) 35kDa subunit mRNA.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 1-39 FROM N.A.
RC   TISSUE=PLACENTA;
RA   Hayes M.P., Murphy F.J., Burd P.R.;
RL   Blood 0:0-0(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Hongyuan J., Meiyun Z.;
RT   "Cloning and sequence analysis of IL-12 cDNA from Chinese.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF101062; AAD16432.1; -.
DR   EMBL; AF050083; AAC05211.1; -.
DR   EMBL; AF180562; AAD56385.1; -.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
FT   VARIANT     247    247       M -> T.
SQ   SEQUENCE   253 AA;  28293 MW;  FAC56ACD2A620BD5 CRC64;

  Query Match             31.1%;  Score 873;  DB 4;  Length 253;
  Best Local Similarity   86.4%;  Pred. No. 3.9e-66;
  Matches  171;  Conservative    7;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        336 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 395
              :||||  || |||| ||:||| ||||||| ||||||||| | ||||||||||||||||||
Db         56 ARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTST 115

Qy        396 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 455
              |||||||||| ||||| ||| | ||||||||| | |||  |||||||||||||:||| |
Db        116 VEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM 175

Qy        456 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 515
              |||||||||||||||||  ||||:|||||| ||||||||||||||||||||||||||||
Db        176 NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHA 235

Qy        516 FRIRAVTINRMMSYLNSS 533
              ||||||||:|:|||||:|
Db        236 FRIRAVTIDRVMSYLNAS 253


RESULT 10
Q28232
ID   Q28232      PRELIMINARY;      PRT;   174 AA.
AC   Q28232;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 (Fragment).
GN   IL-12.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lockhart E.A.;
RT   "Cloning and sequencing of cervine IL-12.";
RL   Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U10160; AAA19658.1; -.
DR   InterPro; IPR002996; CRIA.
FT   NON_TER       1      1
FT   NON_TER     174    174
SQ   SEQUENCE   174 AA;  19684 MW;  389260B3A9067F2E CRC64;

  Query Match             29.2%;  Score 818;  DB 6;  Length 174;
  Best Local Similarity   86.8%;  Pred. No. 1.1e-61;
  Matches  151;  Conservative   14;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         85 AGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW 144
              ||||||||||:|||||||:|||||||||||||||:||| | | |||||||:||| |||||
Db          1 AGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWW 60

Qy        145 LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAE 204
              |||||||||||||||| |||:||||||::|| |:| ||:|:|||||||||||||:||
Db         61 LTAISTDLKFSVKSSRGSSDPRGVTCGAMSLSTEKVIVDHREYKKYTVECQEGSACPAAE 120

Qy        205 ESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWE 258
              |||||||||:|:|||||||||||||||||||||| ||||:|||||| ||||||
Db        121 ESLPIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWE 174


RESULT 11
Q9BG70
ID   Q9BG70      PRELIMINARY;      PRT;   150 AA.
AC   Q9BG70;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Interleukin 12 subunit p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Markus S., Baumgaertner W.;
RT   "Expression of canine interleukin-12 subunit p40 mRNA in a continuous
RT   macrophage cell line.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF333121; AAK01441.1; -.
DR   InterPro; IPR003600; Ig_like.
DR   SMART; SM00410; IG_like; 1.
FT   NON_TER       1      1
FT   NON_TER     150    150
SQ   SEQUENCE   150 AA;  16780 MW;  A867903EF16083BA CRC64;

  Query Match             28.5%;  Score 799;  DB 6;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-60;
  Matches  150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         49 TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKE 108
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKE 60

Qy        109 DGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGV 168
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGV 120

Qy        169 TCGAVTLSAERVRVDNRDYKKYTVECQEGS 198
              |||||||||||||||||||||||||||||
Db        121 TCGAVTLSAERVRVDNRDYKKYTVECQEGS 150


RESULT 12
Q924V6
ID   Q924V6      PRELIMINARY;      PRT;   221 AA.
AC   Q924V6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p35 subunit (IL-12 p35).
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HARTLEY;
RA   Shiratori I., Matsumoto M., Tsuji S., Nomura M., Toyoshima K.,
RA   Seya T.;
RT   "Molecular cloning and functional characterization of guinea pig
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RT   Interleukin -12.";
RL   Int. Immunol. 0:0-0(2001).
DR   EMBL; AB025723; BAB63962.1; -.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
SQ   SEQUENCE   221 AA;  24687 MW;  972E59F5A11DE896 CRC64;

  Query Match             27.5%;  Score 770.5;  DB 11;  Length 221;
  Best Local Similarity   74.3%;  Pred. No. 1.7e-57;
  Matches  156;  Conservative   19;  Mismatches   28;  Indels    7;  Gaps    2;

Qy        326 VSCSGGGGGGSRNLPTPTPSP--GMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEI 383
              ||||      :|||| :|:|     || ||||||||||:: | || | | :|||| |||
Db         17 VSCS-----LARNLPRASPAPVTEPVQCFNHSQTLLRAVNSELHKAIQMLAVYSCTPEEI 71

Qy        384 DHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYE 443
              |||||||||||||:||:|||| |||||||  ||  |||||||||| |||  |||:|||| 
Db         72 DHEDITKDKTSTVKACVPLELVKNESCLASGHISFTTNGSCLASGKTSFMMALCLNSIYE 131

Qy        444 DLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFY 503
              |||:||:||| |||:|||||:||||||||||:|||||:|||| : |||||| ||||||||
Db        132 DLKLYQLEFKNMNAQLLMDPQRQIFLDQNMLSAIDELIQALNGSDVTVPQKLSLEEPDFY 191

Qy        504 KTKIKLCILLHAFRIRAVTINRMMSYLNSS 533
              | |:||||||||||||||||:|:|||| ||
Db        192 KIKMKLCILLHAFRIRAVTIDRVMSYLTSS 221


RESULT 13
Q9TV09
ID   Q9TV09      PRELIMINARY;      PRT;   149 AA.
AC   Q9TV09;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Interleukin-12 p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RT   "Cloning and sequencing of canine IL-12 p40 mRNA.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF091134; AAD46992.1; -.
FT   NON_TER       1      1
FT   NON_TER     149    149
SQ   SEQUENCE   149 AA;  16453 MW;  20E2686B0AA37E26 CRC64;

  Query Match             27.4%;  Score 768;  DB 6;  Length 149;
  Best Local Similarity   98.6%;  Pred. No. 1.6e-57;
  Matches  146;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         69 LGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIF 128
              ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LGAGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIF 60

Qy        129 LKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYK 188
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Db         61 LKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYN 120

Qy        189 KYTVECQEGSACPSAEESLPIEVVVDAI 216
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Db        121 KYTVECQEGSACPSAEESLPIEVVVDAI 148


RESULT 14
Q9Z1Y8
ID   Q9Z1Y8      PRELIMINARY;      PRT;   169 AA.
AC   Q9Z1Y8;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   Interleukin 12p40 (Fragment).
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069279; PubMed=9824482;
RA   Wicher V., Scarozza A.M., Ramsingh A.I., Wicher K.;
RT   "Cytokine gene expression in skin of susceptible guinea-pig infected
RT   with Treponema pallidum.";
RL   Immunology 95:242-247(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99144670; PubMed=10025978;
RA   Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;
RT   "Spontaneous cytokine gene expression in normal guinea pig blood and
RT   tissues.";
RL   Cytokine 10:851-859(1998).
DR   EMBL; AF097507; AAC83805.1; -.
FT   NON_TER       1      1
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SQ   SEQUENCE   169 AA;  19128 MW;  0A2DE7480C1281F5 CRC64;

  Query Match             25.9%;  Score 727.5;  DB 11;  Length 169;
  Best Local Similarity   79.3%;  Pred. No. 5.3e-54;
  Matches  138;  Conservative   11;  Mismatches   20;  Indels    5;  Gaps    2;

Qy         91 HKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIST 150
              ||||:||||| ||:||||| |||||||||||  |  | ||||||::|||||||||||||  |
Db          1 HKGGEVLSRSQLLLHKKEDEIWSTDILKEQKGSNGKTFLKCEARSYSGRFTCWWLTAFGT 60

Qy        151 DLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIE 210
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Db         61 DVKFSVKGSRGSSDPSGVTCG----EAERVSGDNQEY-KYSVECQEDSACPTAEESLPIE 115

Qy        211 VVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWS 264
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Db        116 VVVDAIHKFKYENYTSSFYIRDIIKPDPPKNLQLKPSVNSQQVEVSWEYPDTWS 169


RESULT 15
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ID   O62779      PRELIMINARY;      PRT;   143 AA.
AC   O62779;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 p40 subunit (Fragment).
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99322318; PubMed=10391845;
RA   Harley R., Helps C.R., Harbour D.A., Gruffydd-Jones T.J., Day M.J.;
RT   "Cytokine mRNA expression in lesions in cats with chronic
RT   gingivostomatitis.";
RL   Clin. Diagn. Lab. Immunol. 6:471-478(1999).
DR   EMBL; AF054607; AAC15980.1; -.
DR   InterPro; IPR002996; CR1A.
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SQ   SEQUENCE   143 AA;  16122 MW;  E107DF253F5D4D40 CRC64;

  Query Match             24.8%;  Score 695;  DB 6;  Length 143;
  Best Local Similarity   90.9%;  Pred. No. 2.4e-51;
  Matches  130;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy         150 TDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPI 209
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Db          61 TDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPI 120

Qy         210 EVVVDAIHKLKYENYTSSFFIRD 232
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Db         121 EVVVDAIHKLKYENYTSSFFIRD 143


Search completed: July 15, 2003, 11:06:11
Job time : 48.2311 secs
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:59:19 ; Search time 18.283 Seconds
(without alignments)
857.760 Million cell updates/sec

Title: US-09-917-265-62
Perfect score: 2804
Sequence: 1 MHPQQLVISWFSLVLLASPL.....HAFRIRAVTINRMMSYLNSS 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2393.5	85.4	540	2	US-08-751-767A-8	Sequence 8, Appli
2	2393.5	85.4	540	2	US-08-751-767A-10	Sequence 10, Appl
3	2313.5	82.5	519	2	US-08-751-767A-12	Sequence 12, Appl
4	1501.5	53.5	328	1	US-08-265-087-2	Sequence 2, Appli
5	1501.5	53.5	328	1	US-08-186-529-2	Sequence 2, Appli
6	1501.5	53.5	328	1	US-08-621-493-2	Sequence 2, Appli
7	1501.5	53.5	328	1	US-08-640-386A-2	Sequence 2, Appli
8	1501.5	53.5	328	2	US-08-965-688-2	Sequence 2, Appli
9	1501.5	53.5	328	2	US-08-751-767A-4	Sequence 4, Appli
10	1501.5	53.5	328	4	US-09-260-173-2	Sequence 2, Appli
11	1418.5	50.6	306	1	US-08-424-682A-1	Sequence 1, Appli
12	1142.5	40.7	335	2	US-08-385-335A-15	Sequence 15, Appl
13	1132.5	40.4	335	2	US-08-659-206A-3	Sequence 3, Appli
14	1132.5	40.4	335	2	US-08-659-206A-6	Sequence 6, Appli
15	873	31.1	219	1	US-08-186-529-4	Sequence 4, Appli
16	873	31.1	219	1	US-08-640-386A-4	Sequence 4, Appli
17	873	31.1	253	1	US-08-265-087-4	Sequence 4, Appli
18	873	31.1	253	1	US-08-621-493-4	Sequence 4, Appli
19	873	31.1	253	2	US-08-684-687-4	Sequence 4, Appli
20	873	31.1	253	2	US-08-965-688-4	Sequence 4, Appli
21	873	31.1	253	4	US-09-260-173-4	Sequence 4, Appli
22	867	30.9	219	2	US-08-751-767A-2	Sequence 2, Appli
23	549	19.6	215	2	US-08-385-335A-12	Sequence 12, Appl
24	549	19.6	215	2	US-08-659-206A-2	Sequence 2, Appli
25	549	19.6	215	2	US-08-659-206A-5	Sequence 5, Appli
26	211.5	7.5	468	4	US-08-795-473B-5	Sequence 5, Appli
27	211.5	7.5	468	4	US-09-439-856-5	Sequence 5, Appli
28	211.5	7.5	468	6	5171840-2	Patent No. 5171840
29	211.5	7.5	468	6	5480796-2	Patent No. 5480796
30	193	6.9	323	6	5171840-6	Patent No. 5171840
31	193	6.9	323	6	5480796-6	Patent No. 5480796
32	193	6.9	344	6	5171840-7	Patent No. 5171840
33	193	6.9	344	6	5480796-7	Patent No. 5480796
34	170	6.1	372	1	US-07-865-878A-4	Sequence 4, Appli
35	170	6.1	372	1	US-07-676-647-2	Sequence 2, Appli
36	170	6.1	372	1	US-08-449-329-2	Sequence 2, Appli
37	170	6.1	372	2	US-08-445-073-2	Sequence 2, Appli
38	170	6.1	372	2	US-08-585-258-2	Sequence 2, Appli
39	170	6.1	372	2	US-08-603-010-4	Sequence 4, Appli
40	170	6.1	372	4	US-09-211-590-2	Sequence 2, Appli
41	170	6.1	372	5	PCT-US91-03896-2	Sequence 2, Appli
42	159.5	5.7	422	4	US-09-151-102-2	Sequence 2, Appli
43	159.5	5.7	422	4	US-08-929-846-2	Sequence 2, Appli
44	157	5.6	432	4	US-08-702-665A-3	Sequence 3, Appli
45	157	5.6	441	4	US-09-151-102-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-08-751-767A-8
; Sequence 8, Application US/08751767A
; Patent No. 5994104
; GENERAL INFORMATION:
; APPLICANT: ANDERSON, ROBERT J.
; APPLICANT: GRANT, HUGH
; APPLICANT: MACDONALD, IAN D.
; TITLE OF INVENTION: INTERLUKIN-12 FUSION PROTEIN
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22201
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/751,767A
; FILING DATE: 08-NOV-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: SADOFF, B.J.
; REGISTRATION NUMBER: 36,663
; REFERENCE/DOCKET NUMBER: 117-221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 7038164091
; TELEFAX: 7038164100
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 540 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-751-767A-8

Query Match 85.4%; Score 2393.5; DB 2; Length 540;
Best Local Similarity 84.3%; Pred. No. 1.1e-218;
Matches 456; Conservative 28; Mismatches 48; Indels 9; Gaps 2;

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Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
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Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
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Qy         121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Db         121 KEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERV 180

Qy         181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
               | ||::| :|:||||| ||||:||||||||:|||:|||||||||||||||||||||||
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Qy         241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
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Qy         301 CHKDAKIRVQARDRYYSSSWSDWASVSCSGG--------GGGGSRNLPTPTPSPGMFQCL 352
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Qy         413 SREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQN 472
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Qy         533 S 533
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Db         540 S 540


RESULT 2
US-08-751-767A-10
; Sequence 10, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  540 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-10

  Query Match             85.4%;  Score 2393.5;  DB 2;  Length 540;
  Best Local Similarity   84.3%;  Pred. No. 1.1e-218;
  Matches  456;  Conservative   28;  Mismatches   48;  Indels    9;  Gaps    2;

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Qy          61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
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Qy         121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Db         121 KEPKNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERV 180

Qy         181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
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Db         181 RGDNKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPK 239

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Qy         473 MLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNS 532
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Qy         533 S 533
               |
Db         540 S 540


RESULT 3
US-08-751-767A-12
; Sequence 12, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
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;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  519 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-12

  Query Match             82.5%;  Score 2313.5;  DB 2;  Length 519;
  Best Local Similarity   84.4%;  Pred. No. 4.2e-211;
  Matches  439;  Conservative   27;  Mismatches   45;  Indels    9;  Gaps    2;

Qy         22 AIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKE 81
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Qy         82 FGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFT 141
              |||||||||||||:||| ||||:|||||||||||||:||| ||| ||:|||||||||||
Db         61 FGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFT 120

Qy        142 CWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP 201
              ||||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||
Db        121 CWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACP 179

Qy        202 SAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPD 261
              :|||||||||:|||:|||||||||||||||||||||||| ||||||||||| ||||||||
Db        180 AAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPD 239

Qy        262 TWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 321
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||
Db        240 TWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWS 299

Qy        322 DWASVSCSGG--------GGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTL 373
              :|||| ||||        |||||||||  || |||| ||:||| ||||||| ||||||||
Db        300 EWASVPCSGGGGSGGGGSGGGGSRNLPLATPDPGMFPCLHHSQNLLRAVSNMLQKARQTL 359

Qy        374 ELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFM 433
              | | |||||||||||||||||||||||||||| ||||| ||| | |||||||||| | |||
Db        360 EFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFM 419

Qy        434 TVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQ 493
                |||||||||||||:||| |||||||||||||||||||  ||||:|||||| ||||
Db        420 MALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQ 479

Qy        494 KSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533
              |||||||||||||||||||||||||||||:|: ||||:|
Db        480 KSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNAS 519


RESULT 4
US-08-265-087-2
; Sequence 2, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-265-087-2

  Query Match             53.5%;  Score 1501.5;  DB 1;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 2.7e-134;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| ||||:|||||:|||||||||:|||||||||| |||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| ||||:|||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||| ||||| |||||||| |||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:|||| |||:|||||||:|||:||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:|||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 5
US-08-186-529-2
; Sequence 2, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
```

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;       COUNTRY:  USA
;       ZIP:  02140
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/186,529
;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McDaniels, Patricia A.
;       REGISTRATION NUMBER:  33,194
;       REFERENCE/DOCKET NUMBER:  GI 5225
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-498-8401
;       TELEFAX:  617-876-5851
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  328 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-186-529-2

  Query Match             53.5%;  Score 1501.5;  DB 1;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 2.7e-134;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||  |||||:|||||:||||||||||:||||||||||| |||||  ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||||||||||||||||||||||||:|||  ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||  |||||  ||||||||  |||||||||  ||||||||  |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::|  :|:|||||  ||||:|||||||||:|||:|||||||||||||||||||||||  |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              ||||||||  ||||||||||||||||||||||:|  |||:  ||||||:  |||||  |:|  |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :|  |  |:|:|||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 6
US-08-621-493-2
; Sequence 2, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-621-493-2

  Query Match             53.5%;  Score 1501.5;  DB 1;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 2.7e-134;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||  |||||:|||||:||||||||||:||||||||||| |||||  ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              |||||||||||||||||||||||||||||:|||  ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||  |||||  ||||||||  |||||||||  ||||||||  |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::|  :|:|||||  ||||:|||||||||:|||:|||||||||||||||||||||||  |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              ||||||||  ||||||||||||||||||||||:|  |||:  ||||||:  |||||  |:|  |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :|  |  |:|:|||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 7
US-08-640-386A-2
; Sequence 2, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
```

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;       ZIP:  02140
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/640,386A
;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Brown, Scott A.
;       REGISTRATION NUMBER:  32,724
;       REFERENCE/DOCKET NUMBER:  GI 5225A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-498-8224
;       TELEFAX:  617-876-5851
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  328 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-640-386A-2

  Query Match             53.5%;  Score 1501.5;  DB 1;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 2.7e-134;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| |||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||:||| |||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:||||||||:|||:|||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 8
US-08-965-688-2
; Sequence 2, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;     APPLICANT:  Scott, Phillip
;     APPLICANT:  Trinchieri, Giorgio
;     TITLE OF INVENTION:  Compositions and Methods for Use of
;     TITLE OF INVENTION:  IL-12 as an Adjuvant
;     NUMBER OF SEQUENCES:  4
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Howson and Howson
;       STREET:  Spring House Corporate Center, PO Box 457
;       CITY:  Spring House
;       STATE:  Pennsylvania
;       COUNTRY:  USA
;       ZIP:  19477
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/965,688
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/621,493
;       FILING DATE:  25-MAR-1996
;       APPLICATION NUMBER:  08/265,087
;       FILING DATE:  17-JUN-1994
;       APPLICATION NUMBER:  US 08/229,282
;       FILING DATE:  18-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bak, Mary E.
;       REGISTRATION NUMBER:  31,215
;       REFERENCE/DOCKET NUMBER:  WST51AUSA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-540-9206
;       TELEFAX:  215-540-5818
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  328 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-965-688-2

  Query Match             53.5%;  Score 1501.5;  DB 2;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 2.7e-134;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              ||||||||||| |||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||||||:||| |||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:||||||||:|||:|||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 9
US-08-751-767A-4
; Sequence 4, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;     APPLICANT:  ANDERSON, ROBERT J.
;     APPLICANT:  GRANT, HUGH
;     APPLICANT:  MACDONALD, IAN D.
;     TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;     NUMBER OF SEQUENCES:  80
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  NIXON & VANDERHYE P.C.
;       STREET:  1100 NORTH GLEBE ROAD
;       CITY:  ARLINGTON
;       STATE:  VA
```

```
;       COUNTRY:  USA
;       ZIP:  22201
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/751,767A
;       FILING DATE:  08-NOV-1996
;       CLASSIFICATION:  536
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  SADOFF, B.J.
;       REGISTRATION NUMBER:  36,663
;       REFERENCE/DOCKET NUMBER:  117-221
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  7038164091
;       TELEFAX:  7038164100
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  328 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-751-767A-4

  Query Match             53.5%;  Score 1501.5;  DB 2;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 2.7e-134;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| |||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| ||||:|||||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| ||||:||||||||:|||:|||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||:| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:|||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 10
US-09-260-173-2
; Sequence 2, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;       APPLICANT: Scott, Phillip
;                  Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 328 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-260-173-2

  Query Match             53.5%;  Score 1501.5;  DB 4;  Length 328;
  Best Local Similarity   85.3%;  Pred. No. 2.7e-134;
  Matches  278;  Conservative   22;  Mismatches   25;  Indels    1;  Gaps    1;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| |||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| ||||:|||||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| ||||:||||||||:|||:|||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| ||||||||||||||||||||||:| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCS 329
              :| | |:|:|||||||||:|||| ||
Db        303 NASISVRAQDRYYSSSWSEWASVPCS 328


RESULT 11
US-08-424-682A-1
; Sequence 1, Application US/08424682A
; Patent No. 5650492
;  GENERAL INFORMATION:
;    APPLICANT:  Gately, Maurice K
;    APPLICANT:  Hakimi, John
;    APPLICANT:  Ling, Ping
;    TITLE OF INVENTION:  P40 HOMODIMER OF INTERLEUKIN-12
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
```

```
;       ADDRESSEE:  Hoffmann-La Roche Inc.
;       STREET:  340 Kingsland Street
;       CITY:  Nutley
;       STATE:  New Jersey
;       COUNTRY:  United States of America
;       ZIP:  07110-1199
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/424,682A
;       FILING DATE:  18-APR-1995
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/087,832
;       FILING DATE:  02-JUL-1993
;       CLASSIFICATION:  530
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kass, Alan P
;       REGISTRATION NUMBER:  32142
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (201) 235-4205
;       TELEFAX:  (201) 235-3500
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  306 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-424-682A-1

  Query Match             50.6%;  Score 1418.5;  DB 1;  Length 306;
  Best Local Similarity   85.0%;  Pred. No. 1.8e-126;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82
              ||||:|||||||||||:|||||||||||| ||||| |||| |||||||||||||||||||
Db          1 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 60

Qy         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142
              |||||||||||:||| ||||:||||||||||||||:||| ||| ||:|||||||||||||
Db         61 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 120

Qy        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202
              |||| ||||| |||||||| |||||||||| |||||||| ||:|| :|:|||| ||||:
Db        121 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 179

Qy        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262
              |||||||||:|||:||||||||||||||||||||||| |||||||||| |||||||||
Db        180 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 239

Qy        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322
              |||||||||||||:| |||: |||||: |||| |:| |:| | |:|:||||||||:
Db        240 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 299

Qy        323 WASVSCS 329
              |||| ||
Db        300 WASVPCS 306


RESULT 12
US-08-385-335A-15
; Sequence 15, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-385-335A-15

  Query Match             40.7%;  Score 1142.5;  DB 2;  Length 335;
  Best Local Similarity   65.5%;  Pred. No. 3.4e-100;
  Matches  220;  Conservative   38;  Mismatches   65;  Indels   13;  Gaps    4;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              | ||:| ||||::||| ||||||:||||||||||:|| |||||| | ||| |||||||||
Db          1 MGPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |   |:||||||||| |||| ||||||||||: || | ||:||||:|||||:||
Db         61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              |  ||| ||||| |||||||| ||   : ||||::|||    | : ||||  :||||:|
Db        118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKV 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              :| |||:||:| |||   ||:|||:||||: ::|  : |||||::||||||||||||
Db        178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
              |||:|||||: ||||||||||:|||||||||| | :: | |  : |        |    |
Db        238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLV 296

Qy        293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
              :||| :| | |   : |||:||||:|| | || | |
Db        297 EKTSTEVQC-KGGNVCVQAQDRYYNSSCSKWACVPC 331


RESULT 13
US-08-659-206A-3
; Sequence 3, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
```

```
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-3

  Query Match             40.4%;  Score 1132.5;  DB 2;  Length 335;
  Best Local Similarity   65.2%;  Pred. No. 3.1e-99;
  Matches  219;  Conservative   38;  Mismatches   66;  Indels   13;  Gaps    4;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              | ||:| ||||::||| |||||:||||||||||:|| |||||| | ||| |||||||||
Db          1 MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |   |:||||||||: |||| ||||||||||: || | ||:||||:|||||:||
Db         61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              |  ||| |||||| |||||||| ||   : ||||::|||    | : ||||  :||||:|
Db        118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKV 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              :| |||:||:| |||   ||:|||:|||| ::|  : |||||::||||||||||||
Db        178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
              |||:||||||: |||||||||:|||||||||| | :: | |  : |        |    |
Db        238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLV 296

Qy        293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
              :||| :| | |   : |||:|| |:|| | || | |
Db        297 EKTSTEVQC-KGGNVCVQAQDRCYNSSCSKWACVPC 331


RESULT 14
US-08-659-206A-6
; Sequence 6, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-6

  Query Match             40.4%;  Score 1132.5;  DB 2;  Length 335;
  Best Local Similarity   65.2%;  Pred. No. 3.1e-99;
  Matches  219;  Conservative   38;  Mismatches   66;  Indels   13;  Gaps    4;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              | ||:| ||||::||| |||||:||||||||||:|| |||||| | ||| |||||||||
Db          1 MCPQKLTISWFAIVLLVSPLMAMWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |   |:||||||||: |||| ||||||||||: || | ||:||||:|||||:||
Db         61 TSDQRHGVIGSGKTLTITVKEFLDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL--- 117

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
              |  ||| |||||| |||||||| ||   : ||||::|||    | : ||||  :||||:|
Db        118 KNFKNKTFLKCEAPNYSGRFTCSWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKV 177

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              :| |||:||:| |||   ||:|||:|||| ::|  : |||||::||||||||||||
Db        178 TLDQRDYEKYSVSCQEDVTCPTAEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPK 237

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREK--------KDRLCV 292
              |||:||||||: |||||||||:|||||||||| | :: | |  : |        |    |
Db        238 NLQMKPLKNSQ-VEVSWEYPDSWSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLV 296

Qy        293 DKTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSC 328
              :||| :| | |   : |||:|| |:|| | || | |
Db        297 EKTSTEVQC-KGGNVCVQAQDRCYNSSCSKWACVPC 331


RESULT 15
US-08-186-529-4
; Sequence 4, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
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;       FILING DATE:
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McDaniels, Patricia A.
;       REGISTRATION NUMBER:  33,194
;       REFERENCE/DOCKET NUMBER:  GI 5225
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-498-8401
;       TELEFAX:  617-876-5851
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  219 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-186-529-4

  Query Match             31.1%;  Score 873;  DB 1;  Length 219;
  Best Local Similarity   86.4%;  Pred. No. 6.9e-75;
  Matches  171;  Conservative    7;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        336 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 395
              :||||  || |||| ||:||| ||||||| ||||||||| | ||||||||||||||||||
Db         22 ARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTST 81

Qy        396 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 455
              |||||||||| ||||| ||| | ||||||||| | |||  |||||||||||||:||| |
Db         82 VEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM 141

Qy        456 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 515
              ||||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||
Db        142 NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHA 201

Qy        516 FRIRAVTINRMMSYLNSS 533
              |||||||:|:|||||:|
Db        202 FRIRAVTIDRVMSYLNAS 219


Search completed: July 15, 2003, 11:10:02
Job time : 19.283 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 11:03:04 ; Search time 24.8852 Seconds
(without alignments)
2493.521 Million cell updates/sec

Title: US-09-917-265-62
Perfect score: 2804
Sequence: 1 MHPQQLVISWFSLVLLASPL.....HAFRIRAVTINRMMSYLNSS 533

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2804	100.0	533	10	US-09-917-265-62	Sequence 62, Appl
2	2693	96.0	511	10	US-09-917-265-67	Sequence 67, Appl
3	2643	94.3	533	10	US-09-917-265-39	Sequence 39, Appl
4	2546	90.8	511	10	US-09-917-265-44	Sequence 44, Appl
5	2392	85.3	537	10	US-09-828-825-8	Sequence 8, Appli
6	2392	85.3	537	10	US-09-828-825-16	Sequence 16, Appl
7	2389.5	85.2	542	10	US-09-828-825-6	Sequence 6, Appli
8	2389.5	85.2	542	10	US-09-828-825-14	Sequence 14, Appl
9	2387	85.1	547	10	US-09-828-825-10	Sequence 10, Appl
10	2387	85.1	547	10	US-09-828-825-12	Sequence 12, Appl
11	2358	84.1	527	10	US-09-828-825-2	Sequence 2, Appli
12	2354	84.0	526	10	US-09-828-825-4	Sequence 4, Appli
13	1764	62.9	329	10	US-09-917-265-59	Sequence 59, Appl
14	1764	62.9	329	10	US-09-917-265-108	Sequence 108, App
15	1657	59.1	329	10	US-09-917-265-30	Sequence 30, Appl
16	1653	59.0	307	10	US-09-917-265-53	Sequence 53, Appl
17	1653	59.0	328	10	US-09-917-265-56	Sequence 56, Appl
18	1651	58.9	329	12	US-10-079-616-1	Sequence 1, Appli
19	1554	55.4	307	12	US-10-079-616-2	Sequence 2, Appli
20	1546	55.1	307	10	US-09-917-265-27	Sequence 27, Appl
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22	1501.5	53.5	328	9	US-10-247-463-6	Sequence 6, Appli
23	1501.5	53.5	328	10	US-09-754-014-1	Sequence 1, Appli
24	1501.5	53.5	328	10	US-09-836-866-1	Sequence 1, Appli
25	1501.5	53.5	328	10	US-09-924-703-4	Sequence 4, Appli
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27	1141.5	40.7	335	9	US-10-172-399-4	Sequence 4, Appli
28	1141.5	40.7	335	9	US-10-247-463-7	Sequence 7, Appli
29	970	34.6	222	10	US-09-917-265-47	Sequence 47, Appl
30	970	34.6	222	10	US-09-917-265-105	Sequence 105, App
31	969	34.6	197	10	US-09-917-265-50	Sequence 50, Appl
32	964	34.4	222	12	US-10-079-616-3	Sequence 3, Appli
33	963	34.3	197	12	US-10-079-616-4	Sequence 4, Appli
34	961	34.3	222	10	US-09-917-265-33	Sequence 33, Appl
35	960	34.2	197	10	US-09-917-265-36	Sequence 36, Appl
36	903	32.2	187	10	US-09-917-265-102	Sequence 102, App
37	873	31.1	253	10	US-09-924-703-6	Sequence 6, Appli
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43	206	7.3	592	9	US-09-935-868-8	Sequence 8, Appli
44	206	7.3	592	9	US-10-287-035-8	Sequence 8, Appli
45	197	7.0	1168	9	US-09-935-868-24	Sequence 24, Appl

ALIGNMENTS

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RESULT 1
US-09-917-265-62
; Sequence 62, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-62

  Query Match            100.0%;  Score 2804;  DB 10;  Length 533;
  Best Local Similarity  100.0%;  Pred. No. 4.2e-218;
  Matches  533;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db         361 AVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLIT 420

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Db         481 LQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533


RESULT 2
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; Sequence 67, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-67

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Qy         143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202
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Qy         203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262
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Qy         503 YKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533
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Db         481 YKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511


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; Sequence 39, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-39

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Qy         121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Db         121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKV 180

Qy         181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
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Qy         241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
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Qy         481 LQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533
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RESULT 4
US-09-917-265-44
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; Sequence 44, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-44

  Query Match             90.8%;  Score 2546;  DB 10;  Length 511;
  Best Local Similarity   94.3%;  Pred. No. 2.7e-197;
  Matches  482;  Conservative   12;  Mismatches   17;  Indels    0;  Gaps    0;

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Db         61 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 120

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Db        121 WWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 180

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Db        241 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 300

Qy        323 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEE 382
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Db        301 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEE 360

Qy        383 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIY 442
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Db        361 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIY 420

Qy        443 EDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDF 502
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Db        421 EDLKMYQVEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDF 480

Qy        503 YKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533
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Db        481 YKTKIKLCILLHAFRIRAVTINRMMSYLNAS 511


RESULT 5
US-09-828-825-8
; Sequence 8, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 537
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-8

  Query Match             85.3%;  Score 2392;  DB 10;  Length 537;
  Best Local Similarity   85.2%;  Pred. No. 8e-185;
  Matches  456;  Conservative   28;  Mismatches   45;  Indels    6;  Gaps    3;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
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Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
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Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGG---GGGGS--RNLPTPTPSPGMFQCLNHSQTL 358
              :| | |:|:|||||||||:|||| ||||   |||||  ||||  || |||| ||:||| |
Db        303 NASISVRAQDRYYSSSWSEWASVPCSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNL 362

Qy        359 LRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISL 418
              |||||| |||||||||  | ||||||||||||||||||||||||||| ||||| ||| |
Db        363 LRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSF 422

Qy        419 ITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAID 478
              |||||||||  | |||  |||||||||||||||:||| ||||||||||||||||||  ||
Db        423 ITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVID 482

Qy        479 ELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533
              ||:|||||||| ||||||||||||||||||||||||||||||:|:|||||:|
Db        483 ELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 537


RESULT 6
US-09-828-825-16
; Sequence 16, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 537
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-16
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  Query Match           85.3%;  Score 2392;  DB 10;  Length 537;
  Best Local Similarity  85.2%;  Pred. No. 8e-185;
  Matches  456;  Conservative   28;  Mismatches   45;  Indels    6;  Gaps    3;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| ||||:|||||:||||||||||:|||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:||||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| ||||:||||||||:|||:||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||:| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGG---GGGGS--RNLPTPTPSPGMFQCLNHSQTL 358
              :| | |:|:|||||||||:|||| ||||   |||||  ||||  || |||| ||:||| |
Db        303 NASISVRAQDRYYSSSWSEWASVPCSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNL 362

Qy        359 LRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISL 418
              |||||| |||||||| | ||||||||||||||||||||||||||||| ||||| ||| |
Db        363 LRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSF 422

Qy        419 ITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAID 478
              |||||||| | |||  |||||||||||||:||| ||||||||||||||||||  ||
Db        423 ITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVID 482

Qy        479 ELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533
              ||:||||||| ||||||||||||||||||||||||||||||:|:||||||:|
Db        483 ELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 537


RESULT 7
US-09-828-825-6
; Sequence 6, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 542
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-6

  Query Match           85.2%;  Score 2389.5;  DB 10;  Length 542;
  Best Local Similarity  84.4%;  Pred. No. 1.3e-184;
  Matches  456;  Conservative   28;  Mismatches   45;  Indels   11;  Gaps    3;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| ||||:|||||:||||||||||:|||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:||||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| ||||:||||||||:|||:||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||:| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGG--------GGGGS--RNLPTPTPSPGMFQCLN 353
              :| | |:|:|||||||||:|||| ||||         |||||  ||||  || |||| ||:
Db        303 NASISVRAQDRYYSSSWSEWASVPCSGGGGSGGGGSGGGGSPWRNLPVATPDPGMFPCLH 362

Qy        354 HSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS 413
              ||| ||||||| |||||||| | ||||||||||||||||||||||||||||| ||||| |
Db        363 HSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNS 422

Qy        414 REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNM 473
              || | |||||||| | |||  |||||||||||||:||| ||||||||||||||||||
Db        423 RETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNM 482

Qy        474 LTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533
              |  ||||:||||||| ||||||||||||||||||||||||||||||:|:||||||:|
Db        483 LAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 542


RESULT 8
US-09-828-825-14
; Sequence 14, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 542
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-14

  Query Match           85.2%;  Score 2389.5;  DB 10;  Length 542;
  Best Local Similarity  84.4%;  Pred. No. 1.3e-184;
  Matches  456;  Conservative   28;  Mismatches   45;  Indels   11;  Gaps    3;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| ||||:|||||:||||||||||:|||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:||||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
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Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
                |||||||| |||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGG--------GGGGS--RNLPTPTPSPGMFQCLN 353
                :| | |:|:|||||||||:|||| ||||        |||||  ||||  || |||| ||:
Db        303 NASISVRAQDRYYSSSWSEWASVPCSGGGGSGGGGSGGGGSPWRNLPVATPDPGMFPCLH 362

Qy        354 HSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS 413
                ||| ||||||| |||||||||  | ||||||||||||||||||||||||||| ||||| |
Db        363 HSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNS 422

Qy        414 REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNM 473
                || | |||||||||  | |||  |||||||||||||:||| ||||||||||||||||||
Db        423 RETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNM 482

Qy        474 LTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533
                |  ||||:|||||| |||||||||||||||||||||||||||||:|:|||||:|
Db        483 LAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 542


RESULT 9
US-09-828-825-10
; Sequence 10, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 547
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-10

  Query Match            85.1%;  Score 2387;  DB 10;  Length 547;
  Best Local Similarity   83.7%;  Pred. No. 2.1e-184;
  Matches  456;  Conservative   28;  Mismatches   45;  Indels   16;  Gaps    3;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
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Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:|||||||||:|||:|||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGG-------------GGGGS--RNLPTPTPSPGM 348
              :| | |:|:|||||||||:|||| ||||             |||||  ||||  || |||
Db        303 NASISVRAQDRYYSSSWSEWASVPCSGGGGSGGGGSGGGGSGGGGSPWRNLPVATPDPGM 362

Qy        349 FQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNE 408
              | ||:||| ||||||| ||||||||| | |||||||||||||||||||||||||||| ||
Db        363 FPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNE 422

Qy        409 SCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIF 468
              ||| ||| | ||||||||| | |||  |||||||||||||:||| ||||||||||||||
Db        423 SCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIF 482

Qy        469 LDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMS 528
              ||||||  ||||:||||||| |||||||||||||||||||||||||||||||:|:||
Db        483 LDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMS 542

Qy        529 YLNSS 533
              |||:|
Db        543 YLNAS 547


RESULT 10
US-09-828-825-12
; Sequence 12, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 547
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-12

  Query Match            85.1%;  Score 2387;  DB 10;  Length 547;
  Best Local Similarity   83.7%;  Pred. No. 2.1e-184;
  Matches  456;  Conservative   28;  Mismatches   45;  Indels   16;  Gaps    3;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||||| |||||:|||||:||||||||||:|||||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:||||| |||||:|||||||||:|||:|||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 303
              |||||||| |||||||||||||||||||||||:| |||: |||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGG-------------GGGGS--RNLPTPTPSPGM 348
              :| | |:|:|||||||||:|||| ||||             |||||  ||||  || |||
Db        303 NASISVRAQDRYYSSSWSEWASVPCSGGGGSGGGGSGGGGSGGGGSPWRNLPVATPDPGM 362

Qy        349 FQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNE 408
              | ||:||| ||||||| ||||||||| | |||||||||||||||||||||||||||| ||
Db        363 FPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNE 422
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Qy        409 SCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIF 468
              ||| ||| | ||||||||| | |||  |||||||||||||||:||| ||||||||||||||
Db        423 SCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIF 482

Qy        469 LDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMS 528
              ||||||  ||||:|||||||  ||||||||||||||||||||||||||||||||||:|:||
Db        483 LDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMS 542

Qy        529 YLNSS 533
              |||:|
Db        543 YLNAS 547


RESULT 11
US-09-828-825-2
; Sequence 2, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 527
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-09-828-825-2

  Query Match            84.1%;  Score 2358;  DB 10;  Length 527;
  Best Local Similarity  84.7%;  Pred. No. 4.3e-182;
  Matches  449;  Conservative   28;  Mismatches   47;  Indels    6;  Gaps    2;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| ||||:|||||:||||||||||:|||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKES 123
              ||||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
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Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
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Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVS 363
              :| | |:|:||||||||:|||| ||       |||| || |||| ||:||| ||||||
Db        303 NASISVRAQDRYYSSSWSEWASVPCSPW-----RNLPVATPDPGMFPCLHHSQNLLRAVS 357

Qy        364 NTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGS 423
              | |||||||| | |||||||||||||||||||||||||||| ||||| ||| | |||||
Db        358 NMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGS 417

Qy        424 CLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQA 483
              |||| | |||  ||||||||||||:||| ||||||||||||||||||  ||||:||
Db        418 CLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQA 477

Qy        484 LNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533
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Db        478 LNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 527


RESULT 12
US-09-828-825-4
; Sequence 4, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 526
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-4

  Query Match            84.0%;  Score 2354;  DB 10;  Length 526;
  Best Local Similarity  84.7%;  Pred. No. 9.1e-182;
  Matches  448;  Conservative   28;  Mismatches   47;  Indels    6;  Gaps    2;

Qy          4 QQLVISWFSLVLLASPLMAIWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSA 63
              |||||||||| ||||:|||||:||||||||||:|||||||||| ||||| ||||
Db          4 QQLVISWFSLVFLASPLVAIWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLD 63

Qy         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123
              ||||||||||||||||||||||||||||||:||| ||||:|||||||||||||:|||
Db         64 QSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEP 123

Qy        124 KNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 183
              ||| ||:|||||||||||||||| ||||| |||||||| |||||||||| |||||||| |
Db        124 KNKTFLRCEAKNYSGRFTCWWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGD 183

Qy        184 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 243
              |::| :|:|||||  ||||:|||||||||:|||:||||||||||||||||||||||| |||
Db        184 NKEY-EYSVECQEDSACPAAEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQ 242

Qy        244 LKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHK 303
              |||||||| |||||||||||||||||||:| |||: ||||||:  ||||| |:| |
Db        243 LKPLKNSRQVEVSWEYPDTWSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRK 302

Qy        304 DAKIRVQARDRYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVS 363
              :| | |:|:||||||||:|||| ||       |||| || |||| ||:||| ||||||
Db        303 NASISVRAQDRYYSSSWSEWASVPCSPW-----RNLPVATPDPGMFPCLHHSQNLLRAVS 357

Qy        364 NTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGS 423
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Db        358 NMLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGS 417

Qy        424 CLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQA 483
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Db        418 CLASRKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQA 477

Qy        484 LNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNS 532
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Db        478 LNFNSETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNA 526


RESULT 13
US-09-917-265-59
; Sequence 59, Application US/09917265
; Patent No. US20020052030A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-59

  Query Match             62.9%;  Score 1764;  DB 10;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-134;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYYVELDWHPDAPGEMVVLTCHTPEEDDITW 60
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Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYYVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
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Db         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
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Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
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Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
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RESULT 14
US-09-917-265-108
; Sequence 108, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-108

  Query Match             62.9%;  Score 1764;  DB 10;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-134;
  Matches  329;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYYVELDWHPDAPGEMVVLTCHTPEEDDITW 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MHPQQLVISWFSLVLLASPLMAIWELEKDVYYVELDWHPDAPGEMVVLTCHTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
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Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
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Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
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Db        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329


RESULT 15
US-09-917-265-30
; Sequence 30, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-30

  Query Match             59.1%;  Score 1657;  DB 10;  Length 329;
  Best Local Similarity   93.6%;  Pred. No. 9.3e-126;
  Matches  308;  Conservative   10;  Mismatches   11;  Indels    0;  Gaps    0;

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Db          1 MHPQQLVIAWFSLVLLAPPLMAIWELEKNVYYVELDWHPDAPGEMVVLTCNTPEEDDITW 60

Qy         61 TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQ 120
              || |||||||||||||||| ||||||||||:||| | |||||||||||||||:||
Db         61 TSDQSSEVLGSGKTLTIQVKEFADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQ 120

Qy        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERV 180
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Db        121 KESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFTVKSSRGSSDPQGVTCGAATLSAEKV 180

Qy        181 RVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPT 240
              ||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||
Db        181 RVDNRDYKKYTVECQEGSACPAAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPK 240

Qy        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVV 300
              |||||||||||||||||||||||||||||||| :| |||||||||||| |||||||||
Db        241 NLQLKPLKNSRHVEVSWEYPDTWSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVV 300

Qy        301 CHKDAKIRVQARDRYYSSSWSDWASVSCS 329
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Db        301 CHKDAKIRVQARDRYYSSSWSNWASVSCS 329
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Search completed: July 15, 2003, 11:11:46
Job time : 25.8852 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:54:38 ; Search time 51.3678 Seconds
(without alignments)
1325.559 Million cell updates/sec

Title: US-09-917-265-67
Perfect score: 2693
Sequence: 1 IWELEKDVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNSS 511

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2309.5	85.8	540	21	AAY54921	Interleukin-12 fus
2	2309	85.7	537	23	AAE19820	Human IL-12.2 prot
3	2306.5	85.6	542	23	AAE19819	Human IL-12.3 prot
4	2304	85.6	547	23	AAE19821	Human IL-12.4 prot
5	2275	84.5	527	23	AAE19817	Human IL-12.1 prot
6	2271	84.3	526	23	AAE19818	Human IL-12.0 prot
7	1653	61.4	329	19	AAW41791	Canine IL-12 P40 s
8	1653	61.4	329	20	AAY02342	Canine Interleukin
9	1653	61.4	329	20	AAW84373	Canine interleukin
10	1653	61.4	329	22	AAG66482	Canine protein #3.
11	1644	61.0	329	19	AAW41790	Canine IL-12 P40 s
12	1644	61.0	329	20	AAY02339	Canine Interleukin
13	1644	61.0	329	20	AAW84371	Canine interleukin
14	1644	61.0	329	22	AAG66480	Canine protein #1.
15	1618.5	60.1	308	20	AAW74323	Canine mature CLAF
16	1618.5	60.1	330	20	AAW74322	Canine full length
17	1554	57.7	307	19	AAW76174	Feline FLAFp40 mat
18	1554	57.7	329	19	AAW76173	Feline FLAFp40 pro
19	1484	55.1	329	22	AAE08602	Modified human cyt
20	1451	53.9	327	22	AAE08599	Modified human cyt
21	1429	53.1	327	22	AAE08598	Modified human cyt
22	1421	52.8	327	22	AAE08597	Modified human cyt
23	1419.5	52.7	328	23	AAU75579	Human interleukin
24	1418.5	52.7	306	16	AAR63018	IL-12 p40 subunit.
25	1418.5	52.7	306	19	AAW71244	Human IL-12p40. H
26	1418.5	52.7	306	19	AAW58707	Cytotoxic lymphocy
27	1418.5	52.7	328	13	AAR22769	Natural killer cel
28	1418.5	52.7	328	16	AAR79186	Human interleukin-
29	1418.5	52.7	328	17	AAW07398	Human interleukin-
30	1418.5	52.7	328	18	AAW24235	40 kDa subunit of
31	1418.5	52.7	328	18	AAW36941	40 kDa subunit of
32	1418.5	52.7	328	18	AAW36939	40 kDa subunit of
33	1418.5	52.7	328	19	AAW62992	Human interleukin-
34	1418.5	52.7	328	19	AAW58725	Cytotoxic lymphocy
35	1418.5	52.7	328	19	AAW51311	Human Interleukin-
36	1418.5	52.7	328	19	AAW57482	Human interleukin-
37	1418.5	52.7	328	19	AAW51221	Human interleukin-
38	1418.5	52.7	328	19	AAW44324	Heterodimeric huma
39	1418.5	52.7	328	20	AAY42487	Human interleukin
40	1418.5	52.7	328	21	AAB23796	Human interleukin
41	1418.5	52.7	328	21	AAY54919	Human p40 protein
42	1418.5	52.7	328	21	AAY44181	Human interleukin-
43	1418.5	52.7	328	22	AAE11198	Human interleukin-
44	1418.5	52.7	328	22	AAE08603	Human cytokine p40
45	1418.5	52.7	328	22	AAB67262	IL-12 vaccine adju

ALIGNMENTS

RESULT 1
AAY54921
ID AAY54921 standard; Protein; 540 AA.
XX
AC AAY54921;
XX
DT 14-FEB-2000 (first entry)
XX
DE Interleukin-12 fusion protein, Flexi-12.
XX
KW Interleukin-12; IL-12; fusion protein; IL-12 p35 subunit; B7 protein;
KW IL-12 p40 subunit; gene therapy; tumour; leukaemia; Flexi-12.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN US5994104-A.
XX
PD 30-NOV-1999.
XX
PF 08-NOV-1996; 96US-0751767.
XX
PR 08-NOV-1996; 96US-0751767.
XX
PA (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
XX
PI Anderson RJ, Prentice HG, MacDonald ID;
XX
DR WPI; 2000-038261/03.
DR N-PSDB; AAZ40023.
XX
PT Nucleic acid constructs encoding interleukin-12 fusion proteins useful
PT for treating leukemia and other cancers -

```
XX
PS   Example; Fig 11; 73pp; English.
XX
CC   This sequence is the human interleukin-12 fusion protein sequence,
CC   designated Flexi-12. The invention relates to an isolated nucleic acid
CC   construct (I) comprising a region encoding an interleukin-12 (IL-12)
CC   fusion protein (comprising an IL-12 p35 subunit, an IL-12 p40 subunit and
CC   a linker peptide (joining the subunits)) and a region encoding a B7
CC   protein. (I) may be used to produce IL-12 fusion proteins according to
CC   standard recombinant DNA methodologies. The fusion proteins may be
CC   produced either in vitro in a fermentation culture or in vivo as part of
CC   a gene therapy protocol (in this case (I) is used to transform a patients
CC   cells, which then secrete the functional polypeptide to supplement the
CC   patients own production of IL-12 or to rectify mutations which lead to
CC   the expression of inactive polypeptides). The fusion proteins produced in
CC   this way may be used to treat any disease which responds to IL-12 such as
CC   tumours (both solid and dispersed of the kidney, breast, colon, ovarian
CC   and cervical tumours and melanomas) and in particular, tumours of the
CC   blood such as leukaemia. Alternatively, the polypeptides may be used as
CC   antigens in the production of antibodies to IL-12 and to assay for
CC   agonists and antagonists of its activity. The antibodies and antagonists
CC   may be used to inhibit the activity of IL-12. (I) may also be used
CC   diagnostically as a probe which hybridizes to sequences encoding IL-12
CC   and the antibodies may be used to detect the presence of IL-12
CC   polypeptides in samples. They may be used diagnostically to quantitate
CC   the expression of the polypeptide by patients and hence which subjects
CC   may be in need of restorative therapy.
XX
SQ   Sequence   540 AA;

  Query Match            85.8%;  Score 2309.5;  DB 21;  Length 540;
  Best Local Similarity  84.4%;  Pred. No. 1e-187;
  Matches  438;  Conservative   27;  Mismatches   45;  Indels    9;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| ||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG--------GGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLE 352
              |||| ||||        |||||||||  || |||| ||:||| ||||||| |||||||||
Db        322 WASVPCSGGGGSGGGGSGGGGSRNLPLATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLE 381

Qy        353 LYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMT 412
              | |||||||||||||||||||||||||||| ||||| ||| | ||||||||| | |||
Db        382 FYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMM 441

Qy        413 VLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQK 472
              ||||||||||||||:||| ||||||||||||||||||  ||||:||||||| |||||
Db        442 ALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQK 501

Qy        473 SSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              |||||||||||||||||||||||||||||:|: ||||:|
Db        502 SSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNAS 540


RESULT 2
AAE19820
```

```
ID   AAE19820 standard; Protein; 537 AA.
XX
AC   AAE19820;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human IL-12.2 protein.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12.2; human.
XX
OS   Homo sapiens.
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
DR   N-PSDB; AAD31548.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
PT   operably linked to promoter that directs the expression of DNA molecule
PT   -
XX
PS   Example 1; Fig 9; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is a protein encoded by human IL-12.2
CC   DNA present in pIRES-hB7-1-IL12.2 vector.
XX
SQ   Sequence   537 AA;

  Query Match            85.7%;  Score 2309;  DB 23;  Length 537;
  Best Local Similarity  85.1%;  Pred. No. 1.1e-187;
  Matches  439;  Conservative   27;  Mismatches   44;  Indels    6;  Gaps    3;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| ||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
```

```
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG---GGGGS--RNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYS 355
              |||| ||||   |||||  |||| || |||| ||:||| ||||||| ||||||||| |
Db        322 WASVPCSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYP 381

Qy        356 CTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLC 415
              |||||||||||||||||||||||||||| ||||| ||| | |||||||||| | |||  ||
Db        382 CTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALC 441

Qy        416 LSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSL 475
              |||||||||||:||| |||||||||||||||||||  ||||:||||||| |||||||
Db        442 LSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSL 501

Qy        476 EEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              |||||||||||||||||||||||||||:|:|||||:|
Db        502 EEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 537


RESULT 3
AAE19819
ID   AAE19819 standard; Protein; 542 AA.
XX
AC   AAE19819;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human IL-12.3 protein.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12.3; human.
XX
OS   Homo sapiens.
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
DR   N-PSDB; AAD31547.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
PT   operably linked to promoter that directs the expression of DNA molecule
PT   -
XX
PS   Example 1; Fig 8; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is a protein encoded by human IL-12.3
CC   DNA present in pIRES-hB7-1-IL12.3 vector.
XX
SQ   Sequence   542 AA;

  Query Match             85.6%;  Score 2306.5;  DB 23;  Length 542;
  Best Local Similarity   84.3%;  Pred. No. 1.8e-187;
  Matches  439;  Conservative   27;  Mismatches   44;  Indels   11;  Gaps    3;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||:|||||||||||| |||| |||| |||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| ||||:||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| |||||||||:
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  |||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG--------GGGGS--RNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQT 350
              |||| ||||        |||||  |||| || |||| ||:||| ||||||| |||||||
Db        322 WASVPCSGGGGSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQT 381

Qy        351 LELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASF 410
              || | |||||||||||||||||||||||||||||| ||||| ||| | |||||||| | ||
Db        382 LEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSF 441

Qy        411 MTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVP 470
              |  ||||||||||||||:||| |||||||||||||||||  ||||:||||||| |||
Db        442 MMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVP 501

Qy        471 QKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              |||||||||||||||||||||||||||||:|:|||||:|
Db        502 QKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 542


RESULT 4
AAE19821
ID   AAE19821 standard; Protein; 547 AA.
XX
AC   AAE19821;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human IL-12.4 protein.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12.4; human.
XX
OS   Homo sapiens.
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
DR   N-PSDB; AAD31549.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
```

```
PT   operably linked to promoter that directs the expression of DNA molecule
PT   -
XX
PS   Example 1; Fig 10; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is a protein encoded by human IL-12.4
CC   DNA present in pIRES-hB7-1-IL12.4 vector.
XX
SQ   Sequence   547 AA;

  Query Match            85.6%;  Score 2304;  DB 23;  Length 547;
  Best Local Similarity  83.5%;  Pred. No. 3.1e-187;
  Matches  439;  Conservative   27;  Mismatches   44;  Indels   16;  Gaps    3;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| |||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG----------GGGGS--RNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQ 345
              |||| ||||              |||||  ||||  || |||| ||:||| ||||||| ||
Db        322 WASVPCSGGGGSGGGGSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNLLRAVSNMLQ 381

Qy        346 KARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLAS 405
              ||||||| | |||||||||||||||||||||||||||||| ||||| ||| | |||||||||
Db        382 KARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLAS 441

Qy        406 GKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFN 465
               | |||  |||||||||||||:||| |||||||||||||||||||  ||||:||||||
Db        442 RKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFN 501

Qy        466 SVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              | |||||||||||||||||||||||||||||||:|:|||||:|
Db        502 SETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 547


RESULT 5
AAE19817
ID   AAE19817 standard; Protein; 527 AA.
XX
AC   AAE19817;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human IL-12.1 protein.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12.1; human.
XX
OS   Homo sapiens.
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
DR   N-PSDB; AAD31545.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
PT   operably linked to promoter that directs the expression of DNA molecule
PT   -
XX
PS   Example 1; Fig 6; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is a protein encoded by human IL-12.1
CC   DNA present in pIRES-hB7-1-IL12.1 vector.
XX
SQ   Sequence   527 AA;

  Query Match            84.5%;  Score 2275;  DB 23;  Length 527;
  Best Local Similarity  84.5%;  Pred. No. 8.5e-185;
  Matches  432;  Conservative   27;  Mismatches   46;  Indels    6;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| |||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEE 360
              |||| ||       |||| || |||| ||:||| ||||||| ||||||||| | |||||
Db        322 WASVPCSPW-----RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE 376

Qy        361 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIY 420
              |||||||||||||||||||||| ||||| ||| | ||||||||| | |||  |||||||
Db        377 IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIY 436
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```
Qy        421 EDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDF 480
              |||||||:||| |||||||||||||||||||||  ||||:|||||||  ||||||||||||
Db        437 EDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDF 496

Qy        481 YKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              |||||||||||||||||||:|:|||||:|
Db        497 YKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 527


RESULT 6
AAE19818
ID   AAE19818 standard; Protein; 526 AA.
XX
AC   AAE19818;
XX
DT   18-JUN-2002  (first entry)
XX
DE   Human IL-12.0 protein.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12; human.
XX
OS   Homo sapiens.
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
DR   N-PSDB; AAD31546.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
PT   operably linked to promoter that directs the expression of DNA molecule
PT   -
XX
PS   Example 1; Fig 7; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is a protein encoded by human IL-12.0
CC   DNA present in pIRES-hB7-1-IL12.0 vector.
XX
SQ   Sequence   526 AA;

  Query Match             84.3%;  Score 2271;  DB 23;  Length 526;
  Best Local Similarity   84.5%;  Pred. No. 1.9e-184;
  Matches  431;  Conservative   27;  Mismatches   46;  Indels    6;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||||:|||||||||||| |||||  ||||  |||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| ||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| |||||  |||||||| |||||||||  |||||||| ||:::| :|:|||||  ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||:| |||: ||||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEE 360
              |||| ||       ||||  || |||| ||:||| ||||||| ||||||||| | |||||
Db        322 WASVPCSPW-----RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE 376

Qy        361 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIY 420
              |||||||||||||||||||||||| ||||| ||| | ||||||||| | |||  |||||||
Db        377 IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIY 436

Qy        421 EDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDF 480
              |||||||:||| |||||||||||||||||||||  ||||:|||||||  ||||||||||||
Db        437 EDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDF 496

Qy        481 YKTKIKLCILLHAFRIRAVTINRMMSYLNS 510
              |||||||||||||||||||:|:|||||:
Db        497 YKTKIKLCILLHAFRIRAVTIDRVMSYLNA 526


RESULT 7
AAW41791
ID   AAW41791 standard; peptide; 329 AA.
XX
AC   AAW41791;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant.
XX
OS   Canis sp.
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   N-PSDB; AAV13817.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 2; Pages 10-11; 12pp; Japanese.
XX
CC   The present sequence is a canine interleukin-12 (IL-12) P40
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
```

```
XX
SQ   Sequence   329 AA;

  Query Match             61.4%;  Score 1653;  DB 19;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-132;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 8
AAY02342
ID   AAY02342 standard; Protein; 329 AA.
XX
AC   AAY02342;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Canine Interleukin-12 (IL-12) protein sequence.
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease.
XX
OS   Canis sp.
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   N-PSDB; AAX35625.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 14-15; 16pp; Japanese.
XX
CC   The present sequence represents canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
```

```
XX
SQ   Sequence   329 AA;

  Query Match             61.4%;  Score 1653;  DB 20;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-132;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 9
AAW84373
ID   AAW84373 standard; Protein; 329 AA.
XX
AC   AAW84373;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Canine interleukin 12 protein.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis.
XX
OS   Canis sp.
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03162.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 30-32; 45pp; Japanese.
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XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   329 AA;

  Query Match             61.4%;  Score 1653;  DB 20;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-132;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 10
AAG66482
ID   AAG66482 standard; Protein; 329 AA.
XX
AC   AAG66482;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #3.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Signal_peptide
FT   Protein         23..329
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64388.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian -
XX
PS   Disclosure; Page 17; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence   329 AA;

  Query Match             61.4%;  Score 1653;  DB 22;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-132;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 11
AAW41790
ID   AAW41790 standard; peptide; 329 AA.
XX
AC   AAW41790;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P40 subunit.
XX
KW   Canine; interleukin-12 P40 subunit; IL-12 P40 subunit; antitumour;
KW   antiviral; vaccine adjuvant.
XX
OS   Canis sp.
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
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PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   N-PSDB; AAV13816.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 2; Page 8; 12pp; Japanese.
XX
CC   The present sequence is a canine interleukin-12 (IL-12) P40
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence   329 AA;

  Query Match             61.0%;  Score 1644;  DB 19;  Length 329;
  Best Local Similarity   99.3%;  Pred. No. 2.2e-131;
  Matches  305;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLENSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||| ||
Db        323 WASVPCS 329


RESULT 12
AAY02339
ID   AAY02339 standard; Protein; 329 AA.
XX
AC   AAY02339;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Canine Interleukin-12 (IL-12) protein sequence.
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease.
XX
OS   Canis sp.
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   N-PSDB; AAX35615.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 12; 16pp; Japanese.
XX
CC   The present sequence represents canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence   329 AA;

  Query Match             61.0%;  Score 1644;  DB 20;  Length 329;
  Best Local Similarity   99.3%;  Pred. No. 2.2e-131;
  Matches  305;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLENSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||| ||
Db        323 WASVPCS 329


RESULT 13
AAW84371
ID   AAW84371 standard; Protein; 329 AA.
XX
AC   AAW84371;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Canine interleukin 12 protein.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis.
XX
OS   Canis sp.
XX
PN   WO9851327-A1.
```

```
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   N-PSDB; AAX03152.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 23-25; 45pp; Japanese.
XX
CC   The present sequence represents a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence   329 AA;

  Query Match             61.0%;  Score 1644;  DB 20;  Length 329;
  Best Local Similarity   99.3%;  Pred. No. 2.2e-131;
  Matches  305;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLENSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||| ||
Db        323 WASVPCS 329


RESULT 14
AAG66480
ID   AAG66480 standard; Protein; 329 AA.
XX
AC   AAG66480;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine protein #1.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1..22
FT                   /label= Signal_peptide
FT   Protein         23..329
FT                   /label= Mature_protein
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   N-PSDB; AAI64378.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Disclosure; Page 14; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence   329 AA;

  Query Match             61.0%;  Score 1644;  DB 22;  Length 329;
  Best Local Similarity   99.3%;  Pred. No. 2.2e-131;
  Matches  305;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLENSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||| ||
Db        323 WASVPCS 329


RESULT 15
AAW74323
ID   AAW74323 standard; Protein; 308 AA.
XX
AC   AAW74323;
```

XX
DT 07-MAY-1999 (first entry)
XX
DE Canine mature CLAF p40 subunit.
XX
KW CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis.
XX
OS Canis sp.
XX
PN WO9855511-A1.
XX
PD 10-DEC-1998.
XX
PF 26-MAY-1998; 98WO-JP02295.
XX
PR 03-JUN-1997; 97JP-0161936.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Eda Y, Imamura T, Maeda H, Tokiyoshi S;
XX
DR WPI; 1999-070260/06.
DR N-PSDB; AAX18177.
XX
PT Canine cytokine protein which activates canine cytotoxic T
PT lymphocytes - is useful for treatment of viral and autoimmune
PT diseases in dogs
XX
PS Claim 1; Page 24-26; 51pp; Japanese.
XX
CC This sequence is the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs.
XX
SQ Sequence 308 AA;

Query Match 60.1%; Score 1618.5; DB 20; Length 308;
Best Local Similarity 98.4%; Pred. No. 3e-129;
Matches 303; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

```
Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60

Qy         61 GDAGQYTCHKGGKVLSRSLLL-IHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFT 119
              |||||||||||||||||||    ||:|||||||||||||||||||||||||||||||||||
Db         61 GDAGQYTCHKGGKVLSRSLLFDSTKKKDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFT 120

Qy        120 CWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP 179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP 180

Qy        180 SAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPD 239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 SAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPD 240

Qy        240 TWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 299
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 300

Qy        300 DWASVSCS 307
              ||||||||
Db        301 DWASVSCS 308
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Search completed: July 15, 2003, 11:02:56
Job time : 52.3678 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:49 ; Search time 22.3973 Seconds
(without alignments)
2193.328 Million cell updates/sec

Title: US-09-917-265-67
Perfect score: 2693
Sequence: 1 IWELEKDVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNSS 511

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1418.5	52.7	328	2	A38957	interleukin 12B pr
2	1058.5	39.3	335	2	I72789	interleukin 12 p40
3	873	32.4	253	2	B38957	interleukin 12A pr
4	549	20.4	215	2	I56135	interleukin 12 p35
5	211.5	7.9	468	1	A41242	interleukin-6 rece
6	194	7.2	440	2	JL0144	interleukin-6 rece
7	190	7.1	460	2	JL0145	interleukin-6 rece
8	178	6.6	362	2	S60614	growth promoting a
9	177	6.6	372	2	I58141	ciliary neurotroph
10	170	6.3	372	1	UHHUCN	ciliary neurotroph
11	159.5	5.9	422	2	I37891	interleukin-11 rec
12	157	5.8	432	2	I48343	interleukin-11 rec
13	143	5.3	812	2	H96544	hypothetical prote
14	123.5	4.6	739	2	JS0675	vascular cell adhe
15	122.5	4.5	1277	2	T30532	neural cell adhesi
16	122	4.5	462	1	A37986	interleukin-6 rece
17	120	4.5	1197	2	T30581	neural cell adhesi
18	115.5	4.3	977	2	I45877	protein-tyrosine k
19	114	4.2	831	2	JQ1655	prolactin receptor
20	112.5	4.2	1323	2	PN0568	connectin 3B - chi
21	111.5	4.1	310	2	A29884	prolactin receptor
22	111.5	4.1	412	2	A41070	prolactin receptor
23	111.5	4.1	610	2	A34631	lactogen receptor
24	111.5	4.1	610	2	A36116	prolactin receptor
25	111	4.1	279	2	B32985	somatotropin-bindi
26	111	4.1	638	2	A33505	somatotropin recep
27	111	4.1	1323	2	E88257	protein let-23 [im
28	111	4.1	1374	2	S70712	protein-tyrosine k
29	111	4.1	2670	2	A46719	inositol 1,4,5-tri
30	110.5	4.1	718	2	T26646	hypothetical prote
31	109.5	4.1	1181	2	T19736	hypothetical prote
32	108	4.0	581	2	I45971	prolactin receptor
33	107.5	4.0	615	2	T20187	hypothetical prote
34	107.5	4.0	635	2	A45266	MPL-P protein prec
35	107.5	4.0	638	2	S12136	somatotropin recep
36	106	3.9	288	2	B59405	prolactin receptor
37	106	3.9	376	2	A59405	prolactin receptor
38	106	3.9	622	2	A40144	prolactin receptor
39	106	3.9	739	2	JN0581	vascular cell adhe
40	106	3.9	978	1	A49814	protein-tyrosine k
41	105.5	3.9	1232	2	T43027	neural cell adhesi
42	104.5	3.9	638	2	B28176	somatotropin recep
43	104.5	3.9	677	2	S33608	somatotropin-bindi
44	104	3.9	1484	2	T42632	breast cancer tumo
45	103.5	3.8	468	2	A45268	interleukin-9 rece

ALIGNMENTS

RESULT 1
A38957
interleukin 12B precursor [validated] - human
N;Alternate names: cytotoxic lymphocyte maturation factor 40K chain; natural killer c
C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Nov-2000
C;Accession: A38957; B39359; S21688; B36055
R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.
i, G.; Perussia, B.
J. Immunol. 146, 3074-3081, 1991
A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric
A;Reference number: A38957; MUID:91201875; PMID:1673147
A;Accession: A38957
A;Molecule type: mRNA
A;Residues: 1-328 <WOL>
A;Cross-references: GB:M65290
R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nab
Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
A;Title: Coexpression of two distinct genes is required to generate secreted bioactiv
A;Reference number: A39359; MUID:91239523; PMID:1674604
A;Accession: B39359
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-328 <GUB>
A;Cross-references: GB:M65272; GB:M38444; NID:g180625; PIDN:AAA35695.1; PID:g180626
R;Podlaski, F.J.; Nanduri, V.B.; Hulmes, J.D.; Pan, Y.C.E.; Levin, W.; Danho, W.; Chi
Arch. Biochem. Biophys. 294, 230-237, 1992
A;Title: Molecular characterization of interleukin 12.
A;Reference number: S21688; MUID:92198015; PMID:1347984
A;Accession: S21688
A;Molecule type: protein
A;Residues: 23-28;46-59;74-80,'X',94-130;161-169,'X',171-180;213-235;240-250;289-299,
A;Experimental source: lymphoblastoid cell line NC-37
R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A;Title: Purification to homogeneity and partial characterization of cytotoxic lympho
A;Reference number: A36055; MUID:90370873; PMID:2204066
A;Accession: B36055
A;Molecule type: protein
A;Residues: 23-45 <STE>
A;Experimental source: lymphoblastoid cell line NC-37
C;Genetics:
A;Gene: GDB:IL12B; NKSF2
A;Cross-references: GDB:127870; OMIM:161561
A;Map position: 5q31.1-5q33.1
C;Keywords: cytokine; glycoprotein; heparin binding; heterodimer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-328/Product: interleukin 12B #status predicted <MAT>
F;27-30/Region: heparin binding #status predicted
F;125/Binding site: carbohydrate (Asn) (covalent) #status absent
F;135,303/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;222/Binding site: carbohydrate (Asn) (covalent) #status experimental

```
F;319/Modified site: 2'-mannosyl-tryptophan (Trp) (partial) #status experimental

  Query Match            52.7%;  Score 1418.5;  DB 2;  Length 328;
  Best Local Similarity  85.0%;  Pred. No. 8.9e-102;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| |||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:|||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 2
I72789
interleukin 12 p40 subunit - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C;Accession: I72789
R;Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K.;
J. Immunol. 148, 3433-3440, 1992
A;Title: Cloning and Expression of Murine IL-12.
A;Reference number: I56135; MUID:92268481; PMID:1350290
A;Accession: I72789
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-335 <RES>
A;Cross-references: GB:M86671; NID:g293663; PIDN:AAA39296.1; PID:g293664

  Query Match            39.3%;  Score 1058.5;  DB 2;  Length 335;
  Best Local Similarity  65.0%;  Pred. No. 5.5e-74;
  Matches  204;  Conservative   35;  Mismatches   62;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| |||||||||| |   |:||||||| ||||
Db         23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               ||||||||||: || | ||:||||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||   : ||||::|||    | : ||||  :||||:| :| |||:||:| |||   ||:
Db        140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:||||: ::|  : |||||::||||||||||| |||:|||||: ||||||||:
Db        200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |  : |        |    |:||| :| | |   : |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
              ||:|| | || | |
Db        318 YYNSSCSKWACVPC 331


RESULT 3
B38957
interleukin 12A precursor [validated] - human
N;Alternate names: cytotoxic lymphocyte maturation factor 35K chain; natural killer c
C;Species: Homo sapiens (man)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 01-Dec-2000
C;Accession: B38957; A39359; A36055
R;Wolf, S.F.; Temple, P.A.; Kobayashi, M.; Young, D.; Dicig, M.; Lowe, L.; Dzialo, R.
i, G.; Perussia, B.
J. Immunol. 146, 3074-3081, 1991
A;Title: Cloning of cDNA for natural killer cell stimulatory factor, a heterodimeric
A;Reference number: A38957; MUID:91201875; PMID:1673147
A;Accession: B38957
A;Molecule type: mRNA
A;Residues: 1-253 <WOL>
A;Cross-references: GB:M65290
A;Note: it is uncertain whether Met-1 or Met-35 is the initiator
R;Gubler, U.; Chua, A.O.; Schoenhaut, D.S.; Dwyer, C.M.; McComas, W.; Motyka, R.; Nab
Proc. Natl. Acad. Sci. U.S.A. 88, 4143-4147, 1991
A;Title: Coexpression of two distinct genes is required to generate secreted bioactiv
A;Reference number: A39359; MUID:91239523; PMID:1674604
A;Accession: A39359
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 35-246,'T',248-253 <GUB>
A;Cross-references: GB:M65271; GB:M38443; NID:g180623; PIDN:AAA35694.1; PID:g180624
R;Stern, A.S.; Podlaski, F.J.; Hulmes, J.D.; Pan, Y.C.E.; Quinn, P.M.; Wolitzky, A.G.
Proc. Natl. Acad. Sci. U.S.A. 87, 6808-6812, 1990
A;Title: Purification to homogeneity and partial characterization of cytotoxic lympho
A;Reference number: A36055; MUID:90370873; PMID:2204066
A;Accession: A36055
A;Status: preliminary
A;Molecule type: protein
A;Residues: 'X',58-70,'X',72-82 <STE>
C;Genetics:
A;Gene: GDB:IL12A; NKSF1
A;Cross-references: GDB:127869; OMIM:161560
A;Map position: 3p12-3q13.2
C;Keywords: cytokine; glycoprotein; heterodimer
F;57-253/Product: interleukin 12A #status predicted <MAT>
F;127,141,251/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match            32.4%;  Score 873;  DB 2;  Length 253;
  Best Local Similarity  86.4%;  Pred. No. 7.6e-60;
  Matches  171;  Conservative    7;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        314 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 373
              :|||  || |||| ||:||| |||||||| |||||||| | ||||||||||||||||||
Db         56 ARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTST 115

Qy        374 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 433
              |||||||||| ||||| ||| | |||||||| | |||  |||||||||||||:||| |
Db        116 VEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM 175

Qy        434 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 493
              |||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||||
Db        176 NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHA 235

Qy        494 FRIRAVTINRMMSYLNSS 511
              ||||||||:|:||||:|
Db        236 FRIRAVTIDRVMSYLNAS 253


RESULT 4
I56135
interleukin 12 p35 subunit - mouse
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
C;Accession: I56135
R;Schoenhaut, D.S.; Chua, A.O.; Wolitzky, A.G.; Quinn, P.M.; Dwyer, C.M.; Gately, M.K
```

J. Immunol. 148, 3433-3440, 1992
A;Title: Cloning and Expression of Murine IL-12.
A;Reference number: I56135; MUID:92268481; PMID:1350290
A;Accession: I56135
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-215 <RES>
A;Cross-references: GB:M86672; NID:g198336; PIDN:AAA39292.1; PID:g198337

Query Match 20.4%; Score 549; DB 2; Length 215;
Best Local Similarity 57.4%; Pred. No. 6e-35;
Matches 109; Conservative 29; Mismatches 52; Indels 0; Gaps 0;

```
Qy        322 PSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLE 381
Db         26 PVSGPARCLSQSRNLLKTTDDMVKTAREKLKHYSCTAEDIDHEDITRDQTSTLKTCLPLE 85

Qy        382 LTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDP 441
Db         86 LHKNESCLATRETSSTTRGSCLPPQKTSLMMTLCLGSIYEDLKMYQTEFQAINAALQNHN 145

Qy        442 KRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTI 501
Db        146 HQQIILDKGMLVAIDELMQSLNHNGETLRQKPPVGEADPYRVKMKLCILLHAFSTRVVTI 205

Qy        502 NRMMSYLNSS 511
Db        206 NRVMGYLSSA 215
```

RESULT 5
A41242
interleukin-6 receptor precursor - human
N;Contains: interleukin-6 receptor, soluble form
C;Species: Homo sapiens (man)
C;Date: 27-Mar-1992 #sequence_revision 02-Dec-1994 #text_change 21-Jul-2000
C;Accession: A41242; JU0080; S17468; A61459; S14621
R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.
Science 241, 825-828, 1988
A;Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor.
A;Reference number: A41242; MUID:88305347; PMID:3136546
A;Accession: A41242
A;Molecule type: mRNA
A;Residues: 1-468 <YAM>
A;Cross-references: GB:M20566; NID:g33845; PIDN:CAA31312.1; PID:g33846
R;Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Kawanishi, Y.; Seed, B.; Taniguchi, T.
Proc. Jpn. Acad. 64, 209-211, 1988
A;Title: Molecular structure of interleukin 6 receptor.
A;Reference number: JU0080
A;Accession: JU0080
A;Molecule type: mRNA
A;Residues: 1-468 <YA2>
R;Schooltink, H.; Stoyan, T.; Lenz, D.; Schmitz, H.; Hirano, T.; Kishimoto, T.; Heinrich
Biochem. J. 277, 659-664, 1991
A;Title: Structural and functional studies on the human hepatic interleukin-6 receptor.
A;Reference number: S17468; MUID:91336983; PMID:1872801
A;Accession: S17468
A;Molecule type: mRNA
A;Residues: 1-468 <SCH>
A;Cross-references: EMBL:X58298; NID:g32580; PIDN:CAA41231.1; PID:g32581
A;Experimental source: hepatoma cell line HepG2
R;Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.
J. Exp. Med. 170, 1409-1414, 1989
A;Title: Soluble cytokine receptors are present in normal human urine.
A;Reference number: A61459; MUID:90010793; PMID:2529343
A;Accession: A61459
A;Molecule type: protein
A;Residues: 20-49 <NOV>
C;Comment: Through this receptor, interleukin-6 induces proliferation, activation, and d
C;Comment: This growth factor receptor does not have a tyrosine kinase domain.
C;Genetics:
A;Gene: GDB:IL6R
A;Cross-references: GDB:127966; OMIM:147880
A;Map position: 1q21-1q21
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-468/Product: interleukin-6 receptor #status predicted <MAT>
F;20-363/Domain: extracellular #status predicted <EXT>
F;40-98/Domain: immunoglobulin homology <IMM2>
F;121-309/Domain: cytokine receptor homology <CRS>
F;364-386/Domain: transmembrane #status predicted <TMM>
F;387-468/Domain: intracellular #status predicted <INT>
F;47-96/Disulfide bonds: #status predicted
F;55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.9%; Score 211.5; DB 1; Length 468;
Best Local Similarity 21.1%; Pred. No. 2e-08;
Matches 92; Conservative 79; Mismatches 157; Indels 109; Gaps 19;

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Qy         20 PGEMVVLTCHTPEEDD---ITW------TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHK 70
Db         39 PGDSVTLTCPGVEPEDNATVHWVLRKPAAGSHPSRWAGMGRRLLLRSVQLHDSGNYSCYR 98

Qy         71 GGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW-------L 123
Db         99 AGRPAGTVHLLV----------DVPPEEPQ------LSCFRKSPLSNVVCEWGPRSTPSL 142

Qy        124 T--AISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS---AC 178
Db        143 TTKAVLLVRKFQNSPAEDFQEP----C-----------------QYSQESQKFSCQLAV 180

Qy        179 PSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEY 237
Db        181 PEGDSSFYIVSMCVASSVGSKFSKTQTFQGCGILQPDPPANITVTAVARNPRWLSVTWQD 240

Qy        238 PDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDA------KIRVQARD 291
Db        241 PHSWNS--SFYRLRFELRYRAERSKTFTTWMVKDLQHHCVI--HDAWSGLRHVVQLRAQE 296

Qy        292 RYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTL 351
Db        297 EFGQGEWSEW-SPEAMGTPWTESRSPPAE----------NEVSTPMQAL---------- 334

Qy        352 ELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFM 411
Db        335 -----TTNKDDDNILFRDSANATS--LPVQ--------DSSSVPLPT--FLVAGGSLAFG 377

Qy        412 TVLCLSSIYEDLKMYQM 428
Db        378 TLLCIAIVLRFKKTWKL 394
```

RESULT 6
JL0144
interleukin-6 receptor precursor (clone lambda P1) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C;Accession: JL0144
R;Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto,
J. Exp. Med. 171, 2001-2009, 1990
A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle
A;Reference number: JL0144; MUID:90278354; PMID:2112585
A;Accession: JL0144
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-440 <SUG>
A;Cross-references: GB:X51976; NID:g53548; PIDN:CAA36238.1; PID:g53549
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-440/Product: interleukin-6 receptor #status predicted <MAT>
F;40-94/Domain: immunoglobulin homology <IMM>
F;117-306/Domain: cytokine receptor homology <CRS>
F;358-385/Domain: transmembrane #status predicted <TRA>

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  Query Match             7.2%;  Score 194;  DB 2;  Length 440;
  Best Local Similarity   20.7%;  Pred. No. 4e-07;
  Matches   94;  Conservative   70;  Mismatches  165;  Indels  126;  Gaps   20;

Qy         20 PGEMVVLTCHTPE-EDDIT----WTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKV 74
              ||  | | |   |   ::|    :: :|: |   :| || ::  :  | | | |     :
Db         39 PGATVTLICPGKEAAGNVTIHWVYSGSQNREWTTTGNTLVLRDVQLSDTGDYLCSLNDHL 98

Qy         75 LSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSV 134
              :   ||:          |:  |: :     | |  ||       | |
Db         99 VGTVPLLV----------DVPPEEPK------LSCFRKNPLVNAICEW------------ 130

Qy        135 KSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVV-DA 193
                | | |   |     | |:::   |     : | ||       |   |  :|::  |
Db        131 ---RPSSTPSPTT--KAVLFAKKINTTN-GKSDFQVPCQYSQQLKSF--SCQVEILEGDK 182

Qy        194 IHKL----------KYENYTSSFFIRDIIKPDPPTNLQLKPLK-NSRHVEVSWEYPDTWS 242
              :: :            ::  :|    :::|||| || :  :    | ::|||::|:||
Db        183 VYHIVSLCVANSVGSKSSHNEAFHSLKMVQPDPPANLVVSAIPGRPRWLKVSWQHPETWD 242

Qy        243 TPHSYFSLTFCIQAQGKNNREKKDRL-------CVDKTSAKVVCHKDAKIRVQARDRYYS 295
              ||: | | :: :   ::|    |       ||   : : | |    ::|: ::
Db        243 P--SYYLLQFQLRYRPVWSKEFTVLLLPVAQYQCVIHDALRGVKH---VVQVRGKEELDL 297

Qy        296 SSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYS 355
              ||:|:            | | :| : :     |   : | | :
Db        298 GQWSEWS--------------PEVTGTPWIAE---PRTTPAGILWNPTQVS-------- 331

Qy        356 CTSEEIDHEDITKDKTSTVEACLPLELTMNES----------------------CLASR 392
              :  :|||  :  |       |:: : : |                        |   |
Db        332 -VEDSANHEDQYESSTEATSVLAPVQESSSMSLPTFLVAGGSLAFGLLLCVFIILCWEPR 390

Qy        393 EISLITNG--SCLASGK---------ASFMTVLCL 416
                | :|  ||: |||          | : ||||
Db        391 PHSPLQDGADSCVLSGKQIICACAEGGSPLHVLCL 425


RESULT 7
JL0145
interleukin-6 receptor precursor (clone lambda 301) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C;Accession: JL0145; S14543
R;Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto, T.
J. Exp. Med. 171, 2001-2009, 1990
A;Title: Functional murine interleukin 6 receptor with the intracisternal a particle gen
A;Reference number: JL0144; MUID:90278354; PMID:2112585
A;Accession: JL0145
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-460 <SUG>
A;Cross-references: GB:X51975; NID:g49725; PIDN:CAA36237.1; PID:g49726
A;Experimental source: clone lambda 301
R;Fiorillo, M.T.; Ciliberto, G.; Dente, L.
submitted to the EMBL Data Library, July 1990
A;Description: Cloning and expression of murine IL-6 receptor.
A;Reference number: S14543
A;Accession: S14543
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373,'R',375-460 <FIO>
A;Cross-references: EMBL:X53802; NID:g52692; PIDN:CAA37810.1; PID:g52693
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C;Keywords: cytokine receptor; transmembrane protein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-460/Product: interleukin-6 receptor #status predicted <MAT>
F;40-94/Domain: immunoglobulin homology <IMM>
F;117-306/Domain: cytokine receptor homology <CRS>
F;358-385/Domain: transmembrane #status predicted <TRA>

  Query Match             7.1%;  Score 190;  DB 2;  Length 460;
  Best Local Similarity   20.9%;  Pred. No. 8.7e-07;
  Matches   88;  Conservative   69;  Mismatches  162;  Indels  102;  Gaps   19;

Qy         20 PGEMVVLTCHTPE-EDDIT----WTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKV 74
              ||  | | |   |   ::|    :: :|: |   :| || ::  :  | | | |     :
Db         39 PGATVTLICPGKEAAGNVTIHWVYSGSQNREWTTTGNTLVLRDVQLSDTGDYLCSLNDHL 98

Qy         75 LSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSV 134
              :   ||:          |:  |: :     | |  ||       | |
Db         99 VGTVPLLV----------DVPPEEPK------LSCFRKNPLVNAICEW------------ 130

Qy        135 KSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVV-DA 193
                | | |   |     | |:::   |     : | ||       |   |  :|::  |
Db        131 ---RPSSTPSPTT--KAVLFAKKINTTN-GKSDFQVPCQYSQQLKSF--SCQVEILEGDK 182

Qy        194 IHKL----------KYENYTSSFFIRDIIKPDPPTNLQLKPLK-NSRHVEVSWEYPDTWS 242
              :: :            ::  :|    :::|||| || :  :    | ::|||::|:||
Db        183 VYHIVSLCVANSVGSKSSHNEAFHSLKMVQPDPPANLVVSAIPGRPRWLKVSWQHPETWD 242

Qy        243 TPHSYFSLTFCIQAQGKNNREKKDRL-------CVDKTSAKVVCHKDAKIRVQARDRYYS 295
              ||: | | :: :   ::|    |       ||   : : | |    ::|: ::
Db        243 P--SYYLLQFQLRYRPVWSKEFTVLLLPVAQYQCVIHDALRGVKH---VVQVRGKEELDL 297

Qy        296 SSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYS 355
              ||:|:            | | :| : :     |   : | | :
Db        298 GQWSEWS--------------PEVTGTPWIAE---PRTTPAGILWNPTQVS-------- 331

Qy        356 CTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLC 415
              :  :|||  :  |       |::         |  :|| |    :| |  :|  :||
Db        332 -VEDSANHEDQYESSTEATSVLAPVQ--------ESSSMSLPT--FLVAGGSLAFGLLLC 380

Qy        416 L 416
              :
Db        381 V 381


RESULT 8
S60614
growth promoting activity receptor alpha precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
C;Accession: S60614
R;Heller, S.; Finn, T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pueschel, A.W.; Rohrer,
Development 121, 2681-2693, 1995
A;Title: Analysis of function and expression of the chick GPA receptor (GPARalpha) su
A;Reference number: S60614; MUID:95401882; PMID:7671828
A;Accession: S60614
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-362 <HEL>
A;Cross-references: EMBL:248168; NID:g971417; PIDN:CAA88184.1; PID:g3063774
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: growth factor receptor
F;2-89/Domain: immunoglobulin homology <IMM>
F;114-294/Domain: cytokine receptor homology <CRS>

  Query Match             6.6%;  Score 178;  DB 2;  Length 362;
  Best Local Similarity   23.9%;  Pred. No. 5.2e-06;
  Matches   73;  Conservative   48;  Mismatches  112;  Indels   72;  Gaps   14;

Qy         21 GEMVVLTCHTPEED-DITWTSAQSSEVLGS---GKTLTIQVKEFGDAGQYTCHKGGKVLS 76
              |  | : | : : |  :||| |  :::  |   |  | :: :   :|||:|::|
Db         37 GADVTMKCGSMDWDAAVTWT-ANGTDIDDSHLNGSYLILKNVDLTQSGQYSCYEGSS--- 92

Qy         77 RSLLLIHKKEDGIWSTDILKEQKESK-----NKIFLKCEAKNYSGRFTCWWLTAISTDLK 131
                          |   || |   :     :  | | : ||   | | |     | :
Db         93 ------------WH---LKYQTYLRVGVPPKEPVLMCRSNNYPKGFYCSWHLPSPTYIP 136

Qy        132 FSVKSSRGFSDPQGVTCGAVTLSAER-VRVDNRDYKKYTVECQEGSACPSAEESLPIEVV 190
              |   |         |  |   :  |: :   || : :|                ::  :|
Db        137 NSFNIS--------VIHGTREMVCEKDIFPKNRCHIRYL----------QLFSTVKYKVT 178

Qy        191 VDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNS-RHVEVSWEYPDTWSTPHSYFS 249
              :   : |   : | :|    |:|||||  ::  ||: |: | :||||: | :|  | | |
Db        179 LTVTNALGKNSTTLTFDEFAIVKPDPPESVVAKPVPNNPRRLEVSWQNPSSWPDPES-FP 237
```

```
Qy        250 LTFCIQAQGKNNREKKDRLCVDK-----------TSAKVVCHKDAKIRVQARDRYYSSS 297
Db        238 LKFFLRYR---------PLILDQWQHVELSDGTSHTITDAYAGKEYIIQVAAKDNDI-GT 287

Qy        298 WSDWA 302
Db        288 WSDWS 292
```

RESULT 9
I58141
ciliary neurotrophic factor receptor alpha chain - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C;Accession: I58141; A47387
R;Ip, N.Y.; McClain, J.; Barrezueta, N.X.; Aldrich, T.H.; Pan, L.; Li, Y.; Wiegand, S.J.
Neuron 10, 89-102, 1993
A;Title: The alpha component of the CNTF receptor is required for signaling and defines
A;Reference number: I58141; MUID:93152175; PMID:8381290
A;Accession: I58141
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-372 <IPN>
A;Cross-references: GB:S54212; NID:g265055; PIDN:AAB25290.1; PID:g265056
R;Clatterbuck, R.E.; Price, D.L.; Koliatsos, V.E.
Proc. Natl. Acad. Sci. U.S.A. 90, 2222-2226, 1993
A;Title: Ciliary neurotrophic factor prevents retrograde neuronal death in the adult cen
A;Reference number: A47387; MUID:93211934; PMID:8460125
A;Accession: A47387
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 185-260,'D',262-277 <CLA>
A;Cross-references: GB:S57711; NID:g299331; PIDN:AAB25918.1; PID:g299332
A;Experimental source: Sprague-Dawley, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:128471, NCBIP:128472)
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
C;Keywords: growth factor receptor
F;39-91/Domain: immunoglobulin homology <IMM>
F;116-296/Domain: cytokine receptor homology <CRS>

  Query Match 6.6%; Score 177; DB 2; Length 372;
  Best Local Similarity 23.2%; Pred. No. 6.5e-06;
  Matches 75; Conservative 48; Mismatches 136; Indels 64; Gaps 13;

```
Qy         21 GEMVVLTCHTPEED-DITW--TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSR 77
Db         39 GTDVTLPCGTASWDAAVTWRVNGTDLAPDLLNGSQLILRSLELGHSGLYACFHRDSWHLR 98

Qy         78 SLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL--KFSVK 135
Db         99 HQVLLHV---GL-----------PPREPVLSCRSNTYPKGFYCSWHLSAPTYIPNTFNVT 144

Qy        136 SSRGFSDPQGVTCGAVTLSAER-VRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAI 194
Db        145 ----------VLHGSKMMVCEKDPALKNRCHIRYM----------HLFSTIKYKVSISVS 184

Qy        195 HKLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEYPDTWSTPHSYFSLTFC 253
Db        185 NALGHNTTAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPES-FPLKFF 243

Qy        254 IQAQGKNNREKKDRLCVDK-----------TSAKVVCHKDAKIRVQARDRYYSSSWSDW 301
Db        244 LRYR---------PLILDQWQHVELSNGTAHTITDAYAGKEYIIQVAAKDNEI-GTWSDW 293

Qy        302 ASVSCSGGGGGGSRNLPTPTPSP 324
Db        294 SVAAHATPWTEEPRHLTTEAQAP 316
```

RESULT 10
UHHUCN
ciliary neurotrophic factor receptor alpha precursor - human
N;Alternate names: CNTF receptor
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 22-Jun-1999
C;Accession: A40854; A56526
R;Davis, S.; Aldrich, T.H.; Valenzuela, D.M.; Wong, V.; Furth, M.E.; Squinto, S.P.; Y
Science 253, 59-63, 1991
A;Title: The receptor for ciliary neurotrophic factor.
A;Reference number: A40854; MUID:91289158; PMID:1648265
A;Accession: A40854
A;Molecule type: mRNA
A;Residues: 1-372 <DAV>
A;Cross-references: GB:M73238
R;Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Brannan, C.I.; McClai
Genomics 25, 157-163, 1995
A;Title: Genomic organization and chromosomal localization of the human and mouse gen
A;Reference number: A56526; MUID:95293367; PMID:7774913
A;Accession: A56526
A;Molecule type: DNA
A;Residues: 1-346,'S',348-372 <VAL>
A;Cross-references: GB:L38025; NID:g608654; PIDN:AAA91337.1; PID:g608656
C;Comment: The CNTF receptor is attached to the membrane by a glycosylphosphatidylino
C;Comment: The CNTF receptor sequence appears to contain several PEST regions.
C;Genetics:
A;Gene: GDB:CNTFR
A;Cross-references: GDB:134652; OMIM:118946
A;Map position: 9p13-9p13
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: glycoprotein; growth factor receptor; membrane protein; phosphatidylinosi
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-372/Product: ciliary neurotrophic factor receptor #status predicted <MAT>
F;39-91/Domain: immunoglobulin homology <IMM>
F;116-296/Domain: cytokine receptor homology <CRS>
F;46-89/Disulfide bonds: #status predicted
F;60,70,142,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match 6.3%; Score 170; DB 1; Length 372;
  Best Local Similarity 23.0%; Pred. No. 2.2e-05;
  Matches 69; Conservative 42; Mismatches 127; Indels 62; Gaps 12;

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Qy         21 GEMVVLTCHTPEED-DITW--TSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSR 77
Db         39 GSDVTLPCGTANWDAAVTWRVNGTDLAPDLLNGSQLVLHGLELGHSGLYACFHRDSWHLR 98

Qy         78 SLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL--KFSVK 135
Db         99 HQVLLHV---GL-----------PPREPVLSCRSNTYPKGFYCSWHLPTPTYIPNTFNVT 144

Qy        136 SSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIEVVVDAIH 195
Db        145 VLHG---------SKIMVCEKDPALKNRCHIRYM----------HLFSTIKYKVSISVSN 185

Qy        196 KLKYENYTSSFFIRDIIKPDPPTNLQLKPL-KNSRHVEVSWEYPDTWSTPHSYFSLTFCI 254
Db        186 ALGHNATAITFDEFTIVKPDPPENVVARPVPSNPRRLEVTWQTPSTWPDPES-FPLKFFL 244

Qy        255 QAQGKNNREKKDRLCVDK-----------TSAKVVCHKDAKIRVQARDRYYSSSWSDWA 302
Db        245 RYR---------PLILDQWQHVELSDGTAHTITDAYAGKEYIIQVAAKDNEI-GTWSDWS 294
```

RESULT 11
I37891
interleukin-11 receptor alpha chain - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Dec-1999
C;Accession: I37891; G01970; G01971
R;Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minviell
Blood 86, 2534-2540, 1995
A;Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic
A;Reference number: I37891; MUID:95399754; PMID:7670098
A;Accession: I37891
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA

```
A;Residues: 1-422 <RES>
A;Cross-references: EMBL:Z38102; NID:g995653; PIDN:CAA86224.1; PID:g995654
R;Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A;Reference number: G08959
A;Accession: G01970
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-422 <VAN>
A;Cross-references: EMBL:U32323; NID:g975334; PIDN:AAB36491.1; PID:g975335
R;Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A;Reference number: G08961
A;Accession: G01971
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-422 <VA2>
A;Cross-references: EMBL:U32324; NID:g975336; PIDN:AAB36492.1; PID:g975337
C;Genetics:
A;Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 390/2; 418/1
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
F;120-310/Domain: cytokine receptor homology <CRS>

  Query Match             5.9%;  Score 159.5;  DB 2;  Length 422;
  Best Local Similarity   20.1%;  Pred. No. 0.00017;
  Matches   76;  Conservative   54;  Mismatches  174;  Indels   75;  Gaps   15;

Qy         15 WHPDA-----PGEMVVLTC-HTPEEDDITWTSAQSSEVL-----GSGKTLTIQVKEFGDA 63
              | |        ||  | | |      | ::|     ::|     | |  | :   :  |
Db         30 WGPPGVQYGQPGRSVKLCCPGVTAGDPVSWFRDGEPKLLQGPDSGLGHELVLAQADSTDE 89

Qy         64 GQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW- 122
              | | |               :  ||     :  :       :  : |:| :|   |:| |
Db         90 GTYIC---------------QTLDGALGGTVTLQLGYPPARPVVSCQAADYE-NFSCTWS 133

Qy        123 -----------LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDY-KKYTV 170
                        ||: .        | |         |    | | |  |   ::  :| :
Db        134 PSQISGLPTRYLTSYRKKTVLGADSQRRSPSTGPWPCPQDPLGAARCVVHGAEFWSQYRI 193

Qy        171 ECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKN-SR 229
                 | :   ::   | :                    :: |::|||  |::: :    |
Db        194 NVTEVNPLGASTRLLDVS-----------------LQSILRPDPPQGLRVESVPGYPR 234

Qy        230 HVEVSWEYPDTW-STPHSYFSLTFCIQAQGKNNR--EKKDRLCVDKTSAKVVCHKDAKIR 286
               :  || || :|   ||  | | | :| :   :      :   :::     |      :|
Db        235 RLRASWTYPASWPCQPH--FLLKFRLQYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVR 292

Qy        287 VQARDRYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQK 346
              | |||   : :|| |   |    |   : :|   |: |      |:|  :    ::
Db        293 VSARDFLDAGTWSTW---SPEAWGTPSTGTIPKEIPAWGQL----HTQPEVEPQVDSPAP 345

Qy        347 ARQTLELYSCTSEEIDHED 365
               | :|: :      :|| .|
Db        346 PRPSLQPH---PRLLDHRD 361


RESULT 12
I48343
interleukin-11 receptor alpha-chain precursor - mouse
N;Alternate names: cytokine type 1 receptor
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Jan-2000
C;Accession: I48343; S51619
R;Neuhaus, H.; Bettenhausen, B.; Bilinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gossle
Dev. Biol. 166, 521-542, 1994
A;Title: et12, a novel putative type-1 cytokine receptor expressed during mouse embryoge
A;Reference number: I48343
A;Accession: I48343
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-432 <RES>
A;Cross-references: EMBL:X74953; NID:g673437; PIDN:CAA52908.1; PID:g673438
R;Hilton, D.J.; Hilton, A.A.; Raicevic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M.;
EMBO J. 13, 4765-4775, 1994
A;Title: Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for hi
A;Reference number: S51619; MUID:95045367; PMID:7957045
A;Accession: S51619
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-432 <HIL>
A;Cross-references: EMBL:U14412; NID:g576454; PIDN:AAA53248.1; PID:g576455
C;Genetics:
A;Gene: Et12/IL11
C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
C;Keywords: cytokine receptor
F;120-310/Domain: cytokine receptor homology <CRS>

  Query Match             5.8%;  Score 157;  DB 2;  Length 432;
  Best Local Similarity   21.4%;  Pred. No. 0.00028;
  Matches   94;  Conservative   52;  Mismatches  154;  Indels  140;  Gaps   22;

Qy         15 WHPDA-----PGEMVVLTC-----HTPEEDDITWTSAQSSEVL-----GSGKTLTIQVKE 59
              | |        ||  |:| |      ||    ::|     | :|     | |  | :   :
Db         30 WGPPGVQYGQPGRPVMLCCPGVSAGTP----VSWFRDGDSRLLQGPDSGLGHRLVLAQVD 85

Qy         60 FGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLK---------- 108
                | | | |               :  ||:           |   : ||
Db         86 SPDEGTYVC---------------QTLDGV-----------SGGMVTLKLGFPPARPEVS 119

Qy        109 CEAKNYSGRFTCWW-----------LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAE 156
              |:| :|   |:| |            ||:         :| |         |    | |
Db        120 CQAVDYE-NFSCTWSPGQVSGLPTRYLTSYRKKTLPGAESQRESPSTGPWPCPQDPLEAS 178

Qy        157 RVRVDNRDY-KKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPD 215
              |  |   ::  :| :   | :   ::   | :                    :: |::||
Db        179 RCVVHGAEFWSEYRINVTEVNPLGASTCLLDVR-----------------LQSILRPD 219

Qy        216 PPTNLQLKPLKN-SRHVEVSWEYPDTW-STPHSYFSLTFCIQAQGKNNR--EKKDRLCVD 271
              ||  |::: :    | :  || || :|   ||  | | | :| :   :      : : ::
Db        220 PPQGLRVESVPGYPRRLHASWTYPASWRRQPH--FLLKFRLQYRPAQHPAWSTVEPIGLE 277

Qy        272 KTSAKVVCHKDAKIRVQARDRYYSSSWSDWASVSCSGGGGGGSRNLPTPTPSPGMFQ--- 328
              :     |      :|| |||   : :|| |:  :               ||| |  |
Db        278 EVITDAVAGLPHAVRVSARDFLDAGTWSAWSPEAWG------------TPSTGPLQDEI 324

Qy        329 ---CLNHSQTLLRAVS--NTLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELT 383
                  | | |   |:  ::   || :|:         :|| |              |||
Db        325 PDWSQGHGQQLEAVVAQEDSPAPARPSLQ---PDPRPLDHRD-------------PLE-- 366

Qy        384 MNESCLASREISLITNGSCL 403
                : |||  |      |||
Db        367 -QVAVLASLGIF-----SCL 380


RESULT 13
H96544
hypothetical protein F8A12.4 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: H96544
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H96544
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-812 <STO>
A;Cross-references: GB:AE005173; NID:g11094686; PIDN:AAG29622.1; GSPDB:GN00141
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C;Genetics:
A;Gene: F8A12.4
A;Map position: 1

Query Match 5.3%; Score 143; DB 2; Length 812;
Best Local Similarity 22.1%; Pred. No. 0.0081;
Matches 97; Conservative 57; Mismatches 174; Indels 110; Gaps 23;

```
Qy         26 LTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKK 85
              ::| ||   | :|       |:|| |||   :   ||   :    | |:  ||
Db        426 ISCDTPMFCD-SW----RKRVVGSAKTLRTSI---GDDTSFV-PSGSKMNRRS------- 469

Qy         86 EDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDL---------------- 130
              |||      : |    |   |:|  ||     |      || |
Db        470 EDG----RKIAEDSTKKRLKFMKSARKNDGS--TMGQKQVISDDADDDDSLTVAQITTLY 523

Qy        131 --KFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACP-SAEESLPI 187
                |:|  |    |:| |           |:  ||   :     ||: |:     :|::|
Db        524 KKKYSENSGGNASEPLG--------KKIRLEADNNGLE----PCQKLSSIRYDGDETVPP 571

Qy        188 EVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWSTPHSY 247
              :    | : |   |  :| :: |   :|    |:   | :::    |:|
Db        572 PEI-----KKRNEETGSKSGMRVVLSPFDESNSSKPPVDFGRAIDIVVSAPET------- 619

Qy        248 FSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKI-RVQAR-DRYYSSSWSDWASVS 305
              :|||    | || |||  :  |    | : |:|  | |  || |:   |      |
Db        620 --MTFCDDVYG-NNAEKKTMIDDDSEELKCLLHEDGTITREMARSDKKCCSE----AEKE 672

Qy        306 CSGGG---------GGGSRNLPTPTPSPGMFQCLNHSQT--------LLRAVSN------ 342
               : ||             :::|    : |   | |  :|        | |:  |
Db        673 DADGGISDKVLASKADNKKSIPYQKLASG---CANGDETSKAYKPKVLKRSDGNQAHACL 729

Qy        343 ---------TLQKARQTLELYSCTSEEIDHEDITKDKTSTVEACL-PLELTMNESCL-AS 391
                     |: : |:::   : ::   |:  | |       |  | |:: |  | |
Db        730 LPDDGIRSEETMKSNEQLKVFEKRNNDLGEGDVDNDTTEKRSQKLNVLALSIEERVLKAE 789

Qy        392 REISLITNGSCLASGKAS 409
              | :: :    :   | :
Db        790 RTVAWLNQRRAIKQRKVA 807
```

RESULT 14
JS0675
vascular cell adhesion molecule-1 precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 05-Nov-1999
C;Accession: JS0675; S19872; S23136
R;Hession, C.; Moy, P.; Tizard, R.; Chisholm, P.; Williams, C.; Wysk, M.; Burkly, L.; Mi
Biochem. Biophys. Res. Commun. 183, 163-169, 1992
A;Title: Cloning of murine and rat vascular cell adhesion molecule-1.
A;Reference number: JS0674; MUID:92181437; PMID:1371918
A;Accession: JS0675
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-739 <HES>
A;Cross-references: GB:M84488; NID:g207642; PIDN:AAA42332.1; PID:g207643
R;Williams, A.; Atkins, R.; Fries, J.; Gimbrone, M.A.; Cybulsky, M.I.; Collins, T.
submitted to the EMBL Data Library, February 1992
A;Description: Nucleotide sequence of rat vascular cell adhesion molecule-1.
A;Reference number: S19872
A;Accession: S19872
A;Molecule type: mRNA
A;Residues: 1-2,'G',4-121,'HL',124-165,'N',167-738,'G' <WIL>
A;Cross-references: EMBL:X63722; NID:g57471; PIDN:CAA45254.1; PID:g57472
R;Williams, A.J.; Atkins, R.C.; Fries, J.W.U.; Gimbrone Jr., M.A.; Cybulsky, M.I.; Colli
Biochim. Biophys. Acta 1131, 214-216, 1992
A;Title: Nucleotide sequence of rat vascular cell adhesion molecule-1 cDNA.
A;Reference number: S23136; MUID:92305064; PMID:1377031
A;Accession: S23136
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-2,'G',4-165,'N',167-738,'G' <WI2>
C;Comment: This protein interacts with the beta-1 integrin very late antigen 4 on leukod

C;Genetics:
A;Gene: VCAM-1
C;Superfamily: immunoglobulin homology
C;Keywords: cell adhesion; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;25-739/Product: vascular cell adhesion molecule 1 #status predicted <VAS>
F;239-293/Domain: immunoglobulin homology <IMM1>
F;328-385/Domain: immunoglobulin homology <IMM2>
F;526-581/Domain: immunoglobulin homology <IMM3>
F;676-696/Domain: transmembrane #status predicted <TRA>
F;697-715/Domain: intracellular #status predicted <INT>

Query Match 4.6%; Score 123.5; DB 2; Length 739;
Best Local Similarity 20.0%; Pred. No. 0.23;
Matches 113; Conservative 85; Mismatches 204; Indels 163; Gaps 31;

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Qy          5 EKDVYV----VELDWHPDA---PGEMVVLTCHT-----PEEDDITWTSAQSS---EVLGS 49
              |  ||      |:  ||      |  | :|| :     ||   | |:    :   ::|
Db        216 ELQVYTSPKNTEISVHPSTRLHEGAAVTMTCASEGLPAPE---IFWSKKLDNGVLQLLSG 272

Qy         50 GKTLTIQVKEFGDAGQYTCHKGGKVLSRSL----LLIHKKEDGIWSTDILKEQK---ESK 102
                |||:      |:| | | :|  :: |      |:: :|    :: ||    :   :
Db        273 NATLTLIAMRMEDSGIYVC-EGVNLVGRDKTEVELIVQEKP---FTVDISPGSQVAAQVG 328

Qy        103 NKIFLKCEAKNY-SGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVD 161
              : : | | |    |  |:  | |   : |   |:        :| |    ||:   | |:
Db        329 DSVVLTCAAVGCDSPSFS--WRTQTDSPLNGEVRD-------EGATS---TLTLSPVGVE 376

Qy        162 NRDYKKYTVECQEGSACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQ 221
              :      || ||        |::: :||              ||       |: |
Db        377 DEHSYLCTVTCQR----RKLEKTIQVEVY--------------SF-------PEDPEIEI 411

Qy        222 LKPLKNSRHVEVSWEYPDTWSTPHSYFSL---------TFCIQAQGKNNREKKDR----- 267
              || : | | |:   |: :   |    |          | :  |  : | |
Db        412 SGPLVHGRPVTVNCTVPNVYPFDHLEIELLKGETTLLNKFLREEIGTKSLETKSLEMTFI 471

Qy        268 LCVDKTSAKVVC---------HKDAKIRVQARDRYYSSSWSD---WAS------------ 303
                : |   :||           : | |   :  | : :   :    | |
Db        472 PTAEDTGKALVCLAKLHSSQMESEPKQRQSTQTLYVNVAPKEPTIWVSPSPVPEEGSPVN 531

Qy        304 VSCSGGGGGGSRNLPTP------TPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCT 357
              ::||  |        |||          |  | |: : ||     : :    :   :| |
Db        532 LTCSSDG------FPTPKILWSRQLKNGELQPLSQNTTL-----SFMATKMEDSGIYVCE 580

Qy        358 SEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLS 417
                                  :||: :: : : ||  |    | |   :||
Db        581 G------------------------INEAGISKKSVELIIQG----SSKDIQLTVFPSK 611

Qy        418 SIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEE 477
              |: |       :   ::      |:  | | :   |  | :|:::|  | |: :|: |::
Db        612 SVKEG------DTVIISCTCGSVPEIWIILKKKAKTG-DMVLKSVN-GSYTI-RKAQLQD 662

Qy        478 PDFYKTKIKLCILLHAFRIRAVTIN 502
              |: : |  :     ::|::|::
Db        663 AGVYECESKTEV---GSQLRSLTLD 684
```

RESULT 15
T30532
neural cell adhesion molecule L1 homolog - Fugu rubripes
C;Species: Fugu rubripes
C;Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Mar-2002
C;Accession: T30532
R;Riboldi Tunnicliffe, G.R.; Platzer, M.; Nyakatura, G.; Elgar, G.S.; Brenner, S.; Ro
submitted to the EMBL Data Library, September 1997
A;Description: Analysis of the genomic loci of Fugu rubripes homologs of the human di
A;Reference number: Z20848
A;Accession: T30532
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1277 <RIB>
A;Cross-references: EMBL:AF026198; NID:g3098263; PID:g3098264; PIDN:AAC15580.1
C;Genetics:

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A;Introns: 42/1; 47/1; 81/2; 149/1; 190/1; 247/1; 285/2; 347/1; 391/1; 440/1; 477/2; 531
/2
A;Note: L1-CAM
C;Superfamily: neural cell adhesion molecule L1; fibronectin type III repeat homology; i

  Query Match             4.5%;  Score 122.5;  DB 2;  Length 1277;
  Best Local Similarity   22.9%;  Pred. No. 0.59;
  Matches   77;  Conservative   44;  Mismatches  122;  Indels   93;  Gaps   15;

Qy         19 APGEMVVLTCHTP--EEDDITWT------SAQSSE---VLGSGKTLTIQVKEFGDAGQYT 67
              |||| | | |         ||||      || | |    |    :| ::   |||   |
Db        361 APGETVKLDCQADGIPSPTITWTVNGVPLSATSLEPRRSLTESGSLILKDVIFGDTAIYQ 420

Qy         68 C---HKGGKVLSRSLLLIHK------KEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRF 118
              |   :| | :|: : : : :       |:|   | :         |  |:||
Db        421 CQASNKHGTILANTNVYVIELPPQILTENGNTYTFV------EGQKALLECETFGSPKPK 474

Qy        119 TCWWLTAIS---TDLKFSVKSSRGFS------DPQGV-TC----GAVTLSAERVRVDNRD 164
              |  ::||    | : :: :: |        | :|: ||      ::::|| | | ||
Db        475 VTWESSSISLLLADPRVNLLTNGGLEIANVSHDDEGIYTCLVQGSNISVNAE-VEVLNRT 533

Qy        165 Y-----------------------------------------------KKYTVECQEGS 176
                                                             |||| :   |
Db        534 VILSPPQALRLQPGKTAIFTCLYVTDPKLSSPLLQWRKNDQKIFESHSDKKYTFD-GPGL 592

Qy        177 ACPSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWE 236
              : |          | ||     :|:  : |  :|||| :||:   |: | | ::|
Db        593 IISNVEPGDEGVYTCQIITKLDMVEASSTLTLCD--RPDPPVHLQVTNAKH-RVVTLNWT 649

Qy        237 YPDTWSTPHSYFSLTFCIQAQGKNNREKKDRLCVDK 272
              |  ::|   : : |  |   :|  |:  |:  ||
Db        650 PGDDNNSPILEYVVEFEDQDMKENGWEELKRVAADK 685


Search completed: July 15, 2003, 11:08:47
Job time : 23.3973 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 10:58:28 ; Search time 11.1987 Seconds
(without alignments)
1892.583 Million cell updates/sec

Title: US-09-917-265-67
Perfect score: 2693
Sequence: 1 IWELEKDVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNSS 511

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1652	61.3	329	1	I12B_CANFA	Q28268 canis famil
2	1546	57.4	329	1	I12B_FELCA	O02744 felis silve
3	1469	54.5	329	1	I12B_HORSE	Q9xsq5 equus cabal
4	1427	53.0	327	1	I12B_CEREL	Q28234 cervus elap
5	1418.5	52.7	328	1	I12B_HUMAN	P29460 homo sapien
6	1411	52.4	327	1	I12B_BOVIN	P46282 bos taurus
7	1407	52.2	327	1	I12B_SHEEP	O02815 ovis aries
8	1406.5	52.2	328	1	I12B_MACMU	P48095 macaca mula
9	1389.5	51.6	324	1	I12B_PIG	Q28938 sus scrofa
10	1368.5	50.8	328	1	I12B_CERTO	P46658 cercocebus
11	1255	46.6	327	1	I12B_MARMO	Q61729 marmota mon
12	1058.5	39.3	335	1	I12B_MOUSE	P43432 mus musculu
13	961	35.7	222	1	I12A_FELCA	O02743 felis silve
14	949	35.2	222	1	I12A_CANFA	Q28267 canis famil
15	873	32.4	219	1	I12A_HUMAN	P29459 homo sapien
16	869	32.3	222	1	I12A_PIG	Q29053 sus scrofa
17	866	32.2	222	1	I12A_HORSE	Q9xsq6 equus cabal
18	829.5	30.8	221	1	I12A_CEREL	Q28233 cervus elap
19	827	30.7	219	1	I12A_MACMU	P48091 macaca mula
20	824.5	30.6	221	1	I12A_BOVIN	P54349 bos taurus
21	824.5	30.6	221	1	I12A_SHEEP	Q9tu27 ovis aries
22	822	30.5	219	1	I12A_CERTO	P46661 cercocebus
23	809.5	30.1	221	1	I12A_CAPHI	O02814 capra hircu
24	614.5	22.8	223	1	I12A_MARMO	Q61728 marmota mon
25	549	20.4	215	1	I12A_MOUSE	P43431 mus musculu
26	211.5	7.9	468	1	IL6A_HUMAN	P08887 homo sapien
27	206	7.6	467	1	IL6A_PIG	O18796 sus scrofa
28	190	7.1	460	1	IL6A_MOUSE	P22272 mus musculu
29	178	6.6	362	1	CNTR_CHICK	P51641 gallus gall
30	177	6.6	372	1	CNTR_RAT	Q08406 rattus norv
31	170	6.3	372	1	CNTR_HUMAN	P26992 homo sapien
32	170	6.3	462	1	IL6A_RAT	P22273 rattus norv
33	123.5	4.6	739	1	VCA1_RAT	P29534 rattus norv
34	122.5	4.5	978	1	KIT_FELCA	Q28889 felis silve
35	115.5	4.3	977	1	KIT_BOVIN	P43481 bos taurus
36	114	4.2	611	1	GHR_COLLI	Q90375 columba liv
37	114	4.2	831	1	PRLR_CHICK	Q04594 gallus gall
38	112.5	4.2	978	1	KIT_CAPHI	Q28317 capra hircu
39	111.5	4.1	610	1	PRLR_RAT	P05710 rattus norv
40	111	4.1	638	1	GHR_RAT	P16310 rattus norv
41	111	4.1	1323	1	LT23_CAEEL	P24348 caenorhabdi
42	111	4.1	2670	1	IP3T_RAT	Q63269 rattus norv
43	108.5	4.0	1093	1	SM5B_MOUSE	Q60519 mus musculu
44	108	4.0	581	1	PRLR_BOVIN	Q28172 bos taurus
45	107.5	4.0	635	1	TPOR_HUMAN	P40238 homo sapien

ALIGNMENTS

RESULT 1
I12B_CANFA
ID I12B_CANFA STANDARD; PRT; 329 AA.
AC Q28268;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE maturation factor 40 kDa subunit) (CLMF p40).
GN IL12B.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98280561; PubMed=9617567;
RA Buettner M., Belke-Louis G.F., Rziha H.J., McInnes C., Kaaden O.R.;
RT "Detection, cDNA cloning and sequencing of canine interleukin 12.";
RL Cytokine 10:241-248(1998).
CC -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC BY RESTING PBMC (BY SIMILARITY).
CC -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC SUBUNITS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC --
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CC --
DR EMBL; U49100; AAA92059.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00408; IGc2; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 329 INTERLEUKIN-12 BETA CHAIN.
FT DOMAIN 43 97 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 236 321 FIBRONECTIN TYPE-III.
FT DISULFID 50 90 POTENTIAL.
FT DISULFID 200 200 INTERCHAIN (PROBABLE).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).

```
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   329 AA;  37410 MW;  79F83ED02B5DA93C CRC64;

  Query Match             61.3%;  Score 1652;  DB 1;  Length 329;
  Best Local Similarity   99.7%;  Pred. No. 4.9e-121;
  Matches  306;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCVQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 2
I12B_FELCA
ID   I12B_FELCA     STANDARD;      PRT;   329 AA.
AC   O02744; O46671;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=97246745; PubMed=9089110;
RA   Schijns V.E.C.J., Wierda C.M.H., Vahlenkamp T.W., Horzinek M.C.;
RT   "Molecular cloning of cat interleukin-12.";
RL   Immunogenetics 45:462-463(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98182592; PubMed=9522125;
RA   Fehr D., Dean G.A., Huder J., Fan Z., Huettner S., Higgins J.W.,
RA   Pedersen N.C., Lutz H.;
RT   "Nucleotide and predicted peptide sequence of feline interleukin-12
RT   (IL-12).";
RL   DNA Seq. 8:77-82(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y07762; CAA69068.1; -.
DR   EMBL; U83184; AAB93835.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    329       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    321       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    11     11       L -> F (IN REF. 2).
FT   CONFLICT    51     51       N -> D (IN REF. 2).
FT   CONFLICT   167    167       E -> G (IN REF. 2).
SQ   SEQUENCE   329 AA;  37374 MW;  12A069BC6322AE08 CRC64;

  Query Match             57.4%;  Score 1546;  DB 1;  Length 329;
  Best Local Similarity   93.5%;  Pred. No. 8.4e-113;
  Matches  287;  Conservative    9;  Mismatches   11;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:||||||||||||||||||:|||||||||| ||||||||||||||||||
Db         23 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||| | ||||||||||||||:|||||||||||||||||||||||||
Db         83 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||:|||||| |||| ||||| |||||:|||||||||||||||||||||:
Db        143 WWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| :| |||||||||||| ||||||||||||||||||||||||||||:
Db        263 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 3
I12B_HORSE
ID   I12B_HORSE     STANDARD;      PRT;   329 AA.
AC   Q9XSQ5;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC   Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20009534; PubMed=10541814;
RA   Nicolson L., Penha-Goncalves M.N., Keanie J.L., Logan N.A.,
RA   Argyle D.J., Onions D.E.;
RT   "Cloning and sequencing of horse interleukin-12 and interleukin-18
RT   cDNAs.";
RL   Immunogenetics 50:94-97(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Y11129; CAA72011.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    329       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   329 AA;  37442 MW;  7104BB0DFF8FA73C CRC64;

  Query Match             54.5%;  Score 1469;  DB 1;  Length 329;
  Best Local Similarity   87.6%;  Pred. No. 8e-107;
  Matches  269;  Conservative   20;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||:||||||||||||:||||: ||||||||:||||||||||||||||
Db         23 IWELEKDVYVVELDWYPDAPGEMVVLTCNTPEEEGITWTSAQSNEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||| |||||||:||| | ||:||||||||||||||:||||||| ||||||||||||||||
Db         83 GDAGWYTCHKGGEVLSHSHLLLHKKEDGIWSTDILKDQKESKNKTFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||||||||| |||:|||||| ||||||| ||:|:|||||||||||||||:
Db        143 WWLTAISTDLKFSVKSSRGSSDPRGVTCGAATLSAERVSVDDREYKKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||:||||:|||||||||| |||||||||||| |||||||||| |||||||||:|
Db        203 AEESLPIEIVVDAVHKLKYENYTSGFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPET 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||| || |||| :|:|||| :|:||| | |||| :||||||||||||||:
Db        263 WSTPHSYFSLTFSIQVQGKNKKERKDRLFMDETSATVTCHKDGQIRVQARDRYYSSSWSE 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 4
I12B_CEREL
ID   I12B_CEREL     STANDARD;      PRT;   327 AA.
AC   Q28234;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99304506; PubMed=10376218;
RA   Lockhart E., Slobbe L., Buchan G.;
RT   "The characterisation of a cervine immunoregulatory cytokine,
RT   interleukin 12.";
RL   DNA Seq. 10:139-148(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U57752; AAB02258.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37145 MW;  53AF5BB288907F06 CRC64;

  Query Match             53.0%;  Score 1427;  DB 1;  Length 327;
  Best Local Similarity   85.7%;  Pred. No. 1.5e-103;
  Matches  263;  Conservative   21;  Mismatches   21;  Indels    2;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:||||||||:|||||| ||| | ||||| ||||| ||||||||||||||:|||||
Db         23 IWELEKNVYVVELDWYPDAPGETVVLRCDTPEEDGITWTSDQSSEVLGSGKTLTVQVKEF 82
```

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Qy          61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               ||||||||||||:|||||||:|||||||||||||||:||| | | |||||||:||| |||
Db          83 GDAGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTC 142

Qy         121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               |||||||||||||||||| |||:|||||| :|| |:| ||:|:|||||||||||||||:
Db         143 WWLTAISTDLKFSVKSSRGSSDPRGVTCGAASLSTEKVIVDHREYKKYTVECQEGSACPA 202

Qy         181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
               ||||||||||:|:|||||||||||||||||||||| ||||:|||||| ||||||||||
Db         203 AEESLPIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDT 262

Qy         241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
               |||||||||||||:| |||| |||| | :|:||||| ||||| ||||||||||:| ||:
Db         263 WSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVTCHKDASIRVQARDRYYNSFWSE 320

Qy         301 WASVSCS 307
               |||||||
Db         321 WASVSCS 327


RESULT 5
I12B_HUMAN
ID   I12B_HUMAN     STANDARD;      PRT;   328 AA.
AC   P29460;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40) (NK cell stimulatory
DE   factor chain 2) (NKSF2).
GN   IL12B OR NKSF2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91239523; PubMed=1674604;
RA   Gubler U., Chua A.O., Schoenhaut D.S., Dwyer C.M., McComas W.,
RA   Motyka R., Nabavi N., Wolitzky A.G., Quinn P.M., Familletti P.C.,
RA   Gately M.K.;
RT   "Coexpression of two distinct genes is required to generate secreted
RT   bioactive cytotoxic lymphocyte maturation factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:4143-4147(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91201875; PubMed=1673147;
RA   Wolf S.F., Temple P.A., Kobayashi M., Young D., Dicig M., Lowe L.,
RA   Dzialo R., Fitz L., Ferenz C., Hewick R.M., Kelleher K.,
RA   Herrmann S.H., Clark S.C., Azzoni L., Chan S.H., Trinchieri G.,
RA   Perussia B.;
RT   "Cloning of cDNA for natural killer cell stimulatory factor, a
RT   heterodimeric cytokine with multiple biologic effects on T and
RT   natural killer cells.";
RL   J. Immunol. 146:3074-3081(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   PubMed=11197695;
RA   Huang D., Cancilla M.R., Morahan G.;
RT   "Complete primary structure, chromosomal localization, and definition
RT   of polymorphisms of the gene encoding the human interleukin 12 p40
RT   subunit.";
RL   Genes Immun. 1:515-520(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RA   Hongyuan J., Meiyun Z.;
RT   "Cloning and sequence analysis of IL-12 cDNA from Chinese.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE OF 23-45.
RX   MEDLINE=90370873; PubMed=2204066;
RA   Stern A.S., Podlaski F.J., Hulmes J.D., Pan Y.C.E., Quinn P.M.,
RA   Wolitzky A.G., Familletti P.C., Stremlo D.L., Truitt T.,
RA   Chizzonite R., Gately M.K.;
RT   "Purification to homogeneity and partial characterization of
RT   cytotoxic lymphocyte maturation factor from human B-lymphoblastoid
RT   cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6808-6812(1990).
RN   [6]
RP   SIMILARITY TO IL-6 RECEPTOR.
RX   MEDLINE=91300556; PubMed=2070420;
RA   Gearing D.P., Cosman D.;
RT   "Homology of the p40 subunit of natural killer cell stimulatory
RT   factor (NKSF) with the extracellular domain of the interleukin-6
RT   receptor.";
RL   Cell 66:9-10(1991).
RN   [7]
RP   CARBOHYDRATE-LINKAGE SITE TRP-319.
RX   MEDLINE=99225373; PubMed=10207176;
RA   Doucey M.A., Hess D., Blommers M.J., Hofsteenge J.;
RT   "Recombinant human interleukin-12 is the second example of a
RT   C-mannosylated protein.";
RL   Glycobiology 9:435-441(1999).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED
CC       T AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC.
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS. NKSF IS ESSENTIALLY A COMPLEX OF CYTOKINE AND SOLUBLE
CC       RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- PTM: KNOWN TO BE C-MANNOSYLATED IN THE RECOMBINANT PROTEIN; IT IS
CC       NOT YET KNOWN FOR SURE IF THE WILD-TYPE PROTEIN IS ALSO MODIFIED.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M65272; AAA35695.1; -.
DR   EMBL; M65290; AAA59938.1; -.
DR   EMBL; AY008847; AAG32620.1; -.
DR   EMBL; AF180563; AAD56386.1; -.
DR   PIR; B39359; B39359.
DR   PIR; B36055; B36055.
DR   GlycoSuiteDB; P29460; -.
DR   Genew; HGNC:5970; IL12B.
DR   MIM; 161561; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22
FT   CHAIN       23    328       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     235    320       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD   135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   222    222       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   319    319       C-LINKED (MAN).
FT                               /FTId=CAR_000187.
FT   CONFLICT   239    239       K -> N (IN REF. 2).
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SQ   SEQUENCE   328 AA;  37169 MW;  118FA801B8F5BB2F CRC64;

  Query Match             52.7%;  Score 1418.5;  DB 1;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 6.7e-103;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||||:|||||||||||| ||||| |||| |||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||||:||| ||||:||||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||:::| :|:|||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 6
I12B_BOVIN
ID   I12B_BOVIN     STANDARD;      PRT;   327 AA.
AC   P46282;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Holstein; TISSUE=Lymphoid;
RX   MEDLINE=95244628; PubMed=7727547;
RA   Zarlenga D.S., Canals A., Aschenbrenner R.A., Gasbarre L.C.;
RT   "Enzymatic amplification and molecular cloning of cDNA encoding the
RT   small and large subunits of bovine interleukin 12.";
RL   Biochim. Biophys. Acta 1270:215-217(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U11815; AAA85792.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     236    319       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD   223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37050 MW;  D484DA36EF6F3D9F CRC64;

  Query Match             52.4%;  Score 1411;  DB 1;  Length 327;
  Best Local Similarity   84.7%;  Pred. No. 2.5e-102;
  Matches  260;  Conservative   22;  Mismatches   23;  Indels    2;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||:|||||||||:|||||| ||||| ||||| ||||| ||||||||||||||||||
Db         23 MWELEKNVYVVELDWYPDAPGETVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||||: |||||||:|||||||||||||||:||| | | |||||||:||| |||
Db         83 GDAGQYTCHKGGEALSRSLLLLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||||||||| |||:|||||  ||||:| :::|:|:| ||||||||||||:
Db        143 WWLTAISTDLKFSVKSSRGSSDPRGVTCGAALLSAEKVSLEHREYNKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||| ||||||:|:|||||||||||||||||||||||| ||||:|||||| ||||||||||
Db        203 AEESLLIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||| |||| | :|:||||| ||||| :|||||||||| ||:
Db        263 WSTPHSYFSLTFCVQVQGKNKREKK--LFMDQTSAKVTCHKDANVRVQARDRYYSSFWSE 320

Qy        301 WASVSCS 307
              |||||||
Db        321 WASVSCS 327


RESULT 7
I12B_SHEEP
ID   I12B_SHEEP     STANDARD;      PRT;   327 AA.
AC   O02815; O18989; Q9TT18;
DT   01-NOV-1997 (Rel. 35, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Ovis aries (Sheep), and
OS   Capra hircus (Goat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Caprinae; Ovis.
OX   NCBI_TaxID=9940, 9925;
RN   [1]
RP   SEQUENCE FROM N.A., AND SUBUNIT.
RC   SPECIES=Sheep; TISSUE=Peripheral blood;
RX   MEDLINE=20480126; PubMed=11023671;
RA   Swinburne S.J., Russ G.R., Krishnan R.;
RT   "Ovine interleukin 12 has biological activity on ovine and human
RT   activated peripheral blood mononuclear cells.";
RL   Cytokine 12:1546-1552(2000).
RN   [2]
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RP   SEQUENCE FROM N.A.
RC   SPECIES=Sheep; STRAIN=Merino; TISSUE=Peripheral blood;
RX   MEDLINE=20344025; PubMed=10888112;
RA   De Rose R., Scheerlinck J.-P.Y., Casey G., Wood P.R., Tennent J.M.,
RA   Chaplin P.J.;
RT   "Ovine interleukin-12: analysis of biologic function and species
RT   comparison.";
RL   J. Interferon Cytokine Res. 20:557-564(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=C.hircus;
RA   Beyer J.C., Cheevers W.P., Kumpula-Mcwhirter N.M.;
RT   "Cloning of caprine IL-12 40 kDa subunit.";
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF004024; AAB61368.2; -.
DR   EMBL; AF209435; AAF20151.1; -.
DR   EMBL; AF007576; AAB62945.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
DR   PROSITE; PS00290; IG_MHC; FALSE_NEG.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       POTENTIAL.
FT   CHAIN        23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      236    319       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    200    200       INTERCHAIN (PROBABLE).
FT   CARBOHYD    223    223       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    290    290       T -> A (IN REF. 2).
SQ   SEQUENCE   327 AA;  36936 MW;  DDCD983A10143A96 CRC64;

  Query Match           52.2%;  Score 1407;  DB 1;  Length 327;
  Best Local Similarity  85.0%;  Pred. No. 5.2e-102;
  Matches  261;  Conservative   22;  Mismatches   22;  Indels    2;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:||||||||:|:|||| ||||| ||||| ||||| ||||||||||||||||||||
Db         23 IWELEKNVYVVELDWYPNAPGETVVLTCDTPEEDGITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||||||||:|||||||||||||||:||| | | |||||||:||| |||
Db         83 GDAGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||:|||||||||| ||| |||||| :|||||:| :|:|:| ||||||||||||:
Db        143 SWLTAISTNLKFSVKSSRGSSDPRGVTCGAASLSAEKVSMDHREYNKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||::|:|||||||||||||||||||||||| ||||:|||||| ||||||||||
Db        203 AEESLPIEVVMEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||| |||| | |:||||| ||||| |||||||||||| ||:
Db        263 WSTPHSYFSLTFCVQVQGKNKREKK--LFTDQTSAKVTCHKDANIRVQARDRYYSSFWSE 320

Qy        301 WASVSCS 307
              |||||||
Db        321 WASVSCS 327


RESULT 8
I12B_MACMU
ID   I12B_MACMU     STANDARD;      PRT;   328 AA.
AC   P48095;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19841; AAB60397.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    328       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      235    320       FIBRONECTIN TYPE-III.
```

```
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD    125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   VARIANT     106    106       K -> I.
FT   VARIANT     206    206       L -> P.
FT   VARIANT     218    218       L -> P.
FT   VARIANT     289    289       I -> T.
FT   VARIANT     295    295       S -> P.
SQ   SEQUENCE   328 AA;  37273 MW;  A46198AAC6D2746B CRC64;

  Query Match             52.2%;  Score 1406.5;  DB 1;  Length 328;
  Best Local Similarity   84.4%;  Pred. No. 5.7e-102;
  Matches  259;  Conservative   20;  Mismatches   27;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||||:||||||||||| ||||| |||| || ||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||: || ||||:|||||||||||:||:||| ||| ||:|||||||||||||
Db         83 GDAGQYTCHKGGEALSHSLLLLHKKEDGIWSTDVLKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |:|||||||||||||||||| ||:::| :|:|||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSNPQGVTCGAVTLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||| |||||:|||||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEERLPIEVMVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||| |||: |||||:  |||| |:| |:|   |||:||||||||:
Db        262 WSTPHSYFSLTFCIQVQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 9
I12B_PIG
ID   I12B_PIG       STANDARD;      PRT;   324 AA.
AC   Q28938;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Sus scrofa (Pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX   NCBI_TaxID=9823;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Spleen;
RX   MEDLINE=97383978; PubMed=9239844;
RA   Foss D.L., Murtaugh M.P.;
RT   "Molecular cloning and mRNA expression of porcine interleukin-12.";
RL   Vet. Immunol. Immunopathol. 57:121-134(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U08317; AAA75356.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    324       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      231    316       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    195    195       INTERCHAIN (PROBABLE).
FT   CARBOHYD    125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    218    218       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   324 AA;  36828 MW;  F0E48B72F700086C CRC64;

  Query Match             51.6%;  Score 1389.5;  DB 1;  Length 324;
  Best Local Similarity   83.4%;  Pred. No. 1.2e-100;
  Matches  256;  Conservative   21;  Mismatches   25;  Indels    5;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:||||||||:|:|:|||||||||:||||| ||||| |||||||:|||||| ||||
Db         23 IWELEKNVYVVELDWYPNAPGEMVVLTCNTPEEDGITWTSDQSSEVLGTGKTLTIHVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||| ||| |||:||||:|||||||||||||||:||| ||| ||||||||||||||
Db         83 GDAGQYTCRKGGAVLSQSLLLLHKKEDGIWSTDILKDQKEPKNKSFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||||||||||||||||| :||:||||| |||      |  :|||| ||||||||||:
Db        143 WWLTAISTDLKFSVKSSRGSTDPRGVTCGTATLSE-----DLGEYKKYRVECQEGSACPA 197

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||::|:|||||||||||||||||||||||| |||| |||||||||:|||||
Db        198 AEESLPIEVVLEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLNPLKNSRHVEISWEYPDT 257

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||| | :| |||| |||||:|  |: |||| ||||| ||||||||||||||:
Db        258 WSTPHSYFSLMFGVQVQGKNKREKKDKLFTDQISAKVTCHKDANIRVQARDRYYSSSWSE 317

Qy        301 WASVSCS 307
              |||||||:
Db        318 WASVSCN 324


RESULT 10
I12B_CERTO
ID   I12B_CERTO     STANDARD;      PRT;   328 AA.
AC   P46658;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Cercocebus.
OX   NCBI_TaxID=9531;
RN   [1]
```

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RP   SEQUENCE FROM N.A.
RC   TISSUE=Blood;
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   use  by  non-profit  institutions as long  as its content  is  in  no  way
CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U19834; AAA86701.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    328       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      235    320       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD    125    125       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    135    135       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    222    222       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    303    303       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   328 AA;  37252 MW;  A2DE98E844435B14 CRC64;

  Query Match             50.8%;  Score 1368.5;  DB 1;  Length 328;
  Best Local Similarity   82.1%;  Pred. No. 5.1e-99;
  Matches  252;  Conservative   22;  Mismatches   32;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| || ||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSGEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||: || |||| ||||||||||||||:||| ||: ||:|||||||| ||
Db         83 GDAGQYTCHKGGEALSHSLLLPHKKEDGIWSTDILKDQKEPKNETFLRCEAKNYSGRITC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||: ||||| ||: |||| |:|||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLSTISTDLTFSIISSRGSSNPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||| ||||||:|||||||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEERLPIEVMVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||| |||: |||||:  ||||| |:| |:|   |||:||||||||::
Db        262 WSTPHSYFSLTFCIQVQGKSKREKKDRIFTDKTSATVICRKNASFSVQAQDRYYSSSWNE 321

Qy        301 WASVSCS 307
              | || ||
Db        322 WTSVPCS 328


RESULT 11
I12B_MARMO
ID   I12B_MARMO     STANDARD;      PRT;   327 AA.
AC   Q61729;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RA   Laxton C.D., Foster G.R., Shanmuganathan S., Mills J.S.,
RA   Ackrill A.M.;
RL   Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute.  There are no  restrictions on  its
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CC   modified and this statement is not removed.  Usage  by  and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X97019; CAA65747.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL        1     22       BY SIMILARITY.
FT   CHAIN        23    327       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN       43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN      235    319       FIBRONECTIN TYPE-III.
FT   DISULFID     50     90       POTENTIAL.
FT   DISULFID    199    199       INTERCHAIN (PROBABLE).
FT   CARBOHYD    134    134       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    152    152       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   327 AA;  37172 MW;  9A15445915AB90E6 CRC64;

  Query Match             46.6%;  Score 1255;  DB 1;  Length 327;
  Best Local Similarity   74.8%;  Pred. No. 3.3e-90;
  Matches  229;  Conservative   34;  Mismatches   41;  Indels    2;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:||||||||||| ||| ||||| ||||| ||||| |||||||||||||| ||||
Db         23 IWELEKNVYVVELDWHPDTPGEKVVLTCDTPEEDGITWTSEQSSEVLGSGKTLTILVKEF 82
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Qy          61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               ||| ||| :||:||| |||:|| |||||||||| :|| :||  : ||||||||||
Db          83 EDAGHYTCRRGGEVLSQMLLLLHKNEDGIWSTDILK-KKEPENKNLVTCEAKNYSGRFTC 141

Qy         121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||||||||: ||||| || |||||||||  |||||||::: |:||||:|:||| :|||:
Db         142 WWLTAISTDVNFSVKSHRGSSDPQGVTCGEATLSAERVKIEQREYKKYSVQCQEDNACPT 201

Qy         181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
               |||:||| |||||:|||||||| |||||||||||||| ||::|| |  : |||:|||||:
Db         202 AEETLPITVVVDAVHKLKYENYISSFFIRDIIKPDPPKNLKMKPSKTPQQVEVTWEYPDS 261

Qy         241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
               |||||||||||| :| |||  ::: : | |||||  | | | ||: |||||||:||||:
Db         262 WSTPHSYFSLTFSVQVQGK-KKKRSNTLHVDKTSVTVTCQKGAKVSVQARDRYYNSSWSE 320

Qy         301 WASVSC 306
               ||::||
Db         321 WATMSC 326


RESULT 12
I12B_MOUSE
ID   I12B_MOUSE     STANDARD;      PRT;   335 AA.
AC   P43432;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 beta chain precursor (IL-12B) (Cytotoxic lymphocyte
DE   maturation factor 40 kDa subunit) (CLMF p40).
GN   IL12B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Spleen;
RX   MEDLINE=92268481; PubMed=1350290;
RA   Schoenhaut D.S., Chua A.O., Wolitzky A.G., Quinn P.M., Dwyer C.M.,
RA   Gately M.K., Gubler U.;
RT   "Cloning and expression of murine IL-12.";
RL   J. Immunol. 148:3433-3440(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=96257799; PubMed=8647196;
RA   Tone Y., Thompson S.A., Babik J.M., Nolan K.F., Tone M., Raven C.,
RA   Waldmann H.;
RT   "Structure and chromosomal location of the mouse interleukin-12 p35
RT   and p40 subunit genes.";
RL   Eur. J. Immunol. 26:1222-1227(1996).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC   -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC   -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; M86671; AAA39296.1; -.
DR   EMBL; S82426; AAB37383.1; -.
DR   EMBL; S82421; AAB37383.1; JOINED.
DR   EMBL; S82422; AAB37383.1; JOINED.
DR   EMBL; S82424; AAB37383.1; JOINED.
DR   EMBL; S82425; AAB37383.1; JOINED.
DR   MGD; MGI:96540; Il12b.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR003598; Ig_c2.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW   Cytokine; Glycoprotein; Immunoglobulin domain; Signal.
FT   SIGNAL       1     22       BY SIMILARITY.
FT   CHAIN       23    335       INTERLEUKIN-12 BETA CHAIN.
FT   DOMAIN      43     97       IG-LIKE C2-TYPE DOMAIN.
FT   DOMAIN     233    324       FIBRONECTIN TYPE-III.
FT   DISULFID    50     90       POTENTIAL.
FT   DISULFID   197    197       INTERCHAIN (PROBABLE).
FT   CARBOHYD    47     47       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   122    122       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   132    132       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   220    220       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   DOMAIN     155    159       POLY-SER.
SQ   SEQUENCE   335 AA;  38235 MW;  19E4FA5EF0CFC82A CRC64;

  Query Match             39.3%;  Score 1058.5;  DB 1;  Length 335;
  Best Local Similarity   65.0%;  Pred. No. 6.2e-75;
  Matches  204;  Conservative   35;  Mismatches   62;  Indels   13;  Gaps    4;

Qy           1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
               :|||||||||||:|| |||||| | ||| |||||||||| |   |:|||||||| ||||
Db          23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy          61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||: || | ||:||||:|||||:||   |  ||| |||||| ||||||||
Db          83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy         121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||   : ||||::|||    | : |||  :||||:| :| |||:||:| |||   ||:
Db         140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy         181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
               |||:||||: ::|  : ||||||:|||||||||||| |||:||||||: |||||||||:
Db         200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258

Qy         241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
               |||||||||| | :: | |  : |        |    |:||| :| | |   : |||:||
Db         259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy         293 YYSSSWSDWASVSC 306
               ||:|| | || | |
Db         318 YYNSSCSKWACVPC 331


RESULT 13
I12A_FELCA
ID   I12A_FELCA     STANDARD;      PRT;   222 AA.
AC   O02743; O46672;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Peripheral blood;
RX   MEDLINE=97246745; PubMed=9089110;
RA   Schijns V.E.C.J., Wierda C.M.H., Vahlenkamp T.W., Horzinek M.C.;
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RT   "Molecular cloning of cat interleukin-12.";
RL   Immunogenetics 45:462-463(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98182592; PubMed=9522125;
RA   Fehr D., Dean G.A., Huder J., Fan Z., Huettner S., Higgins J.W.,
RA   Pedersen N.C., Lutz H.;
RT   "Nucleotide and predicted peptide sequence of feline interleukin-12
RT   (IL-12).";
RL   DNA Seq. 8:77-82(1997).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; Y07761; CAA69067.1; -.
DR   EMBL; U83185; AAB93836.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    222       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    99     99       INTERCHAIN (PROBABLE).
FT   CARBOHYD    42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   183    183       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    66     66       S -> P (IN REF. 2).
FT   CONFLICT   221    221       A -> S (IN REF. 2).
SQ   SEQUENCE   222 AA;  25076 MW;  223CF8FE0D30BF17 CRC64;

  Query Match             35.7%;  Score 961;  DB 1;  Length 222;
  Best Local Similarity   94.9%;  Pred. No. 1.3e-67;
  Matches  188;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        314 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 373
              :||||||||||||||||||||||||:||||||||||| ||||||||||||||||||||
Db         25 ARNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTST 84

Qy        374 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 433
              |||||||||||||||||||||||||||||| | |||| ||||||||||||:|||||
Db         85 VEACLPLELTMNESCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAM 144

Qy        434 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 493
              |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||||||
Db        145 NAKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHA 204

Qy        494 FRIRAVTINRMMSYLNSS 511
              ||||||||||||||:|
Db        205 FRIRAVTINRMMSYLNAS 222


RESULT 14
I12A_CANFA
ID   I12A_CANFA     STANDARD;      PRT;   222 AA.
AC   Q28267;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35).
GN   IL12A.
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98280561; PubMed=9617567;
RA   Buettner M., Belke-Louis G.F., Rziha H.J., McInnes C., Kaaden O.R.;
RT   "Detection, cDNA cloning and sequencing of canine interleukin 12.";
RL   Cytokine 10:241-248(1998).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED T
CC       AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC (BY SIMILARITY).
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U49085; AAA92058.1; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL       1     25       BY SIMILARITY.
FT   CHAIN       26    222       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID    99     99       INTERCHAIN (PROBABLE).
FT   CARBOHYD    42     42       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    96     96       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   110    110       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   222 AA;  24992 MW;  48C7E53ECFD6ACE5 CRC64;

  Query Match             35.2%;  Score 949;  DB 1;  Length 222;
  Best Local Similarity   94.4%;  Pred. No. 1.1e-66;
  Matches  187;  Conservative    6;  Mismatches    5;  Indels    0;  Gaps    0;

Qy        314 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 373
              :|:||| :||||:|||||||| |||||||||||||||:   ||||||||||||||||||
Db         25 ARSLPTASPSPGIFQCLNHSQNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTST 84

Qy        374 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 433
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         85 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 144

Qy        434 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 493
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 204

Qy        494 FRIRAVTINRMMSYLNSS 511
              ||||||||:|||||||||
Db        205 FRIRAVTIDRMMSYLNSS 222


RESULT 15
I12A_HUMAN
ID   I12A_HUMAN     STANDARD;      PRT;   219 AA.
AC   P29459; Q96QZ1;
DT   01-APR-1993 (Rel. 25, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Interleukin-12 alpha chain precursor (IL-12A) (Cytotoxic lymphocyte
DE   maturation factor 35 kDa subunit) (CLMF p35) (NK cell stimulatory
DE   factor chain 1) (NKSF1).
GN   IL12A OR NKSF1.
OS   Homo sapiens (Human).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91239523; PubMed=1674604;
RA   Gubler U., Chua A.O., Schoenhaut D.S., Dwyer C.M., McComas W.,
RA   Motyka R., Nabavi N., Wolitzky A.G., Quinn P.M., Familletti P.C.,
RA   Gately M.K.;
RT   "Coexpression of two distinct genes is required to generate secreted
RT   bioactive cytotoxic lymphocyte maturation factor.";
RL   Proc. Natl. Acad. Sci. U.S.A. 88:4143-4147(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91201875; PubMed=1673147;
RA   Wolf S.F., Temple P.A., Kobayashi M., Young D., Dicig M., Lowe L.,
RA   Dzialo R., Fitz L., Ferenz C., Hewick R.M., Kelleher K.,
RA   Herrmann S.H., Clark S.C., Azzoni L., Chan S.H., Trinchieri G.,
RA   Perussia B.;
RT   "Cloning of cDNA for natural killer cell stimulatory factor, a
RT   heterodimeric cytokine with multiple biologic effects on T and
RT   natural killer cells.";
RL   J. Immunol. 146:3074-3081(1991).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 23-48.
RX   MEDLINE=90370873; PubMed=2204066;
RA   Stern A.S., Podlaski F.J., Hulmes J.D., Pan Y.C.E., Quinn P.M.,
RA   Wolitzky A.G., Familletti P.C., Stremlo D.L., Truitt T.,
RA   Chizzonite R., Gately M.K.;
RT   "Purification to homogeneity and partial characterization of
RT   cytotoxic lymphocyte maturation factor from human B-lymphoblastoid
RT   cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 87:6808-6812(1990).
RN   [5]
RP   SIMILARITY TO IL-6.
RX   MEDLINE=92247293; PubMed=1374259;
RA   Merberg D.M., Wolf S.F., Clark S.C.;
RT   "Sequence similarity between NKSF and the IL-6/G-CSF family.";
RL   Immunol. Today 13:77-78(1992).
CC   -!- FUNCTION: CYTOKINE THAT CAN ACT AS A GROWTH FACTOR FOR ACTIVATED
CC       T AND NK CELLS, ENHANCE THE LYTIC ACTIVITY OF NK/LYMPHOKINE-
CC       ACTIVATED KILLER CELLS, AND STIMULATE THE PRODUCTION OF IFN-GAMMA
CC       BY RESTING PBMC.
CC   -!- SUBUNIT: DISULFIDE-BONDED HETERODIMER OF 40 kDa AND 35 kDa
CC       SUBUNITS. NKSF IS ESSENTIALLY A COMPLEX OF CYTOKINE AND SOLUBLE
CC       RECEPTOR.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: BELONGS TO THE IL-6 SUPERFAMILY.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M65271; AAA35694.1; -.
DR   EMBL; M65291; AAA59937.1; ALT_INIT.
DR   EMBL; AF404773; AAK84425.1; -.
DR   PIR; A39359; A39359.
DR   PIR; A36055; A36055.
DR   Genew; HGNC:5969; IL12A.
DR   MIM; 161560; -.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
KW   Cytokine; Growth factor; Signal.
FT   SIGNAL        1     22
FT   CHAIN        23    219       INTERLEUKIN-12 ALPHA CHAIN.
FT   DISULFID     96     96       INTERCHAIN (PROBABLE).
FT   CARBOHYD     93     93       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD    107    107       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CONFLICT    213    213       M -> T (IN REF. 1).
SQ   SEQUENCE   219 AA;  24874 MW;  7C658AB7716112B2 CRC64;

  Query Match             32.4%;  Score 873;  DB 1;  Length 219;
  Best Local Similarity   86.4%;  Pred. No. 8.8e-61;
  Matches  171;  Conservative    7;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        314 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 373
              :||||  || |||| ||:||| ||||||| ||||||||| | ||||||||||||||||||
Db         22 ARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTST 81

Qy        374 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 433
              |||||||||| ||||| ||| | ||||||||| | |||  ||||||||||||||:||| |
Db         82 VEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM 141

Qy        434 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 493
              ||||||||||||||||||  ||||:||||||| ||||||||||||||||||||||||||||
Db        142 NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHA 201

Qy        494 FRIRAVTINRMMSYLNSS 511
              ||||||||:|:|||||:|
Db        202 FRIRAVTIDRVMSYLNAS 219


Search completed: July 15, 2003, 11:07:04
Job time : 12.1987 secs
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:57:19 ; Search time 45.2816 Seconds
(without alignments)
2325.231 Million cell updates/sec

Title: US-09-917-265-67
Perfect score: 2693
Sequence: 1 IWELEKDVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNSS 511

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1272.5	47.3	332	11	Q924V5	Q924v5 cavia porce
2	1268	47.1	327	11	Q9ET05	Q9et05 marmota mon
3	1208	44.9	327	11	Q91ZK7	Q91zk7 sigmodon hi
4	1065.5	39.6	335	11	Q9R278	Q9r278 rattus norv
5	1063.5	39.5	335	11	Q9QUM1	Q9qum1 mus musculu
6	944	35.1	195	6	Q95N82	Q95n82 canis famil
7	940	34.9	268	11	Q62712	Q62712 rattus norv
8	927.5	34.4	344	11	Q924K7	Q924k7 meriones un
9	873	32.4	253	4	O60595	O60595 homo sapien
10	818	30.4	174	6	Q28232	Q28232 cervus elap
11	799	29.7	150	6	Q9BG70	Q9bg70 canis famil
12	770.5	28.6	221	11	Q924V6	Q924v6 cavia porce
13	768	28.5	149	6	Q9TV09	Q9tv09 canis famil
14	727.5	27.0	169	11	Q9Z1Y8	Q9z1y8 cavia porce
15	695	25.8	143	6	O62779	O62779 felis silve
16	643	23.9	215	11	Q91ZK6	Q91zk6 sigmodon hi
17	610.5	22.7	223	11	Q9ET04	Q9et04 marmota mon
18	558	20.7	215	11	Q9R103	Q9r103 rattus norv
19	525	19.5	210	11	Q924K6	Q924k6 meriones un
20	507	18.8	132	11	O70328	O70328 mesocricetu
21	441	16.4	94	6	O62777	O62777 felis silve
22	429.5	15.9	111	11	P97731	P97731 rattus sp.
23	272	10.1	61	6	Q9MYW1	Q9myw1 bos taurus
24	223	8.3	116	11	Q9QUT1	Q9qut1 mus musculu
25	176	6.5	372	11	O88507	O88507 mus musculu
26	170	6.3	432	11	P70225	P70225 mus musculu
27	159.5	5.9	422	4	Q16542	Q16542 homo sapien
28	157	5.8	432	11	Q64385	Q64385 mus musculu
29	156	5.8	431	11	Q99MF4	Q99mf4 rattus norv
30	143	5.3	812	10	Q9C6J9	Q9c6j9 arabidopsis
31	129.5	4.8	229	4	Q14213	Q14213 homo sapien
32	127.5	4.7	622	6	Q9N0J7	Q9n0j7 callithrix
33	123.5	4.6	739	11	Q63669	Q63669 rattus norv
34	122.5	4.5	1277	13	Q98902	Q98902 fugu rubrip
35	120	4.5	1197	13	Q90478	Q90478 brachydanio
36	118.5	4.4	229	4	O75269	O75269 homo sapien
37	116.5	4.3	978	6	Q9XS93	Q9xs93 canis famil
38	116	4.3	455	4	Q9UIR0	Q9uir0 homo sapien
39	116	4.3	626	5	Q22040	Q22040 caenorhabdi
40	115.5	4.3	1148	13	Q9IBA7	Q9iba7 gallus gall
41	115	4.3	628	11	Q9JKG1	Q9jkg1 cavia porce
42	114	4.2	838	13	Q90YM1	Q90ym1 brachydanio
43	113	4.2	428	5	Q8WPM7	Q8wpm7 oikopleura
44	113	4.2	731	6	Q8SPI6	Q8spi6 macropus eu
45	113	4.2	1146	13	Q9I8V6	Q9i8v6 gallus gall

ALIGNMENTS

RESULT 1
Q924V5
ID Q924V5 PRELIMINARY; PRT; 332 AA.
AC Q924V5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Interleukin-12 p40 subunit (IL-12 p40).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HARTLEY;
RA Shiratori I., Matsumoto M., Tsuji S., Nomura M., Toyoshima K.,
RA Seya T.;
RT "Molecular cloning and functional characterization of guinea pig
RT Interleukin -12.";
RL Int. Immunol. 0:0-0(2001).
DR EMBL; AB025724; BAB63963.1; -.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ SEQUENCE 332 AA; 37632 MW; B75D16B23DE8B9B4 CRC64;

Query Match 47.3%; Score 1272.5; DB 11; Length 332;
Best Local Similarity 77.7%; Pred. No. 4.8e-100;
Matches 240; Conservative 22; Mismatches 40; Indels 7; Gaps 3;

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Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||:|||||||||||| ||||| |||||:| ||| ||||| : |::|||||||||||||
Db         23 MWELKKDVYVVELDWHTDAPGETVVLTCNTAEEDGITWTSDRKSDILGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
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Db         83 EDAGGYTCHKGGEVLSRSQLLLHKKEDEIWSTDILKEQKGSNGKTFLKCEARSYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Db        143 WWLTAFGTDVKFSVKGSRGSSDPSGVTCG----EAERVSGDNQEY-KYSVECQEDSACPT 197

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Db        198 AEESLPIEVVVDAIHKFKYENYTSSFYIRDIIKPDPPKNLQLKPSVNSQQVEVSWEYPDT 257

Qy        241 WSTPHSYFSLTFCIQAQG--KNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSW 298

Db        258 WSTPHSYFSLTFLVQTHGKNKNRREKKYELFTDKTSATVSCHKISKVEVRARDRYYSSSW 317

Qy        299 SDWASVSCS 307

Db        318 SEWASVSCS 326


RESULT 2
Q9ET05
ID   Q9ET05      PRELIMINARY;      PRT;   327 AA.
AC   Q9ET05;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p40 subunit.
OS   Marmota monax (Woodchuck).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;
OC   Marmota.
OX   NCBI_TaxID=9995;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21424491; PubMed=11533170;
RA   Garcia-Navarro R., Blanco-Urgoiti B., Berraondo P.,
RA   Sanchez De La Rosa R., Vales A., Hervas-Stubbs S., Lasarte J.J.,
RA   Borras F., Ruiz J., Prieto J.;
RT   "Protection against Woodchuck Hepatitis Virus (WHV) Infection by Gene
RT   Gun Coimmunization with WHV Core and Interleukin-12.";
RL   J. Virol. 75:9068-9076(2001).
DR   EMBL; AF288519; AAG01023.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003599; Ig.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00041; fn3; 1.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00409; IG; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   327 AA;  37140 MW;  42782B3559C224DD CRC64;

  Query Match           47.1%;  Score 1268;  DB 11;  Length 327;
  Best Local Similarity  75.5%;  Pred. No. 1.1e-99;
  Matches  231;  Conservative   34;  Mismatches   39;  Indels    2;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60

Db         23 IWELEKNVYVVELDWHPDTPGETVVLTCDTPEEDGITWTSEQSSEVLGSGKTLTILVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120

Db         83 EDAGHYTCHRGGEVLSQMLLLLHKNEDGIWSTDILK-KKEPENKNLVTCEAKNYSGRFTC 141

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Db        142 WWLTAISTDVKFSVKSHRGSSDPQGVTCGEATLSAERVKIEQREYKKYSVQCQEDNACPT 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Db        202 AEETLPITVVVDAVHKLKYENYISSFFIRDIIKPDPPKNLKMKPSKTPQQVEVTWEYPDS 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300

Db        262 WSTPHSYFSLTFSVQVQGK-KKKRSNTLHVDKTSVTVTCQKGAKVSVQARDRYYNSSWSE 320

Qy        301 WASVSC 306

Db        321 WATMSC 326


RESULT 3
Q91ZK7
ID   Q91ZK7      PRELIMINARY;      PRT;   327 AA.
AC   Q91ZK7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 12 p40 subunit.
OS   Sigmodon hispidus (Hispid cotton rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC   Sigmodon.
OX   NCBI_TaxID=42415;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pletneva L.M., Bacot S., Blanco J.C., Langley R.J., Prince G.A.;
RT   "Sigmodon hispidus cytokines, chemokines and interferons.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF421395; AAL16936.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ   SEQUENCE   327 AA;  37119 MW;  F096702CC950FD56 CRC64;

  Query Match           44.9%;  Score 1208;  DB 11;  Length 327;
  Best Local Similarity  72.7%;  Pred. No. 1.4e-94;
  Matches  224;  Conservative   34;  Mismatches   46;  Indels    4;  Gaps    3;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60

Db         23 IWELEKDVYVVEVDWSPGAPGERVVLTCDTSEEDDIIWTSDQSSEVVGSGKTLIVQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120

Db         83 SDAGQYTCHKGGETLSHSRLLLHKKEDGIWSTDILKDQKDPKNKTFLKCEAANYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Db        143 WWLTAVSTDLKFSLKSSSSSSDSRSVTCGAASLSTEKVTVDQRDYNKYSVACQEDITCPT 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Db        203 AEETLPIELVMEAQHKYKYENYSTGFFIRDIIKPDPPKNLQLKPLKSSQ-VEVSWEYPDS 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKK-DRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWS 299

Db        262 WSTPHSYFSLKFFVQVYRK--KEKKGESLLVDKPSAKIRCSKGGEVRVRAQDHYYNSSWS 319

Qy        300 DWASVSCS 307

Db        320 EWASVSCN 327


RESULT 4
Q9R278
ID   Q9R278      PRELIMINARY;      PRT;   335 AA.
AC   Q9R278;
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DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p40.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER;
RX   MEDLINE=98273736; PubMed=9613680;
RA   Khalife J., Pierrot C., Cocude C., Cetre C., Godin C., Capron A.;
RT   "Molecular cloning and sequencing of the rat interleukin-12 p40
RT   gene.";
RL   Eur. Cytokine Netw. 9:69-73(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER;
RA   Khalife J., Pierrot C., Cocude C., Cetre C., Godin C., Capron A.;
RL   Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF133197; AAD24190.1; -.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   335 AA;  38413 MW;  39BF5B49AF191007 CRC64;

  Query Match             39.6%;  Score 1065.5;  DB 11;  Length 335;
  Best Local Similarity   64.9%;  Pred. No. 2e-82;
  Matches  205;  Conservative   38;  Mismatches   60;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| :|||||||||| |   |:|||||||| |:||
Db         23 MWELEKDVYVVEVDWRPDAPGETVTLTCDSPEEDDITWTSDQRRGVIGSGKTLTITVREF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||:||: || | ||:||||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHRGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||   :|||||::|||    : : |||| :||||:| :: |||:||:| |||   ||:
Db        140 SWLVHRNTDLKFNIKSSSSSPESRAVTCGRASLSAEKVTLNQRDYEKYSVACQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:||||:||:|  : |||||::||||||||||||| |||:|||||: ||||||||:
Db        200 AEETLPIELVVEAQQQNKYENYSTSFFIRDIIKPDPPKNLQVKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |  : |        |    |:||||:| | | | | |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKTKETEEECNQKGAFLVEKTSAEVQC-KGANICVQAQDR 317

Qy        293 YYSSSWSDWASVSCSG 308
              ||:|| | |  | | |
Db        318 YYNSSCSKWTCVPCRG 333


RESULT 5
Q9QUM1
ID   Q9QUM1      PRELIMINARY;      PRT;   335 AA.
AC   Q9QUM1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin 12B P40 subunit.
GN   IL12B OR LL12B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SJL/J, AND B10.S/J; TISSUE=SPLEEN;
RA   Ma R.Z., Teuscher C.;
RT   "Screening for candidate genes of mouse autoimmnue diseases.";
RL   Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF128215; AAF22556.1; -.
DR   EMBL; AF128214; AAF22555.1; -.
DR   MGD; MGI:96540; Il12b.
DR   InterPro; IPR002996; CR1A.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW   Immunoglobulin domain.
SQ   SEQUENCE   335 AA;  38171 MW;  7D061E116C00FC4A CRC64;

  Query Match             39.5%;  Score 1063.5;  DB 11;  Length 335;
  Best Local Similarity   65.3%;  Pred. No. 3e-82;
  Matches  205;  Conservative   35;  Mismatches   61;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| ||||||||||| |   |:|||||||| ||||
Db         23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||: || | ||:||||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||   : ||||::|||    | : ||||  :||||:| :| |||:||:| |||   ||:
Db        140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGTASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:||||: ::|  : |||||::||||||||||||| |||:|||||: ||||||||:
Db        200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |  : |        |    |:||||:| | | | | |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGALLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
              ||:|| | || | |
Db        318 YYNSSCSKWACVPC 331


RESULT 6
Q95N82
ID   Q95N82      PRELIMINARY;      PRT;   195 AA.
AC   Q95N82;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 subunit p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Fonfara S., Groene A., Koenig M., Baumgaertner W.;
RT   "Sequence of canine interleukin-12-p40 mRNA in DH82-cells.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF349536; AAK54070.1; -.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
FT   NON_TER       1       1
FT   NON_TER     195     195
SQ   SEQUENCE   195 AA;  21943 MW;  46D77A1570B2F8B9 CRC64;
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  Query Match             35.1%;  Score 944;  DB 6;  Length 195;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-72;
  Matches  176;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         20 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 79

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         80 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS 176
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        140 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGS 195


RESULT 7
Q62712
ID   Q62712      PRELIMINARY;      PRT;   268 AA.
AC   Q62712;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin-12p40 (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FISCHER; TISSUE=CULTURED SPLENOCYTES;
RA   Goodman R.E., Toews G.B.;
RT   "A partial cDNA of the coding region of rat IL-12p40, cloned by RT/PCR
RT   from Staphlococcal endotoxin stimulated splenocytes.";
RL   Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U16674; AAA52229.1; -.
DR   InterPro; IPR003598; Ig_c2.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00408; IGc2; 1.
KW   Immunoglobulin domain.
FT   NON_TER     268     268
SQ   SEQUENCE   268 AA;  30644 MW;  9370D4CD28D9C73F CRC64;

  Query Match             34.9%;  Score 940;  DB 11;  Length 268;
  Best Local Similarity   70.4%;  Pred. No. 7.1e-72;
  Matches  176;  Conservative   31;  Mismatches   39;  Indels    4;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| :|||||||||| |   |:|||||||| |:||
Db         23 MWELEKDVYVVEVDWRPDAPGETVTLTCDSPEEDDITWTSDQRRGVIGSGKTLTITVREF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||:||: || | ||:||||:|||||:||   |  ||| ||| || ||||||||
Db         83 LDAGQYTCHRGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKREAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||   :|||||::|||    : : ||||| :||||:| :: |||:||:| |||   ||:
Db        140 SWLVHRNTDLKFNIKSSSSSPESRAVTCGAASLSAEKVTLNQRDYEKYSVACQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:||||:||:|  : |||||::|||||||||||| |||:|||||: |||||||||:
Db        200 AEETLPIELVVEAQQQNKYENYSTSFFIRDIIKPDPPKNLQVKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSL 250
              ||||||||||
Db        259 WSTPHSYFSL 268


RESULT 8
Q924K7
ID   Q924K7      PRELIMINARY;      PRT;   344 AA.
AC   Q924K7;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Interleukin-12 p40 subunit.
OS   Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC   Meriones.
OX   NCBI_TaxID=10047;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Gaucher D., Chadee K.;
RT   "Molecular cloning of gerbil interleukin-12, and its expression as a
RT   bioactive single-chain protein.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288612; AAK83061.1; -.
DR   InterPro; IPR003961; FN_III.
DR   InterPro; IPR003530; Hemtopoptn_L_F3.
DR   InterPro; IPR003006; Ig_MHC.
DR   Pfam; PF00047; ig; 1.
DR   SMART; SM00060; FN3; 1.
DR   PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
SQ   SEQUENCE   344 AA;  39375 MW;  21B513448D73E8CB CRC64;

  Query Match             34.4%;  Score 927.5;  DB 11;  Length 344;
  Best Local Similarity   56.6%;  Pred. No. 1.1e-70;
  Matches  184;  Conservative   51;  Mismatches   67;  Indels   23;  Gaps    8;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||:|||||:||   |  | ||||| | || |||||  |:::|  ||||:||:||:|
Db         23 IWELEKNVYVVEMDWRSGA-NESVVLTCDTSEEGDITWTKDQTTKVEQSGKTVTIEVKDF 81

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              :|||||||| : ||   ||:|||::| || :|||: | |:|: ||||||  ||||||||
Db         82 NEAGQYTCHKGDQTLSHFRLLLHKKKNGYWSNEILKQDKNSENQTFLKCEAANYSGRFTC 141

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRD--YKKYTVECQEGSAC 178
              ||    ||||||:|:|    | : ||||||:|:|||:|: | :|   |:|:| |||   |
Db        142 SWLVE-RTDLKFSIKNSSSSPDSRAVTCGAVSLTAEKVKGDEKDGKLKQYSVTCQEDITC 200

Qy        179 PSAEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYP 238
              |:|||::|| :|::|  : |||||:|||||||| |||| ||::||||| : ||||||||
Db        201 PTAEETVPIGLVLEAQEQNKYENYSTSFFIRDIITPDPPKNLKVKPLKNDK-VEVSWEYP 259

Qy        239 DTWSTPHSYFSLTFCIQAQG---------KNNREKKDR-LC-------VDKTSAKVVCHK 281
              |:|||||||:| | :  :           :|:| | |  |       || || || | |
Db        260 DSWSTPHSYFALKFYVWTESNKENKMRNTNSNKENKMRNACIQNGTWLVDTTSTKVRC-K 318

Qy        282 DAKIRVQARDRYYSSSWSDWASVSC 306
              | :: |:|:||||:| :|  | | |
Db        319 DGRVCVEAQDRYYNSLYSKHACVPC 343


RESULT 9
O60595
ID   O60595         PRELIMINARY;   PRT;   253 AA.
AC   O60595;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin 12 (Interleukin-12 P35 subunit).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Liu Y., Guo Y., Wu M.;
RT   "Human Interleukin-12 (or Natural Killer Cell Stimulatory Factor, or
RT   Cytotoxic Lymphocyte Maturation Factor) 35kDa subunit mRNA.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
```

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RP   SEQUENCE OF 1-39 FROM N.A.
RC   TISSUE=PLACENTA;
RA   Hayes M.P., Murphy F.J., Burd P.R.;
RL   Blood 0:0-0(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Hongyuan J., Meiyun Z.;
RT   "Cloning and sequence analysis of IL-12 cDNA from Chinese.";
RL   Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF101062; AAD16432.1; -.
DR   EMBL; AF050083; AAC05211.1; -.
DR   EMBL; AF180562; AAD56385.1; -.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
FT   VARIANT     247    247       M -> T.
SQ   SEQUENCE   253 AA;  28293 MW;  FAC56ACD2A620BD5 CRC64;

  Query Match             32.4%;  Score 873;  DB 4;  Length 253;
  Best Local Similarity   86.4%;  Pred. No. 3.3e-66;
  Matches  171;  Conservative    7;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        314 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 373
              :|||| || |||| ||:||| ||||||| |||||||| | ||||||||||||||||||
Db         56 ARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTST 115

Qy        374 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 433
              |||||||||| ||||| ||| | |||||||| | |||  ||||||||||||:||| |
Db        116 VEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM 175

Qy        434 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 493
              |||||||||||||||||| ||||:||||||| ||||||||||||||||||||||||||
Db        176 NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHA 235

Qy        494 FRIRAVTINRMMSYLNSS 511
              ||||||||:|:|||||:|
Db        236 FRIRAVTIDRVMSYLNAS 253


RESULT 10
Q28232
ID   Q28232      PRELIMINARY;      PRT;   174 AA.
AC   Q28232;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 (Fragment).
GN   IL-12.
OS   Cervus elaphus (Red deer).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidea;
OC   Cervidae; Cervinae; Cervus.
OX   NCBI_TaxID=9860;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Lockhart E.A.;
RT   "Cloning and sequencing of cervine IL-12.";
RL   Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U10160; AAA19658.1; -.
DR   InterPro; IPR002996; CR1A.
FT   NON_TER       1      1
FT   NON_TER     174    174
SQ   SEQUENCE   174 AA;  19684 MW;  389260B3A9067F2E CRC64;

  Query Match             30.4%;  Score 818;  DB 6;  Length 174;
  Best Local Similarity   86.8%;  Pred. No. 9.5e-62;
  Matches  151;  Conservative   14;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         63 AGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWW 122
              ||||||||||:|||||||:|||||||||||||:||| | | |||||||:||| |||||
Db          1 AGQYTCHKGGEVLSRSLLLLHKKEDGIWSTDILKDQKEPKAKSFLKCEAKDYSGHFTCWW 60

Qy        123 LTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAE 182
              |||||||||||||||| |||:||||||::|| |:| ||:|:|||||||||||||:||
Db         61 LTAISTDLKFSVKSSRGSSDPRGVTCGAMSLSTEKVIVDHREYKKYTVECQEGSACPAAE 120

Qy        183 ESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWE 236
              |||||||||:|:|||||||||||||||||||||| ||||:|||||| ||||||
Db        121 ESLPIEVVVEAVHKLKYENYTSSFFIRDIIKPDPPKNLQLRPLKNSRQVEVSWE 174


RESULT 11
Q9BG70
ID   Q9BG70      PRELIMINARY;      PRT;   150 AA.
AC   Q9BG70;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE   Interleukin 12 subunit p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Markus S., Baumgaertner W.;
RT   "Expression of canine interleukin-12 subunit p40 mRNA in a continuous
RT   macrophage cell line.";
RL   Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF333121; AAK01441.1; -.
DR   InterPro; IPR003600; Ig_like.
DR   SMART; SM00410; IG_like; 1.
FT   NON_TER       1      1
FT   NON_TER     150    150
SQ   SEQUENCE   150 AA;  16780 MW;  A867903EF16083BA CRC64;

  Query Match             29.7%;  Score 799;  DB 6;  Length 150;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-60;
  Matches  150;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         27 TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKE 86
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 TCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKE 60

Qy         87 DGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGV 146
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 DGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGV 120

Qy        147 TCGAVTLSAERVRVDNRDYKKYTVECQEGS 176
              |||||||||||||||||||||||||||||
Db        121 TCGAVTLSAERVRVDNRDYKKYTVECQEGS 150


RESULT 12
Q924V6
ID   Q924V6      PRELIMINARY;      PRT;   221 AA.
AC   Q924V6;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Interleukin-12 p35 subunit (IL-12 p35).
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=HARTLEY;
RA   Shiratori I., Matsumoto M., Tsuji S., Nomura M., Toyoshima K.,
RA   Seya T.;
RT   "Molecular cloning and functional characterization of guinea pig
RT   Interleukin -12.";
RL   Int. Immunol. 0:0-0(2001).
DR   EMBL; AB025723; BAB63962.1; -.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
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DR   InterPro; IPR004281; IL12.
DR   Pfam; PF03039; IL12; 1.
DR   PROSITE; PS00339; AA_TRNA_LIGASE_II_2; UNKNOWN_1.
SQ   SEQUENCE   221 AA;  24687 MW;  972E59F5A11DE896 CRC64;

  Query Match           28.6%;  Score 770.5;  DB 11;  Length 221;
  Best Local Similarity   74.3%;  Pred. No. 1.4e-57;
  Matches  156;  Conservative   19;  Mismatches   28;  Indels    7;  Gaps    2;

Qy        304 VSCSGGGGGGSRNLPTPTPSP--GMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEI 361
              ||||      :||||  :|:|     || |||||||||:: | || | | :|||| |||
Db         17 VSCS-----LARNLPRASPAPVTEPVQCFNHSQTLLRAVNSELHKAIQMLAVYSCTPEEI 71

Qy        362 DHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYE 421
              ||||||||||||||:||:||||  |||||||  .||  ||||||||||| |||  |||:||||
Db         72 DHEDITKDKTSTVKACVPLELVKNESCLASGHISFTTNGSCLASGKTSFMMALCLNSIYE 131

Qy        422 DLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFY 481
              |||:||:||| |||:|||||:||||||||||:|||||:|||| : |||||| ||||||||
Db        132 DLKLYQLEFKNMNAQLLMDPQRQIFLDQNMLSAIDELIQALNGSDVTVPQKLSLEEPDFY 191

Qy        482 KTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              | |:||||||||||||||:|:|||| ||
Db        192 KIKMKLCILLHAFRIRAVTIDRVMSYLTSS 221


RESULT 13
Q9TV09
ID   Q9TV09      PRELIMINARY;      PRT;   149 AA.
AC   Q9TV09;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE   Interleukin-12 p40 (Fragment).
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   German A.J., Helps C.R., Harley R., Hall E.J., Day M.J.;
RT   "Cloning and sequencing of canine IL-12 p40 mRNA.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF091134; AAD46992.1; -.
FT   NON_TER       1      1
FT   NON_TER     149    149
SQ   SEQUENCE   149 AA;  16453 MW;  20E2686B0AA37E26 CRC64;

  Query Match           28.5%;  Score 768;  DB 6;  Length 149;
  Best Local Similarity   98.6%;  Pred. No. 1.4e-57;
  Matches  146;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         47 LGSGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIF 106
              ||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LGAGKTLTIQVKEFGDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIF 60

Qy        107 LKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYK 166
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LKCEAKNYSGRFTCWWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYN 120

Qy        167 KYTVECQEGSACPSAEESLPIEVVVDAI 194
              |||||||||||||||||||||||||||
Db        121 KYTVECQEGSACPSAEESLPIEVVVDAI 148


RESULT 14
Q9Z1Y8
ID   Q9Z1Y8      PRELIMINARY;      PRT;   169 AA.
AC   Q9Z1Y8;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE   Interleukin 12p40 (Fragment).
OS   Cavia porcellus (Guinea pig).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX   NCBI_TaxID=10141;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99069279; PubMed=9824482;
RA   Wicher V., Scarozza A.M., Ramsingh A.I., Wicher K.;
RT   "Cytokine gene expression in skin of susceptible guinea-pig infected
RT   with Treponema pallidum.";
RL   Immunology 95:242-247(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99144670; PubMed=10025978;
RA   Scarozza A.M., Ramsingh A.I., Wicher V., Wicher K.;
RT   "Spontaneous cytokine gene expression in normal guinea pig blood and
RT   tissues.";
RL   Cytokine 10:851-859(1998).
DR   EMBL; AF097507; AAC83805.1; -.
FT   NON_TER       1      1
FT   NON_TER     169    169
SQ   SEQUENCE   169 AA;  19128 MW;  0A2DE7480C1281F5 CRC64;

  Query Match           27.0%;  Score 727.5;  DB 11;  Length 169;
  Best Local Similarity   79.3%;  Pred. No. 4.6e-54;
  Matches  138;  Conservative   11;  Mismatches   20;  Indels    5;  Gaps    2;

Qy         69 HKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIST 128
              ||||:||||| ||:||||| |||||||||| |  | ||||||::||||||||||||  |
Db          1 HKGGEVLSRSQLLLHKKEDEIWSTDILKEQKGSNGKTFLKCEARSYSGRFTCWWLTAFGT 60

Qy        129 DLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPIE 188
              |:||||| ||| ||| |||||     ||||  ||::| ||:||||| ||||:||||||||
Db         61 DVKFSVKGSRGSSDPSGVTCG----EAERVSGDNQEY-KYSVECQEDSACPTAEESLPIE 115

Qy        189 VVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDTWS 242
              |||||||| |||||||||:|||||||||| ||||||  ||: ||||||||||||
Db        116 VVVDAIHKFKYENYTSSFYIRDIIKPDPPKNLQLKPSVNSQQVEVSWEYPDTWS 169


RESULT 15
O62779
ID   O62779      PRELIMINARY;      PRT;   143 AA.
AC   O62779;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Interleukin 12 p40 subunit (Fragment).
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99322318; PubMed=10391845;
RA   Harley R., Helps C.R., Harbour D.A., Gruffydd-Jones T.J., Day M.J.;
RT   "Cytokine mRNA expression in lesions in cats with chronic
RT   gingivostomatitis.";
RL   Clin. Diagn. Lab. Immunol. 6:471-478(1999).
DR   EMBL; AF054607; AAC15980.1; -.
DR   InterPro; IPR002996; CRlA.
FT   NON_TER       1      1
FT   NON_TER     143    143
SQ   SEQUENCE   143 AA;  16122 MW;  E107DF253F5D4D40 CRC64;

  Query Match           25.8%;  Score 695;  DB 6;  Length 143;
  Best Local Similarity   90.9%;  Pred. No. 2.1e-51;
  Matches  130;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy         68 CHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTCWWLTAIS 127
              |||| :||| | :|| :|||||||||||:|||||||||||||||||||||||||||||||
Db          1 CHKGXEVLSHSXVLIXEKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTCWWLTAIS 60
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Qy        128 TDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPSAEESLPI 187
              |||||:|||||| |||||||||| |||||:|||||||||||||||||||||:|||||||
Db         61 TDLKFTVKSSRGSSDPQGVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPAAEESLPI 120

Qy        188 EVVVDAIHKLKYENYTSSFFIRD 210
              |||||||||||||||||||||||
Db        121 EVVVDAIHKLKYENYTSSFFIRD 143


Search completed: July 15, 2003, 11:06:11
Job time : 45.2816 secs
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OM protein - protein search, using sw model

Run on: July 15, 2003, 10:59:19 ; Search time 17.5283 Seconds
(without alignments)
857.760 Million cell updates/sec

Title: US-09-917-265-67
Perfect score: 2693
Sequence: 1 IWELEKDVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNSS 511

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2309.5	85.8	519	2	US-08-751-767A-12	Sequence 12, Appl
2	2309.5	85.8	540	2	US-08-751-767A-8	Sequence 8, Appli
3	2309.5	85.8	540	2	US-08-751-767A-10	Sequence 10, Appl
4	1418.5	52.7	306	1	US-08-424-682A-1	Sequence 1, Appli
5	1418.5	52.7	328	1	US-08-265-087-2	Sequence 2, Appli
6	1418.5	52.7	328	1	US-08-186-529-2	Sequence 2, Appli
7	1418.5	52.7	328	1	US-08-621-493-2	Sequence 2, Appli
8	1418.5	52.7	328	1	US-08-640-386A-2	Sequence 2, Appli
9	1418.5	52.7	328	2	US-08-965-688-2	Sequence 2, Appli
10	1418.5	52.7	328	2	US-08-751-767A-4	Sequence 4, Appli
11	1418.5	52.7	328	4	US-09-260-173-2	Sequence 2, Appli
12	1058.5	39.3	335	2	US-08-385-335A-15	Sequence 15, Appl
13	1049.5	39.0	335	2	US-08-659-206A-3	Sequence 3, Appli
14	1049.5	39.0	335	2	US-08-659-206A-6	Sequence 6, Appli
15	873	32.4	219	1	US-08-186-529-4	Sequence 4, Appli
16	873	32.4	219	1	US-08-640-386A-4	Sequence 4, Appli
17	873	32.4	253	1	US-08-265-087-4	Sequence 4, Appli
18	873	32.4	253	1	US-08-621-493-4	Sequence 4, Appli
19	873	32.4	253	2	US-08-684-687-4	Sequence 4, Appli
20	873	32.4	253	2	US-08-965-688-4	Sequence 4, Appli
21	873	32.4	253	4	US-09-260-173-4	Sequence 4, Appli
22	867	32.2	219	2	US-08-751-767A-2	Sequence 2, Appli
23	549	20.4	215	2	US-08-385-335A-12	Sequence 12, Appl
24	549	20.4	215	2	US-08-659-206A-2	Sequence 2, Appli
25	549	20.4	215	2	US-08-659-206A-5	Sequence 5, Appli
26	211.5	7.9	468	4	US-08-795-473B-5	Sequence 5, Appli
27	211.5	7.9	468	4	US-09-439-856-5	Sequence 5, Appli
28	211.5	7.9	468	6	5171840-2	Patent No. 5171840
29	211.5	7.9	468	6	5480796-2	Patent No. 5480796
30	193	7.2	323	6	5171840-6	Patent No. 5171840
31	193	7.2	323	6	5480796-6	Patent No. 5480796
32	193	7.2	344	6	5171840-7	Patent No. 5171840
33	193	7.2	344	6	5480796-7	Patent No. 5480796
34	170	6.3	372	1	US-07-865-878A-4	Sequence 4, Appli
35	170	6.3	372	1	US-07-676-647-2	Sequence 2, Appli
36	170	6.3	372	1	US-08-449-329-2	Sequence 2, Appli
37	170	6.3	372	2	US-08-445-073-2	Sequence 2, Appli
38	170	6.3	372	2	US-08-585-258-2	Sequence 2, Appli
39	170	6.3	372	2	US-08-603-010-4	Sequence 4, Appli
40	170	6.3	372	4	US-09-211-590-2	Sequence 2, Appli
41	170	6.3	372	5	PCT-US91-03896-2	Sequence 2, Appli
42	159.5	5.9	422	4	US-09-151-102-2	Sequence 2, Appli
43	159.5	5.9	422	4	US-08-929-846-2	Sequence 2, Appli
44	157	5.8	432	4	US-08-702-665A-3	Sequence 3, Appli
45	157	5.8	441	4	US-09-151-102-4	Sequence 4, Appli

ALIGNMENTS

```
RESULT 1
US-08-751-767A-12
; Sequence 12, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  519 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-12

  Query Match             85.8%;  Score 2309.5;  DB 2;  Length 519;
  Best Local Similarity   84.4%;  Pred. No. 3.8e-211;
  Matches  438;  Conservative   27;  Mismatches   45;  Indels    9;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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Db          2 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 61

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
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Db         62 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 121

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| ||||||||| |||||||| ||::| :|:||||| ||||:
Db        122 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 180

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| ||||||||||
Db        181 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 240

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        241 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 300

Qy        301 WASVSCSGG--------GGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLE 352
              |||| ||||        |||||||||  || |||| ||:||| ||||||| |||||||||
Db        301 WASVPCSGGGGSGGGGSGGGGSRNLPLATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLE 360

Qy        353 LYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMT 412
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Db        361 FYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMM 420

Qy        413 VLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQK 472
              ||||||||||||||:||| ||||||||||||||||||  ||||:||||||| |||||
Db        421 ALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQK 480

Qy        473 SSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
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Db        481 SSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNAS 519


RESULT 2
US-08-751-767A-8
; Sequence 8, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  540 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-8

  Query Match             85.8%;  Score 2309.5;  DB 2;  Length 540;
  Best Local Similarity   84.4%;  Pred. No. 4e-211;
  Matches  438;  Conservative   27;  Mismatches   45;  Indels    9;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| ||||:|||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| ||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG--------GGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLE 352
              |||| ||||        |||||||||  || |||| ||:||| ||||||| |||||||||
Db        322 WASVPCSGGGGSGGGGSGGGGSRNLPLATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLE 381

Qy        353 LYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMT 412
              | |||||||||||||||||||||||||||| ||||| ||| | |||||||||| | |||
Db        382 FYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMM 441

Qy        413 VLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQK 472
              ||||||||||||||:||| ||||||||||||||||||  ||||:||||||| |||||
Db        442 ALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQK 501

Qy        473 SSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
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Db        502 SSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNAS 540


RESULT 3
US-08-751-767A-10
; Sequence 10, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
```

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;       TELEFAX:  7038164100
;   INFORMATION FOR SEQ ID NO:  10:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  540 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-751-767A-10

  Query Match             85.8%;  Score 2309.5;  DB 2;  Length 540;
  Best Local Similarity   84.4%;  Pred. No. 4e-211;
  Matches  438;  Conservative   27;  Mismatches   45;  Indels    9;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||||:||| ||||:||||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||:::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| ||||: |||||:  ||||| |:| |:| | |:|:||||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG--------GGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLE 352
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Db        322 WASVPCSGGGGSGGGGSGGGGSRNLPLATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLE 381

Qy        353 LYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMT 412
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Db        382 FYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMM 441

Qy        413 VLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQK 472
              |||||||||||||:||| |||||||||||||||||||  ||||:||||||| |||||
Db        442 ALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQK 501

Qy        473 SSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
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Db        502 SSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVTSYLNAS 540


RESULT 4
US-08-424-682A-1
; Sequence 1, Application US/08424682A
; Patent No. 5650492
;  GENERAL INFORMATION:
;    APPLICANT:  Gately, Maurice K
;    APPLICANT:  Hakimi, John
;    APPLICANT:  Ling, Ping
;    TITLE OF INVENTION:  P40 HOMODIMER OF INTERLEUKIN-12
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  United States of America
;      ZIP:  07110-1199
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/424,682A
;      FILING DATE:  18-APR-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/087,832
;      FILING DATE:  02-JUL-1993
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kass, Alan P
;      REGISTRATION NUMBER:  32142
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4205
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  306 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-424-682A-1

  Query Match             52.7%;  Score 1418.5;  DB 1;  Length 306;
  Best Local Similarity   85.0%;  Pred. No. 9.9e-127;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||
Db          1 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 60

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||||:||| ||||:||||||||||||||:||| ||| ||:|||||||||||
Db         61 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 120

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||:::| :|:||||| ||||:
Db        121 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 179

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| ||||||||||
Db        180 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 239

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| ||||: |||||:  ||||| |:| |:| | |:|:||||||||||:
Db        240 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 299

Qy        301 WASVSCS 307
              ||||:||
Db        300 WASVPCS 306


RESULT 5
US-08-265-087-2
; Sequence 2, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
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;       APPLICATION NUMBER:  US/08/265,087
;       FILING DATE:
;       CLASSIFICATION:  424
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/229,282
;       FILING DATE:  18-APR-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Bak, Mary E.
;       REGISTRATION NUMBER:  31,215
;       REFERENCE/DOCKET NUMBER:  WST51AUSA
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  215-540-9206
;       TELEFAX:  215-540-5818
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  328 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-265-087-2

  Query Match             52.7%;  Score 1418.5;  DB 1;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.1e-126;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||| ||||:||||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: ||||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 6
US-08-186-529-2
; Sequence 2, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-186-529-2

  Query Match             52.7%;  Score 1418.5;  DB 1;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.1e-126;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||| ||||:||||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: ||||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 7
US-08-621-493-2
; Sequence 2, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
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;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-621-493-2

  Query Match             52.7%;  Score 1418.5;  DB 1;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.1e-126;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| |||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||| ||||:||||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 8
US-08-640-386A-2
; Sequence 2, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-640-386A-2

  Query Match             52.7%;  Score 1418.5;  DB 1;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.1e-126;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| |||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||| ||||:||||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 9
US-08-965-688-2
; Sequence 2, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
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;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-965-688-2

  Query Match             52.7%;  Score 1418.5;  DB 2;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.1e-126;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| ||||:||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| ||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 10
US-08-751-767A-4
; Sequence 4, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  328 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-751-767A-4

  Query Match             52.7%;  Score 1418.5;  DB 2;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.1e-126;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| ||||:||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| ||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
              |||| ||
Db        322 WASVPCS 328


RESULT 11
US-09-260-173-2
; Sequence 2, Application US/09260173
; Patent No. 6168923
;  GENERAL INFORMATION:
;      APPLICANT: Scott, Phillip
;                 Trinchieri, Giorgio
;      TITLE OF INVENTION: Compositions and Methods for Use of
;                          IL-12 as an Adjuvant
;      NUMBER OF SEQUENCES: 4
;      CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Howson and Howson
;           STREET: Spring House Corporate Center, PO Box 457
;           CITY: Spring House
;           STATE: Pennsylvania
;           COUNTRY: USA
;           ZIP: 19477
;      COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/260,173
;           FILING DATE: 01-Mar-1999
;           CLASSIFICATION: <Unknown>
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;                          17-JUN-1994
;                          18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 328 amino acids
;            TYPE: amino acid
;            TOPOLOGY: linear
;       MOLECULE TYPE: protein
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-260-173-2

  Query Match             52.7%;  Score 1418.5;  DB 4;  Length 328;
  Best Local Similarity   85.0%;  Pred. No. 1.1e-126;
  Matches  261;  Conservative   21;  Mismatches   24;  Indels    1;  Gaps    1;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:|||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| ||||:||||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||:::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||| |||||||||| |||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||:| ||||: |||||:  |||| |:| |:| | |:|:||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCS 307
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Db        322 WASVPCS 328


RESULT 12
US-08-385-335A-15
; Sequence 15, Application US/08385335A
; Patent No. 5891680
;  GENERAL INFORMATION:
;    APPLICANT:  Lieschke, Graham J.
;    APPLICANT:  Mulligan, Richard C.
;    TITLE OF INVENTION:  Bioactive Fusion Proteins
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/385,335A
;      FILING DATE:  08-FEB-1995
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Granahan, Patricia
;      REGISTRATION NUMBER:  32,227
;      REFERENCE/DOCKET NUMBER:  WHI95-01
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-861-6240
;      TELEFAX:  617-861-9540
;  1NFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  335 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  unknown
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-385-335A-15

  Query Match             39.3%;  Score 1058.5;  DB 2;  Length 335;
  Best Local Similarity   65.0%;  Pred. No. 2.1e-92;
  Matches  204;  Conservative   35;  Mismatches   62;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| |||||| | ||| |||||||||| |   |:||||||| ||||
Db         23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||: || | ||:||||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||   : ||||::|||    | : ||||  :||||:| :| |||:||:| |||   ||:
Db        140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:||||: ::|  : |||||::|||||||||||||| |||:|||||| ||||||||:
Db        200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |  : |         |    |:||| :| | |   : |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
              ||:|| | || | |
Db        318 YYNSSCSKWACVPC 331


RESULT 13
US-08-659-206A-3
; Sequence 3, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
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;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-3

  Query Match             39.0%;  Score 1049.5;  DB 2;  Length 335;
  Best Local Similarity   64.6%;  Pred. No. 1.5e-91;
  Matches  203;  Conservative   35;  Mismatches   63;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| ||||||  | ||| ||||||||||| |   |:||||||| ||||
Db         23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||: || | ||:||||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||   : ||||::|||    | : ||||  :||||:| :| |||:||:| |||   ||:
Db        140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:|||| :::|  : |||||::|||||||||||| |||:||||||: |||||||||:
Db        200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |  : |        |    |:||| :| | |   : |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
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Db        318 CYNSSCSKWACVPC 331


RESULT 14
US-08-659-206A-6
; Sequence 6, Application US/08659206A
; Patent No. 5922685
;  GENERAL INFORMATION:
;    APPLICANT:  Rakhmilevich, Alexander
;    TITLE OF INVENTION:  IL-12 Gene Therapy of Tumors
;    NUMBER OF SEQUENCES:  6
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Quarles & Brady
;      STREET:  1 South Pinckney Street
;      CITY:  Madison
;      STATE:  WI
;      COUNTRY:  US
;      ZIP:  53703
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/659,206A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seay, Nicholas J
;      REGISTRATION NUMBER:  27386
;      REFERENCE/DOCKET NUMBER:  110229.91144
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  608-251-5000
;      TELEFAX:  608-251-9166
;  INFORMATION FOR SEQ ID NO:  6:
;    SEQUENCE CHARACTERISTICS:
;     LENGTH: 335 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-659-206A-6

  Query Match             39.0%;  Score 1049.5;  DB 2;  Length 335;
  Best Local Similarity   64.6%;  Pred. No. 1.5e-91;
  Matches  203;  Conservative   35;  Mismatches   63;  Indels   13;  Gaps    4;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              :|||||||||||:|| ||||||  | ||| ||||||||||| |   |:||||||| ||||
Db         23 MWELEKDVYVVEVDWTPDAPGETVNLTCDTPEEDDITWTSDQRHGVIGSGKTLTITVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
               |||||||||||: || | ||:||||:|||||:||   |  ||| |||||| ||||||||
Db         83 LDAGQYTCHKGGETLSHSHLLLHKKENGIWSTEIL---KNFKNKTFLKCEAPNYSGRFTC 139

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
               ||   : ||||::|||    | : ||||  :||||:| :| |||:||:| |||   ||:
Db        140 SWLVQRNMDLKFNIKSSSSSPDSRAVTCGMASLSAEKVTLDQRDYEKYSVSCQEDVTCPT 199

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||:|||| :::|  : |||||::|||||||||||| |||:||||||: |||||||||:
Db        200 AEETLPIELALEARQQNKYENYSTSFFIRDIIKPDPPKNLQMKPLKNSQ-VEVSWEYPDS 258

Qy        241 WSTPHSYFSLTFCIQAQGKNNREK--------KDRLCVDKTSAKVVCHKDAKIRVQARDR 292
              |||||||||| | :: | |  : |        |    |:||| :| | |   : |||:||
Db        259 WSTPHSYFSLKFFVRIQRKKEKMKETEEGCNQKGAFLVEKTSTEVQC-KGGNVCVQAQDR 317

Qy        293 YYSSSWSDWASVSC 306
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Db        318 CYNSSCSKWACVPC 331


RESULT 15
US-08-186-529-4
; Sequence 4, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
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;       TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;       LENGTH:  219 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-186-529-4

  Query Match             32.4%;  Score 873;  DB 1;  Length 219;
  Best Local Similarity   86.4%;  Pred. No. 4.7e-75;
  Matches  171;  Conservative    7;  Mismatches   20;  Indels    0;  Gaps    0;

Qy        314 SRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEEIDHEDITKDKTST 373
              :||||  || |||| ||:||| ||||||| ||||||||| | ||||||||||||||||||
Db         22 ARNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEEIDHEDITKDKTST 81

Qy        374 VEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAM 433
              |||||||||| ||||| ||| | ||||||||| | ||| ||||||||||||||:||| |
Db         82 VEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIYEDLKMYQVEFKTM 141

Qy        434 NAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHA 493
              |||||||||||||||||||  |||||:||||||| ||||||||||||||||||||||||||
Db        142 NAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDFYKTKIKLCILLHA 201

Qy        494 FRIRAVTINRMMSYLNSS 511
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Db        202 FRIRAVTIDRVMSYLNAS 219


Search completed: July 15, 2003, 11:10:03
Job time : 18.5283 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 15, 2003, 11:03:04 ; Search time 23.858 Seconds
(without alignments)
2493.521 Million cell updates/sec

Title: US-09-917-265-67
Perfect score: 2693
Sequence: 1 IWELEKDVYVVELDWHPDAP.....HAFRIRAVTINRMMSYLNSS 511

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 445758 seqs, 116419773 residues

Total number of hits satisfying chosen parameters: 445758

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
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14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2693	100.0	511	10	US-09-917-265-67	Sequence 67, Appl
2	2693	100.0	533	10	US-09-917-265-62	Sequence 62, Appl
3	2546	94.5	511	10	US-09-917-265-44	Sequence 44, Appl
4	2546	94.5	533	10	US-09-917-265-39	Sequence 39, Appl
5	2309	85.7	537	10	US-09-828-825-8	Sequence 8, Appli
6	2309	85.7	537	10	US-09-828-825-16	Sequence 16, Appl
7	2306.5	85.6	542	10	US-09-828-825-6	Sequence 6, Appli
8	2306.5	85.6	542	10	US-09-828-825-14	Sequence 14, Appl
9	2304	85.6	547	10	US-09-828-825-10	Sequence 10, Appl
10	2304	85.6	547	10	US-09-828-825-12	Sequence 12, Appl
11	2275	84.5	527	10	US-09-828-825-2	Sequence 2, Appli
12	2271	84.3	526	10	US-09-828-825-4	Sequence 4, Appli
13	1653	61.4	307	10	US-09-917-265-53	Sequence 53, Appl
14	1653	61.4	329	10	US-09-917-265-59	Sequence 59, Appl
15	1653	61.4	329	10	US-09-917-265-108	Sequence 108, App
16	1554	57.7	307	12	US-10-079-616-2	Sequence 2, Appli
17	1554	57.7	329	10	US-09-917-265-30	Sequence 30, Appl
18	1554	57.7	329	12	US-10-079-616-1	Sequence 1, Appli
19	1550	57.6	328	10	US-09-917-265-56	Sequence 56, Appl
20	1546	57.4	307	10	US-09-917-265-27	Sequence 27, Appl
21	1419.5	52.7	328	9	US-10-172-399-8	Sequence 8, Appli
22	1418.5	52.7	328	9	US-10-247-463-6	Sequence 6, Appli
23	1418.5	52.7	328	10	US-09-754-014-1	Sequence 1, Appli
24	1418.5	52.7	328	10	US-09-836-866-1	Sequence 1, Appli
25	1418.5	52.7	328	10	US-09-924-703-4	Sequence 4, Appli
26	1418.5	52.7	503	9	US-09-920-262A-9	Sequence 9, Appli
27	1058.5	39.3	335	9	US-10-172-399-4	Sequence 4, Appli
28	1058.5	39.3	335	9	US-10-247-463-7	Sequence 7, Appli
29	970	36.0	222	10	US-09-917-265-47	Sequence 47, Appl
30	970	36.0	222	10	US-09-917-265-105	Sequence 105, App
31	969	36.0	197	10	US-09-917-265-50	Sequence 50, Appl
32	964	35.8	222	12	US-10-079-616-3	Sequence 3, Appli
33	963	35.8	197	12	US-10-079-616-4	Sequence 4, Appli
34	961	35.7	222	10	US-09-917-265-33	Sequence 33, Appl
35	960	35.6	197	10	US-09-917-265-36	Sequence 36, Appl
36	903	33.5	187	10	US-09-917-265-102	Sequence 102, App
37	873	32.4	253	10	US-09-924-703-6	Sequence 6, Appli
38	867	32.2	219	9	US-10-172-399-6	Sequence 6, Appli
39	867	32.2	219	10	US-09-754-014-5	Sequence 5, Appli
40	867	32.2	219	10	US-09-836-866-3	Sequence 3, Appli
41	549	20.4	215	9	US-10-172-399-2	Sequence 2, Appli
42	211.5	7.9	468	9	US-10-247-463-12	Sequence 12, Appl
43	206	7.6	592	9	US-09-935-868-8	Sequence 8, Appli
44	206	7.6	592	9	US-10-287-035-8	Sequence 8, Appli
45	197	7.3	1168	9	US-09-935-868-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-09-917-265-67
; Sequence 67, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 67
; LENGTH: 511
; TYPE: PRT
; ORGANISM: Canis familiaris
US-09-917-265-67

Query Match 100.0%; Score 2693; DB 10; Length 511;
Best Local Similarity 100.0%; Pred. No. 8.5e-211;
Matches 511; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
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Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
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Db        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300

Qy        301 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEE 360
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Db        301 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEE 360

Qy        361 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIY 420
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Db        361 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIY 420

Qy        421 EDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDF 480
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Db        421 EDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDF 480

Qy        481 YKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
                 |||||||||||||||||||||||||||||||
Db        481 YKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511


RESULT 2
US-09-917-265-62
; Sequence 62, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 62
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-62

  Query Match            100.0%;  Score 2693;  DB 10;  Length 533;
  Best Local Similarity  100.0%;  Pred. No. 9.1e-211;
  Matches  511;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEE 360
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEE 382

Qy        361 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIY 420
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIY 442

Qy        421 EDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDF 480
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        443 EDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDF 502

Qy        481 YKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
                 |||||||||||||||||||||||||||||||
Db        503 YKTKIKLCILLHAFRIRAVTINRMMSYLNSS 533


RESULT 3
US-09-917-265-44
; Sequence 44, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
;   LENGTH: 511
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-44

  Query Match            94.5%;  Score 2546;  DB 10;  Length 511;
  Best Local Similarity  94.3%;  Pred. No. 7.8e-199;
  Matches  482;  Conservative   12;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
                 ||||||:|||||||||||||||||||||:|||||||||| ||||||||||||||||||
Db          1 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 60

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
                 ||||||||||:||| | ||||||||||||||:|||||||||||||||||||||||||||
Db         61 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 120

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
                 ||||||||||||:|||||| |||| ||||| |||||:|||||||||||||||||||||:
Db        121 WWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 180

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
                 |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 240

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
                 |||||||||||:| |||||||||||| ||||||||||||||||||||||||||||||:
Db        241 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 300

Qy        301 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEE 360
                 ||||||||||||||||||||||||||||||||||||:||||||||||| |||||||
Db        301 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEE 360

Qy        361 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIY 420
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Db        361 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIY 420

Qy        421 EDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDF 480
                 |||||||:|||||||||||||||||||||||||||||| |||||||||||||||||||
Db        421 EDLKMYQVEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDF 480

Qy        481 YKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
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Db        481 YKTKIKLCILLHAFRIRAVTINRMMSYLNAS 511


RESULT 4
US-09-917-265-39
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; Sequence 39, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
;   LENGTH: 533
;   TYPE: PRT
;   ORGANISM: Felis catus
US-09-917-265-39

  Query Match             94.5%;  Score 2546;  DB 10;  Length 533;
  Best Local Similarity   94.3%;  Pred. No. 8.3e-199;
  Matches  482;  Conservative   12;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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Db         23 IWELEKNVYVVELDWHPDAPGEMVVLTCNTPEEDDITWTSDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||:||| | |||||||||||||:|||||||||||||||||||||||||||||
Db         83 ADAGQYTCHKGGEVLSHSFLLIHKKEDGIWSTDILREQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||:|||||| |||| ||||| |||||:||||||||||||||||||||||:
Db        143 WWLTAISTDLKFTVKSSRGSSDPQEVTCGAATLSAEKVRVDNRDYKKYTVECQEGSACPA 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPKNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
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Db        263 WSTPHSYFSLTFGVQVQGKNNREKKDRLSVDKTSAKVVCHKDAKIRVQARDRYYSSSWSN 322

Qy        301 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEE 360
              ||||||||||||||||||||||||||||||||||||||:||||||||||| |||||||
Db        323 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAISNTLQKARQTLEFYSCTSEE 382

Qy        361 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIY 420
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Db        383 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIY 442

Qy        421 EDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDF 480
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Db        443 EDLKMYQVEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNVNSVTVPQNSSLEEPDF 502

Qy        481 YKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
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Db        503 YKTKIKLCILLHAFRIRAVTINRMMSYLNAS 533


RESULT 5
US-09-828-825-8
; Sequence 8, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
;   LENGTH: 537
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-8

  Query Match             85.7%;  Score 2309;  DB 10;  Length 537;
  Best Local Similarity   85.1%;  Pred. No. 1.6e-179;
  Matches  439;  Conservative   27;  Mismatches   44;  Indels    6;  Gaps    3;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||||:||| ||||:|||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| |||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
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Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG---GGGGS--RNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYS 355
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Db        322 WASVPCSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYP 381

Qy        356 CTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLC 415
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Db        382 CTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALC 441

Qy        416 LSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSL 475
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Db        442 LSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSL 501

Qy        476 EEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
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Db        502 EEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 537


RESULT 6
US-09-828-825-16
; Sequence 16, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 537
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-16
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  Query Match           85.7%;  Score 2309;  DB 10;  Length 537;
  Best Local Similarity  85.1%;  Pred. No. 1.6e-179;
  Matches  439;  Conservative   27;  Mismatches   44;  Indels    6;  Gaps    3;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||| ||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| |||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
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Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG---GGGGS--RNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYS 355
              |||| ||||   ||||| |||| || |||| ||:||| ||||||| |||||||| |
Db        322 WASVPCSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYP 381

Qy        356 CTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLC 415
              |||||||||||||||||||||||||||| ||||| ||| | |||||||| | |||  ||
Db        382 CTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALC 441

Qy        416 LSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSL 475
              ||||||||||:||| ||||||||||||||||||  ||||:|||||| ||||||||
Db        442 LSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSL 501

Qy        476 EEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              |||||||||||||||||||||||||||:|:|||||:|
Db        502 EEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 537


RESULT 7
US-09-828-825-6
; Sequence 6, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 542
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-6

  Query Match           85.6%;  Score 2306.5;  DB 10;  Length 542;
  Best Local Similarity  84.3%;  Pred. No. 2.6e-179;
  Matches  439;  Conservative   27;  Mismatches   44;  Indels   11;  Gaps    3;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
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Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||| ||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| |||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG--------GGGGS--RNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQT 350
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Db        322 WASVPCSGGGGSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQT 381

Qy        351 LELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASF 410
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Db        382 LEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSF 441

Qy        411 MTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVP 470
              |  ||||||||||||||:||| ||||||||||||||||||  ||||:|||||| |||
Db        442 MMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVP 501

Qy        471 QKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              |||||||||||||||||||||||||||||:|:|||||:|
Db        502 QKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 542


RESULT 8
US-09-828-825-14
; Sequence 14, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
;   LENGTH: 542
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-14

  Query Match           85.6%;  Score 2306.5;  DB 10;  Length 542;
  Best Local Similarity  84.3%;  Pred. No. 2.6e-179;
  Matches  439;  Conservative   27;  Mismatches   44;  Indels   11;  Gaps    3;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| |||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||:||| ||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
```

```
                ||||||||||:|||:||||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG--------GGGGS--RNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQT 350
              |||| ||||        |||||  ||||  || |||| ||:||| ||||||| |||||||
Db        322 WASVPCSGGGGSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQT 381

Qy        351 LELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASF 410
              || | |||||||||||||||||||||||||||| ||||| ||| | |||||||| | ||
Db        382 LEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSF 441

Qy        411 MTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVP 470
              |  |||||||||||||:||| ||||||||||||||||||  ||||:||||||| |||
Db        442 MMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVP 501

Qy        471 QKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              ||||||||||||||||||||||||||||||:|:|||||:|
Db        502 QKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 542


RESULT 9
US-09-828-825-10
; Sequence 10, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
;   LENGTH: 547
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-10

  Query Match             85.6%;  Score 2304;  DB 10;  Length 547;
  Best Local Similarity   83.5%;  Pred. No. 4.3e-179;
  Matches  439;  Conservative   27;  Mismatches   44;  Indels   16;  Gaps    3;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| |||||:|||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||||| |||||||||| |||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG-------------GGGGS--RNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQ 345
              |||| ||||             |||||  ||||  || |||| ||:||| ||||||| ||
Db        322 WASVPCSGGGGSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQT 381

Qy        346 KARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLAS 405
              ||||||| | |||||||||||||||||||||||||| ||||| ||| | |||||||||
Db        382 KARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLAS 441

Qy        406 GKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFN 465
              | |||  |||||||||||||:||| ||||||||||||||||||  ||||:||||||
Db        442 RKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFN 501

Qy        466 SVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              | ||||||||||||||||||||||||||||||||||||:|:|||||:|
Db        502 SETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 547


RESULT 10
US-09-828-825-12
; Sequence 12, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 547
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-12

  Query Match             85.6%;  Score 2304;  DB 10;  Length 547;
  Best Local Similarity   83.5%;  Pred. No. 4.3e-179;
  Matches  439;  Conservative   27;  Mismatches   44;  Indels   16;  Gaps    3;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||:||| |||||:|||||||||||||:||| ||| ||:|||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:||||||||||||||||||||||| |||||||||| |||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||:  ||||| |:| |:| | |:|:|||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGG-------------GGGGS--RNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQ 345
              |||| ||||             |||||  ||||  || |||| ||:||| ||||||| ||
Db        322 WASVPCSGGGGSGGGGSGGGGSPWRNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQT 381

Qy        346 KARQTLELYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLAS 405
              ||||||| | |||||||||||||||||||||||||| ||||| ||| | |||||||||
Db        382 KARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLAS 441

Qy        406 GKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFN 465
              | |||  |||||||||||||:||| ||||||||||||||||||  ||||:||||||
Db        442 RKTSFMMALCLSSIYEDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFN 501
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Qy        466 SVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              | ||||||||||||||||||||||||||||||||||:|:||||||:|
Db        502 SETVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 547


RESULT 11
US-09-828-825-2
; Sequence 2, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 527
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-09-828-825-2

  Query Match            84.5%;  Score 2275;  DB 10;  Length 527;
  Best Local Similarity  84.5%;  Pred. No. 9.2e-177;
  Matches  432;  Conservative   27;  Mismatches   46;  Indels    6;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||||:||| ||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:|||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||||:  ||||| |:| |:| | |:|:||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEE 360
              |||| ||       |||| || |||| ||:||| ||||||| |||||||| | |||||
Db        322 WASVPCSPW-----RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE 376

Qy        361 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIY 420
              |||||||||||||||||||||| ||||| ||| | |||||||| | |||  |||||||
Db        377 IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIY 436

Qy        421 EDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDF 480
              |||||||:||| ||||||||||||||||||  ||||:||||||| ||||||||||||||
Db        437 EDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDF 496

Qy        481 YKTKIKLCILLHAFRIRAVTINRMMSYLNSS 511
              |||||||||||||||||||:|:||||||:|
Db        497 YKTKIKLCILLHAFRIRAVTIDRVMSYLNAS 527


RESULT 12
US-09-828-825-4
; Sequence 4, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 526
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-4

  Query Match            84.3%;  Score 2271;  DB 10;  Length 526;
  Best Local Similarity  84.5%;  Pred. No. 2e-176;
  Matches  431;  Conservative   27;  Mismatches   46;  Indels    6;  Gaps    2;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||:||||||||||:|||||||||||| ||||| |||| ||||||||||||||||||||
Db         23 IWELKKDVYVVELDWYPDAPGEMVVLTCDTPEEDGITWTLDQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              |||||||||||||:||| ||||:|||||||||||||:||| ||| ||:||||||||||||
Db         83 GDAGQYTCHKGGEVLSHSLLLLHKKEDGIWSTDILKDQKEPKNKTFLRCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              |||| ||||| |||||||| |||||||||| |||||||| ||::| :|:|||||| ||||:
Db        143 WWLTTISTDLTFSVKSSRGSSDPQGVTCGAATLSAERVRGDNKEY-EYSVECQEDSACPA 201

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              |||||||||:|||:|||||||||||||||||||||| |||||||||| ||||||||||
Db        202 AEESLPIEVMVDAVHKLKYENYTSSFFIRDIIKPDPPNNLQLKPLKNSRQVEVSWEYPDT 261

Qy        241 WSTPHSYFSLTFCVQVQGKSKREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              |||||||||||||:| |||: |||||||:  ||||| |:| |:| | |:|:||||||||:
Db        262 WSTPHSYFSLTFCVQVQGKSKREKKDRVFTDKTSATVICRKNASISVRAQDRYYSSSWSE 321

Qy        301 WASVSCSGGGGGGSRNLPTPTPSPGMFQCLNHSQTLLRAVSNTLQKARQTLELYSCTSEE 360
              |||| ||       |||| || |||| ||:||| ||||||| |||||||| | |||||
Db        322 WASVPCSPW-----RNLPVATPDPGMFPCLHHSQNLLRAVSNMLQKARQTLEFYPCTSEE 376

Qy        361 IDHEDITKDKTSTVEACLPLELTMNESCLASREISLITNGSCLASGKASFMTVLCLSSIY 420
              |||||||||||||||||||||| ||||| ||| | |||||||| | |||  |||||||
Db        377 IDHEDITKDKTSTVEACLPLELTKNESCLNSRETSFITNGSCLASRKTSFMMALCLSSIY 436

Qy        421 EDLKMYQMEFKAMNAKLLMDPKRQIFLDQNMLTAIDELLQALNFNSVTVPQKSSLEEPDF 480
              |||||||:||| ||||||||||||||||||  ||||:||||||| ||||||||||||||
Db        437 EDLKMYQVEFKTMNAKLLMDPKRQIFLDQNMLAVIDELMQALNFNSETVPQKSSLEEPDF 496

Qy        481 YKTKIKLCILLHAFRIRAVTINRMMSYLNS 510
              |||||||||||||||||||:|:||||||:
Db        497 YKTKIKLCILLHAFRIRAVTIDRVMSYLNA 526


RESULT 13
US-09-917-265-53
; Sequence 53, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
```

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;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
;   LENGTH: 307
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-53

  Query Match             61.4%;  Score 1653;  DB 10;  Length 307;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-126;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300

Qy        301 WASVSCS 307
              |||||||
Db        301 WASVSCS 307


RESULT 14
US-09-917-265-59
; Sequence 59, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-59

  Query Match             61.4%;  Score 1653;  DB 10;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 2e-126;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
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Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
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Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
              |||||||
Db        323 WASVSCS 329


RESULT 15
US-09-917-265-108
; Sequence 108, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
;   LENGTH: 329
;   TYPE: PRT
;   ORGANISM: Canis familiaris
US-09-917-265-108

  Query Match             61.4%;  Score 1653;  DB 10;  Length 329;
  Best Local Similarity   100.0%;  Pred. No. 2e-126;
  Matches  307;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 IWELEKDVYVVELDWHPDAPGEMVVLTCHTPEEDDITWTSAQSSEVLGSGKTLTIQVKEF 82

Qy         61 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 GDAGQYTCHKGGKVLSRSLLLIHKKEDGIWSTDILKEQKESKNKIFLKCEAKNYSGRFTC 142

Qy        121 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        143 WWLTAISTDLKFSVKSSRGFSDPQGVTCGAVTLSAERVRVDNRDYKKYTVECQEGSACPS 202

Qy        181 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 240
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Db        203 AEESLPIEVVVDAIHKLKYENYTSSFFIRDIIKPDPPTNLQLKPLKNSRHVEVSWEYPDT 262

Qy        241 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        263 WSTPHSYFSLTFCIQAQGKNNREKKDRLCVDKTSAKVVCHKDAKIRVQARDRYYSSSWSD 322

Qy        301 WASVSCS 307
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Db        323 WASVSCS 329


Search completed: July 15, 2003, 11:11:48
Job time : 25.858 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:27:32 ; Search time 169.963 Seconds
(without alignments)
10273.834 Million cell updates/sec

Title: US-09-917-265-83
Perfect score: 60
Sequence: 1 ctgcagtggtggcggtggcg.....acccctactccatccccggg 60

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
6: gb_pat:*
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8: gb_pl:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		32.8	54.7	1626	12	AF401989	AF401989 Synthetic
2	c	30.4	50.7	4877	3	AY051978	AY051978 Drosophil
3	c	30.4	50.7	83141	3	AC005115	AC005115 Drosophil
4	c	30.4	50.7	174652	3	AC092241	AC092241 Drosophil
5	c	30.4	50.7	180968	2	AC019702	AC019702 Drosophil
6	c	30.4	50.7	261383	3	AE003631	AE003631 Drosophil
7	c	29.2	48.7	1194	10	AF020305	AF020305 Mus muscu
8	c	29.2	48.7	1244	10	AF041842	AF041842 Mus muscu
9	c	29.2	48.7	1867	10	AB008833	AB008833 Mus muscu
10	c	29.2	48.7	1884	10	AF051766	AF051766 Mus muscu
11	c	29.2	48.7	1911	10	AF036163	AF036163 Mus muscu
12	c	29.2	48.7	1932	10	MMTRNR3	Y15110 Mus musculu
13		28.6	47.7	46849	9	AC113358	AC113358 Homo sapi
14		28.6	47.7	145435	9	AC011419	AC011419 Homo sapi
15		27.4	45.7	67856	2	AC121528	AC121528 Mus muscu
16	c	27.4	45.7	111922	2	AL845360	AL845360 Mus muscu
17		27	45.0	174087	2	CNS08CB7	AL845345 Oryza sat
18		26.6	44.3	40977	9	HSAC000362	AC000362 Human cos
19	c	26.6	44.3	191205	2	AC119062	AC119062 Pan trogl
20		26.6	44.3	200688	10	AL671963	AL671963 Mouse DNA
21	c	26	43.3	667	10	AF184920	AF184920 Rattus no
22	c	26	43.3	3729	5	CHKCMGFA	M85034 Chicken mye
23		26	43.3	183132	2	AC113060	AC113060 Mus muscu
24		25.8	43.0	90275	2	AP003978	AP003978 Oryza sat
25		25.8	43.0	116275	2	AP003993	AP003993 Oryza sat
26		25.8	43.0	143436	2	AP004801	AP004801 Oryza sat
27	c	25.8	43.0	161153	9	AC020987	AC020987 Homo sapi
28		25.8	43.0	179910	2	AC016187	AC016187 Homo sapi
29	c	25.8	43.0	185034	2	AC110402	AC110402 Rattus no
30	c	25.8	43.0	196349	2	AC022032	AC022032 Homo sapi
31		25.6	42.7	7895	10	AF236363S3	AF236365 Mus muscu
32		25.6	42.7	117056	2	AP000839	AP000839 Homo sapi
33		25.6	42.7	163156	2	AP004085	AP004085 Oryza sat
34		25.6	42.7	175562	9	AP002833	AP002833 Homo sapi
35	c	25.6	42.7	188750	2	AC108524	AC108524 Rattus no
36	c	25.6	42.7	197561	2	AC093407	AC093407 Mus muscu
37		25.6	42.7	301000	1	AP005376	AP005376 Thermosyn
38		25.6	42.7	317113	2	AC127377	AC127377 Mus muscu
39		25.4	42.3	69	6	AR067951	AR067951 Sequence
40		25.4	42.3	69	6	AR095964	AR095964 Sequence
41		25.4	42.3	70	6	AR078906	AR078906 Sequence
42		25.4	42.3	70	6	AR097700	AR097700 Sequence
43	c	25.4	42.3	3863	3	AF184227	AF184227 Drosophil
44		25.4	42.3	4527	5	AF443296	AF443296 Coturnix
45	c	25.4	42.3	9925	1	AB024335	AB024335 Comamonas

ALIGNMENTS

RESULT 1
AF401989
LOCUS AF401989 1626 bp mRNA linear SYN 14-FEB-2002
DEFINITION Synthetic construct single chain interleukin-12 mRNA, complete cds.
ACCESSION AF401989
VERSION AF401989.1 GI:18656516
KEYWORDS .
SOURCE synthetic construct.
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1 (bases 1 to 1626)
AUTHORS McMonagle,E.L.J., Taylor,S., van Zuilekom,H., Sanders,L., Scholtes,N., Keanie,L.J., Hopkins,C.A., Logan,N.A., Bain,D., Argyle,D.J., Onions,D.E., Schijns,V.E. and Nicolson,L.
TITLE Production of biologically active equine interleukin 12 through

```
          expression of p35, p40 and single chain IL-12 in mammalian and
          baculovirus expression systems
  JOURNAL   Equine Vet. J. 33 (7), 693-698 (2001)
  MEDLINE   21626920
   PUBMED   11770992
REFERENCE   2  (bases 1 to 1626)
  AUTHORS   McMonagle,L.J., Taylor,S., Keanie,L.J., Hopkins,C.A., Logan,N.A.,
          Argyle,D.J., Onions,D.E. and Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-JUL-2001) Veterinary Pathology, Glasgow Veterinary
          School, Bearsden Rd, Glasgow G61 1QH, UK
FEATURES             Location/Qualifiers
     source          1. .1626
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
     CDS             1. .1626
                     /note="derived from Equus caballus; N-terminal p40 subunit
                     linked by (Gly4Ser)3 linker to signal-peptide deleted p35
                     subunit"
                     /codon_start=1
                     /transl_table=11
                     /product="single chain interleukin-12"
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                     /db_xref="GI:18656517"
                     /translation="MGHQWLVLSWFSLVLLASPLMAIWELEKDVYVVELDWYPDAPGE
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                     LLHKKEDGIWSTDILKDQKESKNKTFLKCEAKNYSGRFTCWWLTAISTDLKFSVKSSR
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                     EDLKMYQVEFKAMNAKLLIDPQRQIFLDENMLTAIDKLMQALNFNSETVPQKPSLEGL
                     DFYKTKVKLCILLHAFRIRAVTINRMMGYLNAS"
     primer_bind     1. .14
     misc_feature    15. .987
                     /note="interleukin-12 p40 sequence"
     misc_feature    988. .1032
                     /note="linker"
     misc_feature    1033. .1611
                     /note="interleukin-12 p35 sequence"
     primer_bind     complement(1612. .1626)
BASE COUNT      429 a    425 c    427 g    345 t
ORIGIN

  Query Match             54.7%;  Score 32.8;  DB 12;  Length 1626;
  Best Local Similarity   71.7%;  Pred. No. 0.22;
  Matches   43;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              | |  ||||   ||||||||||||||||||| ||| | || ||  | || |||  ||| ||
Db       1005 CGGTGGTGGATCCGGTGGCGGCGGATCTAGGAACCTCCCCACAGCCACACCAGGCCCAGG 1064


RESULT 2
AY051978/c
LOCUS       AY051978               4877 bp    mRNA    linear   INV 27-AUG-2001
DEFINITION  Drosophila melanogaster LD44770 full length cDNA.
ACCESSION   AY051978
VERSION     AY051978.1  GI:15292266
KEYWORDS    FLI_CDNA.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 4877)
  AUTHORS   Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Carlson,J.,
            Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R.,
            Gonzalez,M., Guarin,H., Li,P., Liao,G., Miranda,A., Mungall,C.J.,
            Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K.,
            Yu,C., Lewis,S.E., Rubin,G.M. and Celniker,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
            Lawrence Berkeley National Laboratory, One Cyclotron Road,
            Berkeley, CA 94720, USA
COMMENT     Sequence submitted by:
            Berkeley Drosophila Genome Project
            Lawrence Berkeley National Laboratory
            Berkeley, CA 94720
            This clone was sequenced as part of a high-throughput process to
            sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
            Science 2000). The sequence has been subjected to integrity checks
            for sequence accuracy, presence of a polyA tail and contiguity
            within 100 kb in the genome. Thus we believe the sequence to
            reflect accurately this particular cDNA clone.  However, there are
            artifacts associated with the generation of cDNA clones that may
            have not been detected in our initial analyses such as internal
            priming, priming from contaminating genomic DNA, retained introns
            due to reverse transcription of unspliced precursor RNAs, and
            reverse transcriptase errors that result in single base changes.
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our Web site
            (http://fruitfly.berkeley.edu) or send email to
            cdna@fruitfly.berkeley.edu.
FEATURES             Location/Qualifiers
     source          1. .4877
                     /organism="Drosophila melanogaster"
                     /strain="y; cn bw sp"
                     /db_xref="taxon:7227"
                     /map="32D4-32D4"
     gene            1. .4877
                     /gene="CG4751"
                     /note="alignment with genomic scaffold AE003631"
                     /db_xref="FLYBASE:FBgn0032348"
     CDS             105. .4343
                     /gene="CG4751"
                     /note="Longest ORF"
                     /codon_start=1
                     /product="LD44770p"
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                     /db_xref="GI:15292267"
                     /db_xref="FLYBASE:FBgn0032348"
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                     SDAGDEDNDDETKENYEGFNGTGRTVTLQTLMAANVLQPGLGLMTIEYLGQKFVGDLL
                     ADGKIKSHETETIFLTPSAWAMHCKRIINPDKKSGCGWASVKYKGKKLDAYKNTYLRK
                     CALQKETPLDDCELDAERKTDTPEIVVKRTVFAHNTVSNRNVVHDANMLIESVPFTSV
                     GKLQPFLITVNSSALLLADFHCHLTVREVCGYLGGTWDMNTHTLSITKTYPCRSTRFD
                     RQRAGEVERDIQKMMIQDQLLLVGWYHSHPKFQAEPTLRDCDAQLDYQIKMRGASDLT
                     YTPCVSLIISPYYDENPTLESVVKCIWIVPPNENRQSMEYGRPMLMQYSVLPDKEIPE
                     EVRSEIQLCVDYYSQYRSEMVKFRNIYNNDVTYNEKLKNTLYPKFPSKQSDKALWNWI
                     CAVLDCEQEDDFIPPKTIKIIDNDDLEVKEEDKPVVLMDLSGDVKINPPKEEQFSEAM
                     GGLEDSGRKAEEESNAQAEQKASELKVMSLQEQLCMPSGLNMNPVRMLSPLATPNPTS
                     LPPVLPNLGAPVLPATPSQLLPPQVPAVTAPPAITPAVTTSALTSALNASPRDSPITI
                     QSNSASPAKFEVPVRASPSPAKSDTSSHASTSRTRNSPAPSPGKFSVSDIARNSPSIT
                     PNKYEAAAAALVPPAAACLPTANDLMAASLAQLAGQLPPNFLQGDLAALFQQQRKDYG
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                     QESLSAMMMKPPKSTTPSSARTRESSASPALERLTPTKSASSGGSGGGGSNSNSGGKY
                     NFSAVDLAISSVPSNTPSPAPSDGSSGSSHRRPSPDIGRLYGELAPPGALLGSGGVPK
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BASE COUNT     1271 a   1320 c   1247 g   1039 t
ORIGIN

  Query Match             50.7%;  Score 30.4;  DB 3;  Length 4877;
  Best Local Similarity   71.4%;  Pred. No. 1.8;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
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              |||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
Db        244 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 189


RESULT 3
AC005115/c
LOCUS       AC005115               83141 bp    DNA     linear   INV 18-SEP-1998
DEFINITION  Drosophila melanogaster DNA sequence (P1 DS06882 (D310)), complete
            sequence.
ACCESSION   AC005115
VERSION     AC005115.1  GI:3628578
KEYWORDS    HTG.
SOURCE      Drosophila melanogaster (Subclones in sac from P1 clone DS06882
            (D310)) DNA.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 83141)
  AUTHORS   Celniker,S.E., George,R.A., Galle,R.F., Hoskins,R.A.,
            Svirskas,R.R., Harris,N.L., Agbayani,A., Arcaina,T.T., Baxter,E.,
            Blazej,R.G., Chavez,C., Chew,M., Doyle,C.M., Farfan,D.E.,
            Flanagan,J., Houston,K.A., Hummasti,S.R., Karra,K., Kearney,L.,
            Kim,S.H., Lee,B., Lomotan,M.A., Mak,J., Mazda,P., Moshrefi,A.R.,
            Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Punch,E.,
            Snir,E., Twomey,B., Wan,K.H., Zhang,R., Zieran,L.L. and Rubin,G.M.
  TITLE     Sequencing of Drosophila chromosome 2L, region 32D2-32D4
  JOURNAL   Unpublished (1997)
REFERENCE   2  (bases 1 to 83141)
  AUTHORS   Celniker,S.E., George,R.A., Galle,R., Svirskas,R.R., Hoskins,R.A.,
            Agbayani,A., Arcaina,T.T., Baxter,E., Blazej,R.G., Chavez,C.,
            Chew,M., Doyle,C.M., Farfan,D.E., Flanagan,J., Houston,K.A.,
            Hummasti,S.R., Karra,K., Kearney,L., Kim,S.H., Lee,B.,
            Lomotan,M.A., Mak,J., Mazda,P., Mok,M.S., Moshrefi,A.R.,
            Moshrefi,M., Nixon,K., Pacleb,J.M., Park,S., Pfeiffer,B., Punch,E.,
            Snir,E., Twomey,B., Wan,K.H., Whitelaw,K.R., Yee,A., Zhang,R.,
            Zieran,L.L. and Kimmel,B.E.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-JUN-1998) Drosophila Genome Center, Lawrence Berkeley
            Laboratory, MS 64-121, Berkeley, CA 94720, USA
COMMENT     On Sep 18, 1998 this sequence version replaced gi:3581676.
            Sequence submitted by:
            Berkeley Drosophila Genome Project
            Lawrence Berkeley National Laboratory, MS 64-121
            Berkeley, CA 94720
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive Web site (http://fruitfly.berkeley.edu/sequence/) or send
            email to bdgp@fruitfly.berkeley.edu.
            Library location: 66-72.
FEATURES             Location/Qualifiers
     source          1. .83141
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /chromosome="2L"
                     /map="32D2-32D4"
                     /clone="P1 DS06882 (D310)"
BASE COUNT    22988 a  17855 c  18248 g  24050 t
ORIGIN

  Query Match             50.7%;  Score 30.4;  DB 3;  Length 83141;
  Best Local Similarity   71.4%;  Pred. No. 2.1;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
Db      36392 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 36337


RESULT 4
AC092241/c
LOCUS       AC092241              174652 bp    DNA     linear   INV 30-JUN-2001
DEFINITION  Drosophila melanogaster, chromosome 2L, region 32F-33A, BAC clone
            BACR09F02, complete sequence.
ACCESSION   AC092241
VERSION     AC092241.1  GI:14578122
KEYWORDS    HTG.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 174652)
  AUTHORS   Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
            Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
            Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
            Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
            Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
            Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
            Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
            Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A.,
            McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
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            Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,
            Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,
            Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
  TITLE     Sequencing of Drosophila chromosome 2L, region 32F-33A
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 174652)
  AUTHORS   Celniker,S.E., Adams,M.D., Kronmiller,B., Tyler,D., Wan,K.H.,
            Holt,R.A., Evans,C.A., Gocayne,J.D., Amanatides,P.G., Brandon,R.C.,
            Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A.,
            Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
            Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D.,
            Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A.,
            Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J.,
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            McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunoo,J.,
            Pacleb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B.,
            Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F.,
            Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M.,
            Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-JUN-2001) Berkeley Drosophila Genome Project, MS
            64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
            Berkeley, CA 94720, US
COMMENT     Sequence submitted by:
            Berkeley Drosophila Genome Project
            Lawrence Berkeley National Laboratory, MS 64-121
            Berkeley, CA 94720
            This sequence was assembled using end sequences from a whole genome
            shotgun and from subclones of this BAC and its neighboring clones.
            For further information about this sequence, including its location
            and relationship to other sequences, please visit our sequence
            archive Web site (http://www.fruitfly.org/sequence/) or send email
            to bdgp@fruitfly.berkeley.edu.
FEATURES             Location/Qualifiers
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                     /clone="BACR09F02 (D1343)"
                     /clone_lib="RPCI-98 (Roswell Park Cancer Institute
                     Drosophila melanogaster BAC library, partial EcoRI in
                     pBACe3.6)"
BASE COUNT    49626 a  37840 c  37886 g  49300 t
ORIGIN

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  Best Local Similarity   71.4%;  Pred. No. 2.1;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
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Db      28726 TGCAGTGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 28671


RESULT 5
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LOCUS       AC019702               180968 bp    DNA     linear   HTG 03-JAN-2000
DEFINITION  Drosophila melanogaster, *** SEQUENCING IN PROGRESS ***, in ordered
            pieces.
ACCESSION   AC019702
VERSION     AC019702.1  GI:6665195
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 180968)
  AUTHORS   Adams,M. and Venter,J.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive,
            Rockville, MD, USA
COMMENT     This sequence was identified as CDM:10210673 by the submitter.
            For more information on this record e-mail to fly@celera.com.
            * NOTE: This is a 'working draft' sequence.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

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Db      96770 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 96715


RESULT 6
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DEFINITION  Drosophila melanogaster genomic scaffold 142000013386055 section 24
            of 63, complete sequence.
ACCESSION   AE003631 AE002690
VERSION     AE003631.2  GI:10728714
KEYWORDS    HTG.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 261383)
  AUTHORS   Adams,M.D., Celniker,S.E., Holt,R.A., Evans,C.A., Gocayne,J.D.,
            Amanatides,P.G., Scherer,S.E., Li,P.W., Hoskins,R.A., Galle,R.F.,
            George,R.A., Lewis,S.E., Richards,S., Ashburner,M., Henderson,S.N.,
            Sutton,G.G., Wortman,J.R., Yandell,M.D., Zhang,Q., Chen,L.X.,
            Brandon,R.C., Rogers,Y.H., Blazej,R.G., Champe,M., Pfeiffer,B.D.,
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            Busam,D.A., Butler,H., Cadieu,E., Center,A., Chandra,I.,
            Cherry,J.M., Cawley,S., Dahlke,C., Davenport,L.B., Davies,P., de
            Pablos,B., Delcher,A., Deng,Z., Mays,A.D., Dew,I., Dietz,S.M.,
            Dodson,K., Doup,L.E., Downes,M., Dugan-Rocha,S., Dunkov,B.C.,
            Dunn,P., Durbin,K.J., Evangelista,C.C., Ferraz,C., Ferriera,S.,
            Fleischmann,W., Fosler,C., Gabrielian,A.E., Garg,N.S.,
            Gelbart,W.M., Glasser,K., Glodek,A., Gong,F., Gorrell,J.H., Gu,Z.,
            Guan,P., Harris,M., Harris,N.L., Harvey,D., Heiman,T.J.,
            Hernandez,J.R., Houck,J., Hostin,D., Houston,K.A., Howland,T.J.,
            Wei,M.H., Ibegwam,C., Jalali,M., Kalush,F., Karpen,G.H., Ke,Z.,
            Kennison,J.A., Ketchum,K.A., Kimmel,B.E., Kodira,C.D., Kraft,C.,
            Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A.,
            Li,J., Li,Z., Liang,Y., Lin,X., Liu,X., Mattei,B., McIntosh,T.C.,
            McLeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C.,
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            Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I.,
            Simpson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C.,
            Stapleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R.,
            Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A.,
            Weinstock,G.M., Weissenbach,J., Williams,S.M., Woodage,T.,
            Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F.,
            Zaveri,J.S., Zhan,M., Zhang,G., Zhao,Q., Zheng,L., Zheng,X.H.,
            Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O.,
            Gibbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
  TITLE     The genome sequence of Drosophila melanogaster
  JOURNAL   Science 287 (5461), 2185-2195 (2000)
  MEDLINE   20196006
   PUBMED   10731132
REFERENCE   2  (bases 1 to 261383)
  AUTHORS   Adams,M.D., Celniker,S.E., Gibbs,R.A., Rubin,G.M. and Venter,C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
            Rockville, MD, USA
COMMENT     On Oct 9, 2000 this sequence version replaced gi:7297810.
FEATURES             Location/Qualifiers
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                KSKEEQERLSVMILGMDSLSHLNFLRQMRRTANYVRKHLSHVEFWGYNKVGDNTFPNL
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                /db_xref="FLYBASE:FBan0004705"

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  Best Local Similarity  71.4%;  Pred. No. 2.2;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
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Db      78377 TGCAGTGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 78322


RESULT 7
AF020305/c
LOCUS       AF020305               1194 bp    mRNA    linear   ROD 03-MAY-2001
DEFINITION  Mus musculus glial cell line-derived neurotrophic factor family
            receptor alpha-3 (gfra-3) mRNA, complete cds.
ACCESSION   AF020305
VERSION     AF020305.1  GI:2429366
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1194)
  AUTHORS   Trupp,M., Raynoschek,C., Belluardo,N. and Ibanez,C.F.
  TITLE     Multiple GPI-anchored receptors control GDNF-dependent and
            independent activation of the c-Ret receptor tyrosine kinase
  JOURNAL   Mol. Cell. Neurosci. 11 (1-2), 47-63 (1998)
  MEDLINE   98271460
   PUBMED   9608533
REFERENCE   2  (bases 1 to 1194)
  AUTHORS   Trupp,M. and Ibanez,C.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-AUG-1997) Neuroscience, Karolinska Institute,
            Doktorsringen 12A, Stockholm 17177, Sweden
FEATURES             Location/Qualifiers
     source          1. .1194
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     CDS             1. .1194
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                     /note="structurally related to members of the GFRa family
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                     /product="glial cell line-derived neurotrophic factor
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BASE COUNT      253 a    372 c    307 g    262 t
ORIGIN

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  Best Local Similarity   69.0%;  Pred. No. 4.6;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
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RESULT 8
AF041842/c
LOCUS       AF041842               1244 bp    mRNA    linear   ROD 16-JUN-1998
DEFINITION  Mus musculus glial cell line-derived neurotrophic factor family
            receptor alpha-3 (gfra3) mRNA, complete cds.
ACCESSION   AF041842
VERSION     AF041842.1  GI:2921578
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1244)
  AUTHORS   Widenfalk,J., Tomac,A., Lindqvist,E., Hoffer,B. and Olson,L.
  TITLE     GFRalpha-3, a protein related to GFRalpha-1, is expressed in
            developing peripheral neurons and ensheathing cells
  JOURNAL   Eur. J. Neurosci. 10 (4), 1508-1517 (1998)
  MEDLINE   98420233
   PUBMED   9749804
REFERENCE   2  (bases 1 to 1244)
  AUTHORS   Tomac,A., Hoffer,B. and Olson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-1998) Neuroscience, Karolinska Institute,
            Doktorsringen 12, Stockholm 17171, Sweden
FEATURES             Location/Qualifiers
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     CDS             51. .1244
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                     /product="glial cell line-derived neurotrophic factor
                     family receptor alpha-3"
                     /protein_id="AAC23558.1"
                     /db_xref="GI:2921579"
                     /translation="MGLSLEPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQA
                     RKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHR
                     RMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCL
                     KFAMLCTLHDKCDRLRKAYGEACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCP
                     PEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILG
                     TCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDECEQLERSFSQ
                     NPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNPALRLQPRLPILSFSILPLIL
                     LQTLW"
BASE COUNT      259 a    394 c    325 g    266 t
ORIGIN

  Query Match           48.7%;  Score 29.2;  DB 10;  Length 1244;
  Best Local Similarity   69.0%;  Pred. No. 4.6;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
Db        629 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 572


RESULT 9
AB008833/c
LOCUS       AB008833               1867 bp    mRNA    linear   ROD 13-FEB-1999
DEFINITION  Mus musculus mRNA for GFRalpha-3, complete cds.
ACCESSION   AB008833
VERSION     AB008833.1  GI:2627159
KEYWORDS    GFRalpha-3.
SOURCE      Mus musculus (strain:C57BL6) adult heart cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (sites)
  AUTHORS   Nomoto,S., Ito,S., Yang,L.X. and Kiuchi,K.
  TITLE     Molecular cloning and expression analysis of GFR alpha-3, a novel
            cDNA related to GDNFR alpha and NTNR alpha
  JOURNAL   Biochem. Biophys. Res. Commun. 244 (3), 849-853 (1998)
  MEDLINE   98205811
REFERENCE   2  (bases 1 to 1867)
  AUTHORS   Nomoto,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-NOV-1997) Satoshi Nomoto, RIKEN (The Institute of
            Physical and Chemical Research), Bio-Mimetic Control Research
            Center; 2271-130 Anagahora, Shimoshidami, Moriyama-ku, Nagoya,
            Aichi 463, Japan (E-mail:nomoto@nagoya.riken.go.jp,
            Tel:81-52-736-5864, Fax:81-52-736-5865)
FEATURES             Location/Qualifiers
     source          1. .1867
                     /organism="Mus musculus"
                     /strain="C57BL6"
                     /db_xref="taxon:10090"
                     /tissue_type="heart"
                     /dev_stage="adult"
     gene            1. .1867
                     /gene="GFRalpha-3"
     mRNA            1. .1867
                     /gene="GFRalpha-3"
     CDS             46. .1239
                     /gene="GFRalpha-3"
                     /codon_start=1
                     /product="GFRalpha-3"
                     /protein_id="BAA23562.1"
                     /db_xref="GI:2627160"
                     /translation="MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQA
                     RKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHR
                     RMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCL
                     KFAMLCTLHDKCDRLRKAYGEACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCA
                     PEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILG
                     TCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDECEQLERSFSQ
                     NPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNPALRLQPRLPILSFSILPLIL
                     LQTLW"
BASE COUNT      384 a    572 c    474 g    437 t
ORIGIN

  Query Match           48.7%;  Score 29.2;  DB 10;  Length 1867;
  Best Local Similarity   69.0%;  Pred. No. 4.7;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
Db        624 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 567


RESULT 10
AF051766/c
```

```
LOCUS       AF051766                1884 bp    mRNA    linear   ROD 26-JUN-1998
DEFINITION  Mus musculus GDNF family receptor alpha 3 mRNA, complete cds.
ACCESSION   AF051766
VERSION     AF051766.1  GI:2961629
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1884)
  AUTHORS   Baloh,R.H., Gorodinsky,A., Golden,J.P., Tansey,M.G., Keck,C.L.,
            Popescu,N.C., Johnson,E.M. Jr. and Milbrandt,J.
  TITLE     GFRalpha3 is an orphan member of the GDNF/neurturin/persephin
            receptor family
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (10), 5801-5806 (1998)
  MEDLINE   98245162
   PUBMED   9576965
REFERENCE   2  (bases 1 to 1884)
  AUTHORS   Baloh,R.H. and Milbrandt,J.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-MAR-1998) Pathology, Washington University, 660 South
            Euclid Ave, St. Louis, MO 63110, USA
FEATURES             Location/Qualifiers
     source          1. .1884
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     CDS             63. .1256
                     /note="GFRalpha3; GPI-linked receptor; related to GFRa1
                     (GDNFRa, TRNR1, RETL1) and GFRa2 (TRNR2, NTNRa, RETL2)"
                     /codon_start=1
                     /product="GDNF family receptor alpha 3"
                     /protein_id="AAC24354.1"
                     /db_xref="GI:2961630"
                     /translation="MGLSWSPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQA
                     RKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHR
                     RMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCL
                     KFAMLCTLHDKCDRLRKAYGEACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCA
                     PEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILG
                     TCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDECEQLERSFSQ
                     NPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNPALRLQPRLPILSFSILPLIL
                     LQTLW"
BASE COUNT      386 a    578 c    483 g    437 t
ORIGIN

  Query Match             48.7%;  Score 29.2;  DB 10;  Length 1884;
  Best Local Similarity   69.0%;  Pred. No. 4.7;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| ||||||| |  | |||| ||| ||  || | | | ||
Db        641 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 584


RESULT 11
AF036163/c
LOCUS       AF036163                1911 bp    mRNA    linear   ROD 26-JUN-1998
DEFINITION  Mus musculus glial cell line-derived neurotrophic factor family
            receptor alpha 3 (gfra3) mRNA, complete cds.
ACCESSION   AF036163
VERSION     AF036163.1  GI:2674176
KEYWORDS    .
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1911)
  AUTHORS   Naveilhan,P., Baudet,C., Mikaels,A., Shen,L., Westphal,H. and
            Ernfors,P.
  TITLE     Expression and regulation of GFRalpha3, a glial cell line-derived
            neurotrophic factor family receptor
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 95 (3), 1295-1300 (1998)
  MEDLINE   98115914
   PUBMED   9448325
REFERENCE   2  (bases 1 to 1911)
  AUTHORS   Naveilhan,P. and Ernfors,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-NOV-1997) Lab. Mol. Neuro. Dept. Medical Biochemistry
            and Biophysics, Karolinska Institute, Doktorsringen 12A, Stockholm
            171 77, Sweden
FEATURES             Location/Qualifiers
     source          1. .1911
                     /organism="Mus musculus"
                     /db_xref="taxon:10090"
     gene            1. .1911
                     /gene="gfra3"
     CDS             62. .1255
                     /gene="gfra3"
                     /function="GDNF family receptor"
                     /codon_start=1
                     /product="glial cell line-derived neurotrophic factor
                     family receptor alpha 3"
                     /protein_id="AAC24468.1"
                     /db_xref="GI:2674177"
                     /translation="MGLSLEPRPPLLMILLLVLSLWLPLGAGNSLATENRFVNSCTQA
                     RKKCEANPACKAAYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHR
                     RMKHQATCLDIYWTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCL
                     KFAMLCTLHDKCDRLRKAYGEACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCP
                     PEDAGCGERRRNTIAPSCALPSVTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILG
                     TCATEQSRCLRAYLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDECEQLERSFSQ
                     NPCLVEAIAAKMRFHRQLFSQDWADSTFSVVQQQNSNPALRLQPRLPILSFSILPLIL
                     LQTLW"
     polyA_site      1884
                     /gene="gfra3"
BASE COUNT      413 a    579 c    482 g    437 t
ORIGIN

  Query Match             48.7%;  Score 29.2;  DB 10;  Length 1911;
  Best Local Similarity   69.0%;  Pred. No. 4.7;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| ||||||| |  | |||| ||| ||  || | | | ||
Db        640 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 583


RESULT 12
MMTRNR3/c
LOCUS       MMTRNR3                 1932 bp    mRNA    linear   ROD 03-MAR-1998
DEFINITION  Mus musculus mRNA for TGF-beta-related neurotrophic factor
            receptor-3.
ACCESSION   Y15110
VERSION     Y15110.1  GI:2959855
KEYWORDS    neurotrophic receptor; TGF-beta related protein; trnR-3 gene.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 1932)
  AUTHORS   Zhong,J., Annies,M., Tolle,A. and Heumann,R.
  TITLE     Molecular cloning of a new member of TrnR family
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1932)
  AUTHORS   Zhong,J.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-OCT-1997) J. Zhong, Molecular Neurobiochemistry
            NC7/172, Ruhr-University Bochum, Universitaetsstr. 150, D-44780
            Bochum, FRG
COMMENT     Related publication:  Lennon G. et al, Genomics 33, 151-152, 1996.
FEATURES             Location/Qualifiers
     source          1. .1932
                     /organism="Mus musculus"
                     /strain="Swiss-Webster /NIH"
                     /db_xref="taxon:10090"
                     /tissue_type="embryo"
                     /dev_stage="15 days old"
     gene            118. .1275
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                     /gene="TrnR-3"
     CDS             118. .1275
                     /gene="TrnR-3"
                     /codon_start=1
                     /product="TGF-beta-related neurotrophic receptor-3"
                     /protein_id="CAA75384.1"
                     /db_xref="GI:2959856"
                     /translation="MILLLVLSLWLPLGAGNSLATENRFVNSCTQARKKCEANPACKA
                     AYQHLGSCTSSLSRPLPLEESAMSADCLEAAEQLRNSSLIDCRCHRRMKHQATCLDIY
                     WTVHPARSLGDYELDVSPYEDTVTSKPWKMNLSKLNMLKPDSDLCLKFAMLCTLHDKC
                     DRLRKAYGEACSGIRCQRHLCLAQLRSFFEKAAESHAQGLLLCPCPPEDAGCGERRRN
                     TIAPSCALPSVTPNCLDLRSFCRADPLCRSRLMDFQTHCHPMDILGTCATEQSRCLRA
                     YLGLIGTAMTPNFISKVNTTVALSCTCRGSGNLQDECEQLERSFSQNPCLVEAIAAKM
                     RFHRQLFSQDWADSTFSVVQQQNSNPALRLQPRLPILSFSILPLILLQTLW"
     sig_peptide     118. .162
                     /gene="TrnR-3"
BASE COUNT      414 a    586 c    491 g    441 t
ORIGIN

  Query Match             48.7%;  Score 29.2;  DB 10;  Length 1932;
  Best Local Similarity   69.0%;  Pred. No. 4.7;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
Db        660 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 603


RESULT 13
AC113358
LOCUS       AC113358               46849 bp    DNA     linear   PRI 30-MAY-2002
DEFINITION  Homo sapiens chromosome 5 clone CTD-3075M2, complete sequence.
ACCESSION   AC113358
VERSION     AC113358.2  GI:21263234
KEYWORDS    HTG.
SOURCE      Homo sapiens.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 46849)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 46849)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (01-MAR-2002) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 46849)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAY-2002) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On May 30, 2002 this sequence version replaced gi:19033472.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 100% of Sequence;
            Estimated Total Number of Errors is 0.
            NOTE:  BACTERIAL TRANSPOSON excised at 35722.
FEATURES             Location/Qualifiers
     source          1. .46849
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTD-3075M2"
BASE COUNT    14722 a   8197 c   8727 g  15203 t
ORIGIN

  Query Match             47.7%;  Score 28.6;  DB 9;  Length 46849;
  Best Local Similarity   79.1%;  Pred. No. 9.3;
  Matches   34;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         15 GTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||| ||| ||| |||||| |||||| | |||| | ||||| |
Db      23383 GTGGAGGCAGATGTAGAAAATTGCCAGCACCTAATACATCCAC 23425


RESULT 14
AC011419
LOCUS       AC011419               145435 bp    DNA     linear   PRI 25-JUN-2002
DEFINITION  Homo sapiens chromosome 5 clone CTD-2029I9, complete sequence.
ACCESSION   AC011419
VERSION     AC011419.7  GI:21553204
KEYWORDS    HTG.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 145435)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 145435)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-OCT-1999) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   3  (bases 1 to 145435)
  AUTHORS   DOE Joint Genome Institute.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAR-2002) Production Sequencing Facility, DOE Joint
            Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE   4  (bases 1 to 145435)
  AUTHORS   DOE Joint Genome Institute and Stanford Human Genome Center.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2002) DOE Joint Genome Institute, 2800 Mitchell
            Drive, Walnut Creek, CA 94598, USA
COMMENT     On Jun 25, 2002 this sequence version replaced gi:19224750.
            Draft Sequence Produced by DOE Joint Genome Institute
            www.jgi.doe.gov
            Finishing Completed at Stanford Human Genome Center
            www-shgc.stanford.edu
            Quality: Phrap Quality >=40 100% of Sequence;
            Estimated Total Number of Errors is 0.
            NOTE:  This insert is not the entire sequence of the clone (entire
            sequence is 169.1kb). It is clipped at the overlap with AC008586.
            The number of bases overlapped is 13259.
FEATURES             Location/Qualifiers
     source          1. .145435
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="5"
                     /clone="CTD-2029I9"
BASE COUNT    44462 a  27173 c  27568 g  46232 t
ORIGIN

  Query Match             47.7%;  Score 28.6;  DB 9;  Length 145435;
  Best Local Similarity   79.1%;  Pred. No. 9.8;
  Matches   34;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         15 GTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||| ||| ||| |||||| |||||| | |||| | ||||| |
Db      20501 GTGGAGGCAGATGTAGAAAATTGCCAGCACCTAATACATCCAC 20543


RESULT 15
AC121528
LOCUS       AC121528               67856 bp    DNA     linear   HTG 20-MAY-2002
DEFINITION  Mus musculus clone RP24-400J11, LOW-PASS SEQUENCE SAMPLING.
ACCESSION   AC121528
VERSION     AC121528.1  GI:20986557
KEYWORDS    HTG; HTGS_PHASE0.
SOURCE      Mus musculus.
  ORGANISM  Mus musculus
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 67856)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus, clone RP24-400J11
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 67856)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
            Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
            Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
            Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D.,
            Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L.,
            Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I.,
            Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K.,
            Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K.,
            Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N.,
            Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J.,
            Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C.,
            Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P.,
            O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
            Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C.,
            Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S.,
            Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N.,
            Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S.,
            Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J.,
            Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
            Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-MAY-2002) Whitehead Institute/MIT Center for Genome
            Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT     All repeats were identified using RepeatMasker:
            Smit, A.F.A. & Green, P. (1996-1997)
            http://ftp.genome.washington.edu/RM/RepeatMasker.html
            -------------- Genome Center
                Center: Whitehead Institute/ MIT Center for Genome Research
                Center code: WIBR
                Web site: http://www-seq.wi.mit.edu
                Contact: sequence_submissions@genome.wi.mit.edu
            -------------- Project Information
                Center project name: L20177
                Center clone name: 400_J_11
            --------------.
            * NOTE: This record contains 84 individual
            * sequencing reads that have not been assembled into
            * contigs. Runs of N are used to separate the reads
            * and the order in which they appear is completely
            * arbitrary. Low-pass sequence sampling is useful for
            * identifying clones that may be gene-rich and allows
            * overlap relationships among clones to be deduced.
            * However, it should not be assumed that this clone
            * will be sequenced to completion. In the event that
            * the record is updated, the accession number will
            * be preserved.
            *        1      695: contig of 695 bp in length
            *      696 795: gap of      100 bp
            *      796     1481: contig of 686 bp in length
            *     1482 1581: gap of      100 bp
            *     1582     2316: contig of 735 bp in length
            *     2317 2416: gap of      100 bp
            *     2417     3076: contig of 660 bp in length
            *     3077 3176: gap of      100 bp
            *     3177     3891: contig of 715 bp in length
            *     3892 3991: gap of      100 bp
            *     3992     4695: contig of 704 bp in length
            *     4696 4795: gap of      100 bp
            *     4796     5492: contig of 697 bp in length
            *     5493 5592: gap of      100 bp
            *     5593     6296: contig of 704 bp in length
            *     6297 6396: gap of      100 bp
            *     6397     7116: contig of 720 bp in length
            *     7117 7216: gap of      100 bp
            *     7217     7897: contig of 681 bp in length
            *     7898 7997: gap of      100 bp
            *     7998     8735: contig of 738 bp in length
            *     8736 8835: gap of      100 bp
            *     8836     9531: contig of 696 bp in length
            *     9532 9631: gap of      100 bp
            *     9632    10348: contig of 717 bp in length
            *    10349 10448: gap of      100 bp
            *    10449    11162: contig of 714 bp in length
            *    11163 11262: gap of      100 bp
            *    11263    11974: contig of 712 bp in length
            *    11975 12074: gap of      100 bp
            *    12075    12786: contig of 712 bp in length
            *    12787 12886: gap of      100 bp
            *    12887    13582: contig of 696 bp in length
            *    13583 13682: gap of      100 bp
            *    13683    14387: contig of 705 bp in length
            *    14388 14487: gap of      100 bp
            *    14488    15198: contig of 711 bp in length
            *    15199 15298: gap of      100 bp
            *    15299    16004: contig of 706 bp in length
            *    16005 16104: gap of      100 bp
            *    16105    16825: contig of 721 bp in length
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            *    16926    17615: contig of 690 bp in length
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            *    17716    18394: contig of 679 bp in length
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            *    18495    19218: contig of 724 bp in length
            *    19219 19318: gap of      100 bp
            *    19319    20049: contig of 731 bp in length
            *    20050 20149: gap of      100 bp
            *    20150    20876: contig of 727 bp in length
            *    20877 20976: gap of      100 bp
            *    20977    21693: contig of 717 bp in length
            *    21694 21793: gap of      100 bp
            *    21794    22499: contig of 706 bp in length
            *    22500 22599: gap of      100 bp
            *    22600    23306: contig of 707 bp in length
            *    23307 23406: gap of      100 bp
            *    23407    24111: contig of 705 bp in length
            *    24112 24211: gap of      100 bp
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            *    24983    25700: contig of 718 bp in length
            *    25701 25800: gap of      100 bp
            *    25801    26526: contig of 726 bp in length
            *    26527 26626: gap of      100 bp
            *    26627    27335: contig of 709 bp in length
            *    27336 27435: gap of      100 bp
            *    27436    28147: contig of 712 bp in length
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            *    28248    28945: contig of 698 bp in length
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            *    29046    29760: contig of 715 bp in length
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            *    32132 32231: gap of      100 bp
            *    32232    32934: contig of 703 bp in length
            *    32935 33034: gap of      100 bp
            *    33035    33766: contig of 732 bp in length
            *    33767 33866: gap of      100 bp
            *    33867    34584: contig of 718 bp in length
            *    34585 34684: gap of      100 bp
            *    34685    35388: contig of 704 bp in length
            *    35389 35488: gap of      100 bp
            *    35489    36214: contig of 726 bp in length
            *    36215 36314: gap of      100 bp
            *    36315    37053: contig of 739 bp in length
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*    37054 37153: gap of      100 bp
*    37154    37883: contig of 730 bp in length
*    37884 37983: gap of      100 bp
*    37984    38698: contig of 715 bp in length
*    38699 38798: gap of      100 bp
*    38799    39499: contig of 701 bp in length
*    39500 39599: gap of      100 bp
*    39600    40302: contig of 703 bp in length
*    40303 40402: gap of      100 bp
*    40403    41100: contig of 698 bp in length
*    41101 41200: gap of      100 bp
*    41201    41905: contig of 705 bp in length
*    41906 42005: gap of      100 bp
*    42006    42734: contig of 729 bp in length
*    42735 42834: gap of      100 bp
*    42835    43561: contig of 727 bp in length
*    43562 43661: gap of      100 bp
*    43662    44350: contig of 689 bp in length
*    44351 44450: gap of      100 bp
*    44451    45162: contig of 712 bp in length
*    45163 45262: gap of      100 bp
*    45263    45997: contig of 735 bp in length
*    45998 46097: gap of      100 bp
*    46098    46818: contig of 721 bp in length
*    46819 46918: gap of      100 bp
*    46919    47639: contig of 721 bp in length
*    47640 47739: gap of      100 bp
*    47740    48454: contig of 715 bp in length
*    48455 48554: gap of      100 bp
*    48555    49272: contig of 718 bp in length
*    49273 49372: gap of      100 bp
*    49373    50069: contig of 697 bp in length
*    50070 50169: gap of      100 bp
*    50170    50876: contig of 707 bp in length
*    50877 50976: gap of      100 bp
*    50977    51697: contig of 721 bp in length
*    51698 51797: gap of      100 bp
*    51798    52531: contig of 734 bp in length
*    52532 52631: gap of      100 bp
*    52632    53359: contig of 728 bp in length
*    53360 53459: gap of      100 bp
*    53460    54158: contig of 699 bp in length
*    54159 54258: gap of      100 bp
*    54259    54959: contig of 701 bp in length
*    54960 55059: gap of      100 bp
*    55060    55772: contig of 713 bp in length
*    55773 55872: gap of      100 bp

  Query Match             45.7%;  Score 27.4;  DB 2;  Length 67856;
  Best Local Similarity   69.8%;  Pred. No. 26;
  Matches  37;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          4 CAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCC 56
              |||  ||   |||||| || ||| |||  |||| |   ||| |||||||||| |
Db      17372 CAGCAGTCAAGGTGGCTGCTGATTTAGGCACTTCCAGCCCCATACTCCATCAC 17424


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Job time : 173.963 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 04:18:07 ; Search time 16.1318 Seconds
(without alignments)
8375.975 Million cell updates/sec

Title: US-09-917-265-83
Perfect score: 60
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		33	55.0	33	17	AAT35197	(Gly6)Ser linker D
2		30.4	50.7	3352	23	ABL10788	Drosophila melanog
c 3		30.4	50.7	4343	23	ABL08253	Drosophila melanog
4		30.4	50.7	6727	23	ABL08252	Drosophila melanog
5		29.2	48.7	42	24	AAL44013	Reproductive recom
c 6		29.2	48.7	1878	19	AAV00256	Mouse Ret ligand r
c 7		29.2	48.7	1889	19	AAV00249	Mouse Ret ligand r
c 8		29.2	48.7	1935	21	AAZ29100	Murine GFRalpha3 c
c 9		28.6	47.7	576	23	ABV54109	Human prostate exp
10		28.2	47.0	1080	20	AAZ21160	Artificial synthet
11		28.2	47.0	1086	20	AAZ21157	Artificial synthet
c 12		28	46.7	42	24	AAL44012	Reproductive recom
13		27.6	46.0	8608	24	AAD31548	pIRES-hB7-1-IL12.2
14		27.6	46.0	8623	24	AAD31547	pIRES-hB7-1-IL12.3
15		27.6	46.0	8629	24	AAD31552	pIRES-IL12.2-hb7-1
16		27.6	46.0	8638	24	AAD31549	pIRES-hB7-1-IL12.4
17		27.6	46.0	8644	24	AAD31551	pIRES-IL12.3-hb7-1
18		27.6	46.0	8659	24	AAD31550	pIRES-IL12.4-hb7-1
c 19		26.2	43.7	409	23	ABV03540	Human prostate exp
c 20		26.2	43.7	412	23	ABV33838	Human prostate exp
c 21		26.2	43.7	412	23	ABV42727	Human prostate exp
c 22		26.2	43.7	433	23	ABV12709	Human prostate exp
23		26.2	43.7	837	20	AAX08493	sFvMHC-1-8k single
c 24		26	43.3	1699	20	AAV99331	cDNA encoding a GD
25		25.4	42.3	69	15	AAQ56574	Human 5' V kappa p
26		25.4	42.3	69	20	AAX08496	5' V kappa primer.
27		25.4	42.3	69	21	AAA74677	Human kappa light
28		25.4	42.3	69	21	AAA90430	Human V-kappa 5' P
c 29		25.4	42.3	3862	23	ABL03155	Drosophila melanog
c 30		25.4	42.3	5343	23	ABL29333	Drosophila melanog
c 31		25.4	42.3	9614	23	ABL03154	Drosophila melanog
32		25.2	42.0	1005	20	AAZ21161	Artificial synthet
33		25.2	42.0	1020	20	AAZ21167	Artificial synthet
34		25.2	42.0	1047	20	AAZ21164	Artificial synthet
35		25.2	42.0	1148	22	AAS26350	Human cDNA encodin
36		25.2	42.0	1179	22	AAS25897	Human cDNA encodin
c 37		25.2	42.0	2704	23	ABL12747	Drosophila melanog
38		25.2	42.0	5950	23	AAS72442	DNA encoding novel
39		25.2	42.0	6791	23	ABL12746	Drosophila melanog
40		25	41.7	816	22	AAS09507	cDNA encoding a hu
41		25	41.7	837	20	AAX08492	sFvMHC-1-5k single
42		25	41.7	1248	22	AAS09508	cDNA encoding a hu
43		25	41.7	8280	23	AAS74108	DNA encoding novel
44		25	41.7	10438	23	AAS74106	DNA encoding novel
c 45		24.8	41.3	825	22	AAK91827	Human cDNA 5'-end

ALIGNMENTS

RESULT 1
AAT35197
ID AAT35197 standard; DNA; 33 BP.
XX
AC AAT35197;
XX
DT 28-NOV-1996 (first entry)
XX
DE (Gly6)Ser linker DNA.
XX
KW Bioactive fusion protein; interleukin-12; IL-12; p35 subunit;
KW p40 subunit; antitumour; cytokine; tumour; melanoma;
KW fibrosarcoma; renal cell carcinoma; immunotherapy; therapy;
KW retrovirus; vector; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_feature 1..6
FT /*tag= a
FT /note= "IL-12p40 3' end"
FT misc_feature 7..27
FT /*tag= b
FT /note= "linker sequence"
FT misc_feature 28..33
FT /*tag= c
FT /note= "IL-12p35 5' end"
XX
PN WO9624676-A1.
XX
PD 15-AUG-1996.
XX

PF 07-FEB-1996; 96WO-US01787.
XX
PR 08-FEB-1995; 95US-0385335.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
XX
PI Lieschke GJ, Mulligan RC;
XX
DR WPI; 1996-384448/38.
DR P-PSDB; AAR99244.
XX
PT New DNA encoding fusion protein, esp. contg. IL-12 p35 and p40
PT subunits - for treatment of established tumours or prevention of
PT tumour establishment
XX
PS Example 4; Page 24; 118pp; English.
XX
CC A nucleic acid sequence (AAT35197) codes for a (Gly6)Ser linker
CC (AAR99245) utilised in interleukin-12 (IL-12) fusion proteins.
CC The bioactive IL-12 fusion protein comprises the IL-12 p40
CC subunit joined to the IL-12 p35 subunit (deleted of the signal
CC peptide) via the linker. DNA encoding such a construct can be
CC incorporated into a vector (pref. SFG-based retroviral vector) to
CC allow prodn. of the IL-12 dimer in transfected cells. Tumour
CC cells (esp. CMS-5, B16 or renal carcinoma cells) secreting IL-12
CC dimer can be used to reduce the size of established tumours and/or
CC increase survival time, esp. in cases of melanoma, fibrosarcoma
CC and renal cell carcinoma.
XX
SQ Sequence 33 BP; 6 A; 6 C; 15 G; 6 T; 0 other;

Query Match 55.0%; Score 33; DB 17; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAAC 34
||||||||||||||||||||||||||||||||
Db 1 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAAC 33

RESULT 2
ABL10788
ID ABL10788 standard; cDNA; 3352 BP.
XX
AC ABL10788;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 26846.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB66685.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 26846; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 3352 BP; 877 A; 808 C; 761 G; 906 T; 0 other;

Query Match 50.7%; Score 30.4; DB 23; Length 3352;
Best Local Similarity 71.4%; Pred. No. 0.22;
Matches 40; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
|||||||| ||||| |||||||| | || | || || || || || | || || ||
Db 285 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 340

RESULT 3
ABL08253/c
ID ABL08253 standard; cDNA; 4343 BP.
XX
AC ABL08253;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 19241.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ss.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
DR WPI; 2001-656860/75.
DR P-PSDB; ABB64150.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
PS Claim 1; SEQ ID NO 19241; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed

```
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 4343 BP; 1099 A; 1216 C; 1171 G; 857 T; 0 other;

  Query Match             50.7%;  Score 30.4;  DB 23;  Length 4343;
  Best Local Similarity   71.4%;  Pred. No. 0.23;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||||||| |||| |||||||| |  || | ||  ||  || || | || || ||
Db        244 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 189


RESULT 4
ABL08252
ID   ABL08252 standard; cDNA; 6727 BP.
XX
AC   ABL08252;
XX
DT   26-MAR-2002  (first entry)
XX
DE   Drosophila melanogaster expressed polynucleotide SEQ ID NO 19238.
XX
KW   Drosophila; developmental biology; cell signalling; insecticide;
KW   pharmaceutical; gene; ss.
XX
OS   Drosophila melanogaster.
XX
PN   WO200171042-A2.
XX
PD   27-SEP-2001.
XX
PF   23-MAR-2001; 2001WO-US09231.
XX
PR   23-MAR-2000; 2000US-191637P.
PR   11-JUL-2000; 2000US-0614150.
XX
PA   (PEKE ) PE CORP NY.
XX
PI   Venter JC,  Adams M,  Li PWD,  Myers EW;
XX
DR   WPI; 2001-656860/75.
DR   P-PSDB; ABB64149.
XX
PT   New isolated nucleic acid detection reagent for detecting 1000 or more
PT   genes from Drosophila and for elucidating cell signalling and cell-cell
PT   interactions -
XX
PS   Claim 1; SEQ ID NO 19238; 21pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated nucleic acid detection reagent
CC   capable of detecting 1000 or more genes from Drosophila. The invention is
CC   useful in developmental biology and in elucidating cell signalling and
CC   cell-cell interactions in higher eukaryotes for the development of
CC   insecticides, therapeutics and pharmaceutical drugs. The invention
CC   discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC   sequences (ABL01840-ABL16175) and the encoded proteins
CC   (ABB57737-ABB72072).
CC   The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 6727 BP; 1645 A; 1611 C; 1680 G; 1791 T; 0 other;

  Query Match             50.7%;  Score 30.4;  DB 23;  Length 6727;
  Best Local Similarity   71.4%;  Pred. No. 0.26;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
Db       5484 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 5539


RESULT 5
AAL44013
ID   AAL44013 standard; DNA; 42 BP.
XX
AC   AAL44013;
XX
DT   27-SEP-2002  (first entry)
XX
DE   Reproductive recombination virus-related oligonucleotide SEQ IN #33.
XX
KW   Gene therapy; ss; reproductive recombination virus; tumour cell killing;
KW   Epstein-Barr virus; cancer-suppressing gene; vascular inhibition gene;
KW   cell factor gene; prodrug-converting enzyme gene; cell death gene;
KW   nasopharyngeal cancer; Hodgkin's lymphoma; gastric cancer; PCR; primer.
XX
OS   Unidentified.
XX
PN   WO200256917-A1.
XX
PD   25-JUL-2002.
XX
PF   17-JAN-2002; 2002WO-CN00025.
XX
PR   18-JAN-2001; 2001CN-0105247.
XX
PA   (VIRG-) VIRGENE BIOTECHNOLOGY LTD.
XX
PI   Qian Q,  Che X,  Sham S,  Wu M;
XX
DR   WPI; 2002-566772/60.
XX
PT   Construction of reproductive recombination virus able to specifically
PT   kill Epstein-Barr associated tumor cells, useful in drugs for treating
PT   e.g. nasopharyngeal cancer, Hodgkin's lymphoma and gastric cancer -
XX
PS   Example 9; Page 23; 44pp; Chinese.
XX
CC   The invention comprises a reproductive recombination virus capable of
CC   killing specifically tumour cells associated with Epstein-Barr (EB)
CC   virus. The virus of the invention comprises an insertion of a target gene
CC   into the non-reproduction-requiring domain in the virus gene group (the
CC   target gene is a cancer-suppressing gene, vascular inhibition gene, cell
CC   factor gene, prodrug-converting enzyme gene or cell death gene). The
CC   reproductive recombination virus of the invention is useful for treating
CC   nasopharyngeal cancer, Hodgkin's lymphoma and gastric cancer. The present
CC   DNA sequence was used in an example of the invention.
XX
SQ   Sequence 42 BP; 6 A; 13 C; 16 G; 7 T; 0 other;

  Query Match             48.7%;  Score 29.2;  DB 24;  Length 42;
  Best Local Similarity   81.0%;  Pred. No. 0.26;
  Matches   34;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          8 GGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACT 49
              |||||||||||||||||||||||||||| | ||     | |||
Db          1 GGTGGCGGTGGCGGCGGATCTAGAAACCTCCCCGTGGCCACT 42


RESULT 6
AAV00256/c
ID   AAV00256 standard; cDNA; 1878 BP.
XX
AC   AAV00256;
XX
DT   21-MAY-1998  (first entry)
XX
DE   Mouse Ret ligand retL3 cDNA partial clone (EST AA50083).
XX
KW   Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
KW   cell growth; renal cell; nerve cell; renal failure; nephritis;
KW   kidney transplant; toxic injury; hypoxic injury;
KW   neurodegeneration; motor neurone disease; multiple sclerosis;
```

```
KW   infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW   cranial nerve injury; spinal cord injury; Down's syndrome;
KW   cerebral palsy; Lyme disease; muscular dystrophy;
KW   myasthenia gravis; tumour; therapy; ss.
XX
OS   Mus musculus.
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FH   Key             Location/Qualifiers
FT   CDS             205..1245
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PN   WO9744356-A2.
XX
PD   27-NOV-1997.
XX
PF   07-MAY-1997;    97WO-US07726.
XX
PR   10-APR-1997;    97US-0017427.
PR   08-MAY-1996;    96US-0017427.
PR   07-JUN-1996;    96US-0019300.
PR   16-JUL-1996;    96US-0021859.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Cate RL,  Hession C,  Sanicola-Nadel M;
XX
DR   WPI; 1998-018431/02.
DR   P-PSDB; AAW37465.
XX
PT   New nucleic acid encoding ret receptor ligands and related proteins
PT   - vectors, transformed cells and antibodies, used for promoting cell
PT   growth and improving survival of injured cells, especially renal or
PT   nerve cells
XX
PS   Disclosure; Page 71-73; 113pp; English.
XX
CC   This sequence comprises EST AA050083, identified as a partial cDNA
CC   for mouse Ret ligand (RetL) RetL3 (see AAW37465), by sceening of
CC   an EST database with rat RetL1 (see AAW37457).  A full-length
CC   mouse retL3 cDNA clone (see AAV00249) was obtained by combining
CC   AA050083 with a clone obtained by 5'RACE.  Rat, mouse and
CC   human retL1, retL2 and retL3 cDNA sequences (see AAV00245-51) and
CC   encoded polypeptides (see AAW37457-63) are claimed and can be used
CC   in methods for promoting cell growth and improving survival of
CC   cells, especially renal or neural cells.
XX
SQ   Sequence 1878 BP; 389 A; 575 C; 478 G; 436 T; 0 other;

  Query Match             48.7%;  Score 29.2;  DB 19;  Length 1878;
  Best Local Similarity   69.0%;  Pred. No. 0.55;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
Db        630 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 573


RESULT 7
AAV00249/c
ID   AAV00249 standard; cDNA; 1889 BP.
XX
AC   AAV00249;
XX
DT   21-MAY-1998  (first entry)
XX
DE   Mouse Ret ligand retL3 cDNA.
XX
KW   Ret ligand; RetL; RetL3; receptor; signal transduction; mouse;
KW   cell growth; renal cell; nerve cell; renal failure; nephritis;
KW   kidney transplant; toxic injury; hypoxic injury;
KW   neurodegeneration; motor neurone disease; multiple sclerosis;
KW   infection; meningitis; myelopathy; Creutzfeldt-Jakob disease;
KW   cranial nerve injury; spinal cord injury; Down's syndrome;
KW   cerebral palsy; Lyme disease; muscular dystrophy;
KW   myasthenia gravis; tumour; therapy; ss.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             41..1234
FT                   /*tag=  a
XX
PN   WO9744356-A2.
XX
PD   27-NOV-1997.
XX
PF   07-MAY-1997;    97WO-US07726.
XX
PR   10-APR-1997;    97US-0017427.
PR   08-MAY-1996;    96US-0017427.
PR   07-JUN-1996;    96US-0019300.
PR   16-JUL-1996;    96US-0021859.
XX
PA   (BIOJ ) BIOGEN INC.
XX
PI   Cate RL,  Hession C,  Sanicola-Nadel M;
XX
DR   WPI; 1998-018431/02.
DR   P-PSDB; AAW37461.
XX
PT   New nucleic acid encoding ret receptor ligands and related proteins
PT   - vectors, transformed cells and antibodies, used for promoting cell
PT   growth and improving survival of injured cells, especially renal or
PT   nerve cells
XX
PS   Claim 1; Page 75-77; 113pp; English.
XX
CC   This sequence comprises cDNA coding for mouse Ret ligand (RetL)
CC   RetL3 (see AAW37461), a key component of the Ret signalling pathway.
CC   It was deduced from a partial clone (see AAV00256) obtained from
CC   from an EST database search with rat RetL1 (see AAW37457) and from
CC   a clone obtained by 5' RACE.  Rat and human retL1, and human retL2
CC   and retL3 DNA sequences are also claimed (see AAV00245-48 and
CC   AAV00250-51).  Vectors containing retL3 DNA and prokaryotic or
CC   eukaryotic host cells transformed or transfected with these vectors
CC   are claimed, as well as a method for production of RetL3, its
CC   soluble variants and fusion proteins with a toxin, imageable
CC   compound or radionuclide.  RetL3, optionally when expressed from
CC   vectors in vivo, is used to promote growth of new tissue and
CC   survival of damaged tissue, particularly kidney or neural tissue.
CC   Typical applications are in renal failure, nephritis, kidney
CC   transplants, toxic or hypoxic injury, neurodegeneration, motor
CC   neurone disease, multiple sclerosis, bacterial, viral or prion
CC   infections (e.g. meningitis, myelopathy associated with HIV or
CC   Creutzfeldt-Jakob disease), cranial nerve or spinal cord injury,
CC   developmental disorders such as Down's syndrome and cerebral palsy,
CC   or conditions involving the peripheral nervous system (Lyme disease,
CC   muscular dystrophy and myasthenia gravis).  Fusion proteins are
CC   used to deliver toxins etc. to Ret-expressing cells, especially
CC   tumours.
XX
SQ   Sequence 1889 BP; 410 A; 569 C; 473 G; 437 T; 0 other;

  Query Match             48.7%;  Score 29.2;  DB 19;  Length 1889;
  Best Local Similarity   69.0%;  Pred. No. 0.55;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
Db        619 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 562


RESULT 8
AAZ29100/c
ID   AAZ29100 standard; cDNA; 1935 BP.
XX
```

```
AC   AAZ29100;
XX
DT   07-FEB-2000  (first entry)
XX
DE   Murine GFRalpha3 cDNA.
XX
KW   Murine GFRalpha3; GFRalpha3; GFRalpha1;
KW   glial-cell-line-derived neurotrophic factor family receptor alpha-3;
KW   probe; homologous DNA; neuronal cell activation; GFRalpha3 ligand;
KW   cell proliferation; cell differentiation; GFRalpha3-containing cell;
KW   Ret-containing cell; peripheral nervous system disease; diabetes;
KW   human immunodeficiency virus; chemotherapeutic agent treatment;
KW   autonomic nervous system dysfunction; transgenic animal; ds.
XX
OS   Mus musculus.
XX
FH   Key             Location/Qualifiers
FT   CDS             89..1282
FT                   /*tag=  a
FT                   /product= "Murine GFRalpha 3"
FT   sig_peptide     89..169
FT                   /*tag=  b
XX
PN   WO9949039-A2.
XX
PD   30-SEP-1999.
XX
PF   19-MAR-1999;   99WO-US06098.
XX
PR   23-MAR-1998;   98US-0079124.
PR   13-APR-1998;   98US-0081569.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   De Sauvage FJ,  Klein RD,  Phillips HS,  Rosenthal A;
XX
DR   WPI; 2000-038358/03.
DR   P-PSDB; AAY15174.
XX
PT   New isolated GFR-alpha3 nucleic acid, used to develop products for
PT   treating diseases or conditions involving peripheral nervous system or
PT   autonomic nervous system -
XX
PS   Example 1; Fig 1; 112pp; English.
XX
CC   The present sequence encodes full length mouse glial-cell-line-derived
CC   neurotrophic factor family receptor alpha-3 (GFRalpha3). This has
CC   sequence identity with GFRalpha1. GFRalpha3 DNA or its fragments can be
CC   used as a probe to screen for homologous DNA. GFRalpha3 possess neuronal
CC   cell activation property. GFRalpha3 ligands can be used to stimulate
CC   proliferation, growth, survival, differentiation, metabolism or
CC   regeneration of GFRalpha3- and Ret-containing cells. They can be useful
CC   in the treatment of peripheral nervous system diseases, eg. those
CC   associated with diabetes, human immunodeficiency virus, or
CC   chemotherapeutic agent treatments. Agonist or antagonists of GFRalpha3
CC   can be used to treat autonomic nervous system dysfunctions. The products
CC   can also be used for detection, diagnosis and production of transgenic
CC   animals.
XX
SQ   Sequence 1935 BP; 418 A; 584 C; 490 G; 443 T; 0 other;

  Query Match             48.7%;  Score 29.2;  DB 21;  Length 1935;
  Best Local Similarity   69.0%;  Pred. No. 0.55;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| |||||||    | | ||||  ||| ||  || | | | ||
Db        667 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 610


RESULT 9
ABV54109/c
ID   ABV54109 standard; cDNA; 576 BP.
XX
AC   ABV54109;
XX
DT   17-SEP-2002  (first entry)
XX
DE   Human prostate expression marker cDNA 54100.
XX
KW   Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker;
KW   pharmacogenomic marker; gene; ss.
XX
OS   Homo sapiens.
XX
PN   WO200160860-A2.
XX
PD   23-AUG-2001.
XX
PF   20-FEB-2001; 2001WO-US05171.
XX
PR   17-FEB-2000; 2000US-183319P.
PR   16-MAR-2000; 2000US-189862P.
PR   25-MAY-2000; 2000US-207454P.
PR   09-JUN-2000; 2000US-211314P.
PR   18-JUL-2000; 2000US-219007P.
PR   13-DEC-2000; 2000US-255281P.
XX
PA   (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
XX
PI   Schlegel R,  Endege WO,  Monahan JE;
XX
DR   WPI; 2001-662795/76.
XX
PT   Novel isolated nucleic acid molecule associated with cancerous state of
PT   prostate cells and correlating with presence of prostate cancer, useful
PT   for detecting presence of prostate cancer, stage of prostate cancer  -
XX
PS   Claim 1; Page 10468; 11750pp; English.
XX
CC   The invention relates to an isolated nucleic acid molecule (I) comprising
CC   a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
CC   specification or its complement. (I) is useful for:
CC   (a) assessing whether a patient is afflicted with prostate cancer;
CC   (b) monitoring the progression of prostate cancer in a patient;
CC   (c) assessing the efficacy of a test compound to inhibit prostate
CC   cancer in a patient;
CC   (d) assessing the efficacy of a therapy for inhibiting prostate cancer
CC   in a patient;
CC   (e) selecting a composition for inhibiting prostate cancer in a patient;
CC   (f) assessing the prostate cell carcinogenic potential of a compound;
CC   (g) determining whether prostate cancer has metastasized in a patient;
CC   (h) assessing the aggressiveness or indolence of prostate cancer in a
CC   patient;
CC   (I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
XX
SQ   Sequence 576 BP; 171 A; 95 C; 100 G; 210 T; 0 other;

  Query Match             47.7%;  Score 28.6;  DB 23;  Length 576;
  Best Local Similarity   79.1%;  Pred. No. 0.72;
  Matches   34;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy         15 GTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||| ||| ||| |||||| |||||| | |||| | ||||| |
Db        211 GTGGAGGCAGATGTAGAAAATTGCCAGCACCTAATACATCCAC 169


RESULT 10
AAZ21160
ID   AAZ21160 standard; DNA; 1080 BP.
XX
AC   AAZ21160;
XX
DT   17-NOV-1999  (first entry)
XX
DE   Artificial synthetic construct DNA sequence SEQ ID NO:39.
```

XX
KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection; ss.
XX
OS Synthetic.
XX
PN WO9946392-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05345.
XX
PR 12-MAR-1998; 98US-0077745.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kwak LW, Biragyn A;
XX
DR WPI; 1999-551418/46.
XX
PT New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX
PS Disclosure; Page 125; 142pp; English.
XX
CC The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion
CC proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and
CC human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)
CC human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human
CC MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and
CC HIV gp120. The fusion proteins, and nucleotide sequences encoding them,
CC can be used for producing an immune response, e.g. an effector T cell
CC immune response. They can also be used for treating cancer or treating
CC or preventing HIV infection. The fusion proteins and/or nucleotide
CC sequences can be used in in vitro diagnostic assays, as well as in
CC screening assays for identifying unknown tumour antigen epitopes and fine
CC mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AAZ21168 are
CC sequences given in the SEQ ID LISTING in the present invention but which
CC are not mentioned further within the specification.
XX
SQ Sequence 1080 BP; 306 A; 262 C; 271 G; 241 T; 0 other;

Query Match 47.0%; Score 28.2; DB 20; Length 1080;
Best Local Similarity 68.4%; Pred. No. 1.1;
Matches 39; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
| |||| |||||||||| |||||||| | | | || | |||||||| |
Db 669 CGGCAGCGGTGGCGGTGGGAGCGGATCTGACATCCAGATGACACAGTCTCCATCCTC 725

RESULT 11
AAZ21157
ID AAZ21157 standard; DNA; 1086 BP.
XX
AC AAZ21157;
XX
DT 17-NOV-1999 (first entry)
XX
DE Artificial synthetic construct DNA sequence SEQ ID NO:36.
XX
KW Chemokine; tumour; viral; antigen; fusion protein; cancer; vaccine;
KW immune response; HIV; infection; ss.
XX
OS Synthetic.
XX
PN WO9946392-A1.
XX
PD 16-SEP-1999.
XX
PF 12-MAR-1999; 99WO-US05345.
XX
PR 12-MAR-1998; 98US-0077745.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Kwak LW, Biragyn A;
XX
DR WPI; 1999-551418/46.
XX
PT New fusion polypeptides comprising a chemokine and a tumour antigen or
PT HIV antigen, used for treating cancers or treating or preventing HIV
PT infection -
XX
PS Disclosure; Page 123; 142pp; English.
XX
CC The present invention describes fusion proteins comprising a chemokine
CC and a tumour antigen or HIV antigen. Specifically claimed fusion
CC proteins comprise: (1) human monocyte chemotactic protein-3 (MCP-3) and
CC human Muc-1; (2) human interferon-induced protein 10 (IP-10) and human
CC Muc-1; (3) human macrophage-derived chemokine (MDC) and human Muc-1; (4)
CC human SDF-1 and human Muc-1; (5) human IP-10 and HIV gp120; (6) human
CC MCP-3 and HIV gp120; (7) human MDC and HIV gp120; and (8) human SDF-1 and
CC HIV gp120. The fusion proteins, and nucleotide sequences encoding them,
CC can be used for producing an immune response, e.g. an effector T cell
CC immune response. They can also be used for treating cancer or treating
CC or preventing HIV infection. The fusion proteins and/or nucleotide
CC sequences can be used in in vitro diagnostic assays, as well as in
CC screening assays for identifying unknown tumour antigen epitopes and fine
CC mapping of tumour antigen epitopes. AAY29916 and AAZ21156 to AAZ21168 are
CC sequences given in the SEQ ID LISTING in the present invention but which
CC are not mentioned further within the specification.
XX
SQ Sequence 1086 BP; 309 A; 252 C; 270 G; 255 T; 0 other;

Query Match 47.0%; Score 28.2; DB 20; Length 1086;
Best Local Similarity 68.4%; Pred. No. 1.1;
Matches 39; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
| |||| |||||||||| |||||||| | | | || | |||||||| |
Db 675 CGGCAGCGGTGGCGGTGGGAGCGGATCTGACATCCAGATGACACAGTCTCCATCCTC 731

RESULT 12
AAL44012/c
ID AAL44012 standard; DNA; 42 BP.
XX
AC AAL44012;
XX
DT 27-SEP-2002 (first entry)
XX
DE Reproductive recombination virus-related oligonucleotide SEQ IN #32.
XX
KW Gene therapy; ss; reproductive recombination virus; tumour cell killing;
KW Epstein-Barr virus; cancer-suppressing gene; vascular inhibition gene;
KW cell factor gene; prodrug-converting enzyme gene; cell death gene;
KW nasopharyngeal cancer; Hodgkin's lymphoma; gastric cancer; PCR; primer.
XX
OS Unidentified.
XX
PN WO200256917-A1.
XX
PD 25-JUL-2002.
XX
PF 17-JAN-2002; 2002WO-CN00025.
XX
PR 18-JAN-2001; 2001CN-0105247.
XX
PA (VIRG-) VIRGENE BIOTECHNOLOGY LTD.
XX
PI Qian Q, Che X, Sham S, Wu M;
XX

```
DR   WPI; 2002-566772/60.
XX
PT   Construction of reproductive recombination virus able to specifically
PT   kill Epstein-Barr associated tumor cells, useful in drugs for treating
PT   e.g. nasopharyngeal cancer, Hodgkin's lymphoma and gastric cancer -
XX
PS   Example 9; Page 23; 44pp; Chinese.
XX
CC   The invention comprises a reproductive recombination virus capable of
CC   killing specifically tumour cells associated with Epstein-Barr (EB)
CC   virus. The virus of the invention comprises an insertion of a target gene
CC   into the non-reproduction-requiring domain in the virus gene group (the
CC   target gene is a cancer-suppressing gene, vascular inhibition gene, cell
CC   factor gene, prodrug-converting enzyme gene or cell death gene). The
CC   reproductive recombination virus of the invention is useful for treating
CC   nasopharyngeal cancer, Hodgkin's lymphoma and gastric cancer. The present
CC   DNA sequence was used in an example of the invention.
XX
SQ   Sequence 42 BP; 10 A; 19 C; 10 G; 3 T; 0 other;

  Query Match             46.7%;  Score 28;  DB 24;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 0.72;
  Matches   28;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCT 28
              ||||||||||||||||||||||||||||
Db         28 CTGCAGTGGTGGCGGTGGCGGCGGATCT 1


RESULT 13
AAD31548
ID   AAD31548 standard; DNA; 8608 BP.
XX
AC   AAD31548;
XX
DT   18-JUN-2002  (first entry)
XX
DE   pIRES-hB7-1-IL12.2 vector DNA.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12.2; chimeric; human; Simian virus 40;
KW   SV40; cytomegalovirus; CMV; ds.
XX
OS   Chimeric - Cytomegalovirus.
OS   Chimeric - Bacteriophage T7.
OS   Chimeric - Homo sapiens.
OS   Chimeric - Bacteriophage T3.
OS   Chimeric - Rhesus macaque polyoma virus.
OS   Chimeric - Unidentified.
XX
FH   Key             Location/Qualifiers
FT   enhancer        1..750
FT                   /*tag=  a
FT                   /note= "CMV enhancer; Also serves as a promoter"
FT   misc_feature    890..1002
FT                   /*tag=  b
FT                   /note= "Intervening sequence"
FT   promoter        1067..1085
FT                   /*tag=  c
FT                   /note= "T7 RNA polymerase promoter"
FT   misc_feature    1090..1984
FT                   /*tag=  d
FT                   /note= "Human B7-1 DNA"
FT   misc_feature    1090..1956
FT                   /*tag=  e
FT                   /note= "Human B7-1 coding region"
FT   RBS             2013..2593
FT                   /*tag=  f
FT                   /note= "IRES sequence"
FT   misc_feature    2627..4263
FT                   /*tag=  g
FT                   /note= "Human IL-12.2 DNA"
FT   CDS             2640..4253
FT                   /*tag=  h
FT                   /product= "Human IL-12.2 protein"
FT   misc_feature    3606..3676
FT                   /*tag=  i
FT                   /note= "Flexible linker of human IL-12.2 sequence"
FT   promoter        4362..4383
FT                   /*tag=  j
FT                   /note= "T3 RNA polymerase promoter"
FT   polyA_signal    4393..4614
FT                   /*tag=  k
FT                   /note= "SV40 fragment containing polyadenylation signal"
FT   rep_origin      4709..5164
FT                   /*tag=  l
FT                   /note= "f1 origin of replication"
FT   misc_feature    5228..6595
FT                   /*tag=  m
FT                   /note= "Neo r expression cassette"
FT   misc_feature    7006..7866
FT                   /*tag=  n
FT                   /note= "Ampicillin resistance"
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
DR   P-PSDB; AAE19820.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
PT   operably linked to promoter that directs the expression of DNA molecule
PT   -
XX
PS   Example 1; Page 31-36; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is pIRES-hB7-1-IL12.2 vector DNA.
CC   This vector comprises cytomegalovirus (CMV) promoter and enhancer,
CC   bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
CC   human IL-12.2 DNA, bacteriophage T3 RNA polymerase promoter,
CC   Simian virus 40 (SV40) fragment containing polyadenylation signal, f1
CC   origin of replication, Neo r expression cassette and ampicillin
CC   resistance sequence.
XX
SQ   Sequence 8608 BP; 2180 A; 2126 C; 2138 G; 2164 T; 0 other;

  Query Match             46.0%;  Score 27.6;  DB 24;  Length 8608;
  Best Local Similarity   67.2%;  Pred. No. 2.8;
  Matches   39;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              | || |||||||||||  ||  ||  |||||| | ||     | ||||||  ||| ||
Db       3634 GAAGCGGTGGCGGTGGAAGCCCATGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGG 3691
```

```
RESULT 14
AAD31547
ID   AAD31547 standard; DNA; 8623 BP.
XX
AC   AAD31547;
XX
DT   18-JUN-2002  (first entry)
XX
DE   pIRES-hB7-1-IL12.3 vector DNA.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12.3; chimeric; human; Simian virus 40;
KW   SV40; cytomegalovirus; CMV; ds.
XX
OS   Chimeric - Cytomegalovirus.
OS   Chimeric - Bacteriophage T7.
OS   Chimeric - Homo sapiens.
OS   Chimeric - Bacteriophage T3.
OS   Chimeric - Rhesus macaque polyoma virus.
OS   Chimeric - Unidentified.
XX
FH   Key             Location/Qualifiers
FT   enhancer        1..750
FT                   /*tag= a
FT                   /note= "CMV enhancer; Also serves as a promoter"
FT   misc_feature    890..1002
FT                   /*tag= b
FT                   /note= "Intervening sequence"
FT   promoter        1067..1085
FT                   /*tag= c
FT                   /note= "T7 RNA polymerase promoter"
FT   misc_feature    1090..1984
FT                   /*tag= d
FT                   /note= "Human B7-1 DNA"
FT   misc_feature    1090..1956
FT                   /*tag= e
FT                   /note= "Human B7-1 coding region"
FT   RBS             2013..2593
FT                   /*tag= f
FT                   /note= "IRES sequence"
FT   misc_feature    2627..4278
FT                   /*tag= g
FT                   /note= "Human IL-12.3 DNA"
FT   CDS             2640..4268
FT                   /*tag= h
FT                   /product= "Human IL-12.3 protein"
FT   misc_feature    3606..3690
FT                   /*tag= i
FT                   /note= "Flexible linker of human IL-12.3 sequence"
FT   promoter        4398..4407
FT                   /*tag= j
FT                   /note= "T3 RNA polymerase promoter"
FT   polyA_signal    4408..4629
FT                   /*tag= k
FT                   /note= "SV40 fragment containing polyadenylation signal"
FT   rep_origin      4724..5179
FT                   /*tag= l
FT                   /note= "f1 origin of replication"
FT   misc_feature    5243..6610
FT                   /*tag= m
FT                   /note= "Neo r expression cassette"
FT   misc_feature    7021..7881
FT                   /*tag= n
FT                   /note= "Ampicillin resistance"
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
DR   P-PSDB; AAE19819.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
PT   operably linked to promoter that directs the expression of DNA molecule
PT   -
XX
PS   Example 1; Page 24-29; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is pIRES-hB7-1-IL12.3 vector DNA.
CC   This vector comprises cytomegalovirus (CMV) promoter and enhancer,
CC   bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
CC   human IL-12.3 DNA, bacteriophage T3 RNA polymerase promoter,
CC   Simian virus 40 (SV40) fragment containing polyadenylation signal, f1
CC   origin of replication, Neo r expression cassette and ampicillin
CC   resistance sequence.
XX
SQ   Sequence 8623 BP; 2182 A; 2128 C; 2147 G; 2166 T; 0 other;

  Query Match             46.0%;  Score 27.6;  DB 24;  Length 8623;
  Best Local Similarity   67.2%;  Pred. No. 2.8;
  Matches   39;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              | || |||||||||||  ||  ||  |||||| | ||     | ||||||  ||| ||
Db       3649 GAAGCGGTGGCGGTGGAAGCCCATGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGG 3706


RESULT 15
AAD31552
ID   AAD31552 standard; DNA; 8629 BP.
XX
AC   AAD31552;
XX
DT   18-JUN-2002  (first entry)
XX
DE   pIRES-IL12.2-hb7-1 vector DNA.
XX
KW   Expression system; interleukin-12; cancer therapy; cellular vaccine;
KW   immunotherapeutic response; IL-12.2; chimeric; human; Simian virus 40;
KW   SV40; cytomegalovirus; CMV; ds.
XX
OS   Chimeric - Cytomegalovirus.
OS   Chimeric - Bacteriophage T7.
OS   Chimeric - Homo sapiens.
OS   Chimeric - Bacteriophage T3.
OS   Chimeric - Rhesus macaque polyoma virus.
OS   Chimeric - Unidentified.
XX
FH   Key             Location/Qualifiers
FT   enhancer        1..750
FT                   /*tag= a
FT                   /note= "CMV enhancer; Also serves as a promoter"
FT   promoter        1067..1085
FT                   /*tag= b
FT                   /note= "T7 RNA polymerase promoter"
FT   misc_feature    1090..2726
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FT                   /*tag=  c
FT                   /note= "Human IL-12.2 DNA"
FT   CDS             1103..2716
FT                   /*tag=  d
FT                   /product= "Human IL-12.2 protein"
FT   misc_feature    2087..2116
FT                   /*tag=  e
FT                   /note= "Linker of human IL-12.2 sequence"
FT   RBS             2752..3332
FT                   /*tag=  f
FT                   /note= "IRES sequence"
FT   misc_feature    3369..4263
FT                   /*tag=  g
FT                   /note= "Human B7-1 DNA"
FT   promoter        4383..4404
FT                   /*tag=  h
FT                   /note= "T3 RNA polymerase promoter"
FT   polyA_signal    4414..4635
FT                   /*tag=  i
FT                   /note= "SV40 fragment containing polyadenylation signal"
FT   rep_origin      4730..5185
FT                   /*tag=  j
FT                   /note= "f1 origin of replication"
FT   misc_feature    5249..6616
FT                   /*tag=  k
FT                   /note= "Neo r expression cassette"
FT   misc_feature    7027..7887
FT                   /*tag=  l
FT                   /note= "Ampicillin resistance"
XX
PN   US2002018767-A1.
XX
PD   14-FEB-2002.
XX
PF   10-APR-2001; 2001US-0828825.
XX
PR   27-JUL-2000; 2000KR-0043498.
XX
PA   (LEES/) LEE S.
PA   (KIMH/) KIM H.
XX
PI   Lee S,  Kim H;
XX
DR   WPI; 2002-239247/29.
DR   P-PSDB; AAE19824.
XX
PT   New expression system, useful as vaccine for treating cancer, comprises
PT   DNA molecule encoding interleukin-12 and costimulatory molecule,
PT   operably linked to promoter that directs the expression of DNA molecule
PT    -
XX
PS   Example 1; Page 59-63; 76pp; English.
XX
CC   The invention relates to an expression system which comprises a DNA
CC   molecule encoding interleukin (IL)-12 and a costimulatory molecule,
CC   operably linked to a promoter that directs the expression of the DNA
CC   molecule. Expression vectors of the invention are useful for in vitro
CC   generation of genetically modified human cancer cells for cancer
CC   therapy. These cells share phenotypes of both antigen presenting cells
CC   and cancer cells and are suitable as a cellular vaccine for certain
CC   types of cancer. Expression vectors are useful for eliciting an anti
CC   tumour immune response in a individual. They are useful for activating
CC   T cells for immunotherapeutic responses against primary or metastatic
CC   cancers. The present sequence is pIRES-IL12.2 hB7-1 vector DNA.
CC   This vector comprises cytomegalovirus (CMV) promoter and enhancer,
CC   bacteriophage T7 RNA polymerase promoter, human B7-1 DNA, IRES sequence,
CC   human IL-12.2 DNA, bacteriophage T3 RNA polymerase promoter,
CC   Simian virus 40 (SV40) fragment containing polyadenylation signal, f1
CC   origin of replication, Neo r expression cassette and ampicillin
CC   resistance sequence.
XX
SQ   Sequence 8629 BP; 2185 A; 2132 C; 2143 G; 2169 T; 0 other;
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  Query Match           46.0%;  Score 27.6;  DB 24;  Length 8629;
  Best Local Similarity  67.2%;  Pred. No. 2.8;
  Matches   39;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              | || |||||||||||  ||  ||  |||||| | ||     | ||||||  ||| ||
Db       2097 GAAGCGGTGGCGGTGGAAGCCCATGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGG 2154


Search completed: July 16, 2003, 06:46:47
Job time : 17.1318 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:30:08 ; Search time 108.731 Seconds
(without alignments)
8936.974 Million cell updates/sec

Title: US-09-917-265-83
Perfect score: 60
Sequence: 1 ctgcagtggtggcggtggcg.....acccctactccatccccggg 60

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	31	51.7	389	13	BI372699	BI372699 RE59742.5
c	2	31	51.7	590	13	BI372718	BI372718 RE59764.5
c	3	30.4	50.7	475	9	AI546686	AI546686 SD10406.5
c	4	30.4	50.7	484	9	AI511787	AI511787 LD43310.5
c	5	30.4	50.7	526	9	AI512758	AI512758 LD44770.5
c	6	30.4	50.7	544	9	AA949039	AA949039 LD27781.5
c	7	30.4	50.7	558	9	AI541995	AI541995 SD07995.5
c	8	30.4	50.7	610	13	BI638233	BI638233 SD20467.5
c	9	30.4	50.7	622	9	AA735618	AA735618 LD21627.5
c	10	29.2	48.7	442	9	AA049894	AA049894 mj11d08.r
	11	29.2	48.7	499	17	AZ758753	AZ758753 1M0550L21
c	12	29.2	48.7	600	13	BI987608	BI987608 3203-65 M
	13	28	46.7	750	12	BG583687	BG583687 EST485440
c	14	27.8	46.3	260	9	AA940899	AA940899 LD23227.5
	15	27.8	46.3	1101	17	CNS00HE3	AL073368 Drosophil
c	16	27.6	46.0	747	12	BE892594	BE892594 601433403
	17	27.2	45.3	637	17	BH268535	BH268535 CH230-122
	18	26.8	44.7	517	9	AI119674	AI119674 uf05g11.y
c	19	26.8	44.7	1101	17	CNS00H7Y	AL073046 Drosophil
c	20	26.6	44.3	395	17	AQ131072	AQ131072 HS_3034_A
	21	26.6	44.3	526	13	BJ519662	BJ519662 BJ519662
c	22	26.6	44.3	527	17	TA158C01Q	AL471964 T. brucei
	23	26.6	44.3	861	17	CNS01FNA	AL142055 Anopheles
	24	26.2	43.7	384	14	R82508	R82508 yj19f05.s1
	25	26	43.3	243	9	AA499721	AA499721 vg05b07.r
	26	26	43.3	609	9	AA667840	AA667840 vs28g10.r
c	27	26	43.3	934	10	BE263153	BE263153 601144896
c	28	25.8	43.0	227	14	D24785	D24785 RICR2555A R
	29	25.6	42.7	146	12	BF363523	BF363523 QV1-NN017
c	30	25.6	42.7	148	12	BF363497	BF363497 QV1-NN017
	31	25.6	42.7	188	12	BF363502	BF363502 QV1-NN017
	32	25.6	42.7	189	12	BF363565	BF363565 QV1-NN017
	33	25.6	42.7	198	12	BF363499	BF363499 QV1-NN017
c	34	25.6	42.7	249	12	BF363632	BF363632 QV1-NN017
	35	25.6	42.7	276	12	BF363540	BF363540 QV1-NN017
c	36	25.6	42.7	280	12	BF363622	BF363622 QV1-NN017
c	37	25.6	42.7	291	12	BF363649	BF363649 QV1-NN017
c	38	25.6	42.7	291	12	BF363654	BF363654 QV1-NN017
	39	25.6	42.7	296	12	BF363630	BF363630 QV1-NN017
c	40	25.6	42.7	296	12	BF363642	BF363642 QV1-NN017
c	41	25.6	42.7	296	12	BF363645	BF363645 QV1-NN017
c	42	25.6	42.7	296	12	BF363647	BF363647 QV1-NN017
c	43	25.6	42.7	297	12	BF363524	BF363524 QV1-NN017
c	44	25.6	42.7	297	12	BF363557	BF363557 QV1-NN017
c	45	25.6	42.7	297	12	BF363650	BF363650 QV1-NN017

ALIGNMENTS

RESULT 1
BI372699/c
LOCUS BI372699 389 bp mRNA linear EST 01-AUG-2001
DEFINITION RE59742.5prime RE Drosophila melanogaster normalized Embryo pFlc-1 Drosophila melanogaster cDNA clone RE59742 5 similar to CG4751: FBan0004751 GO:[] located on: 2L 32D4-32D4;: 05/16/2001, mRNA sequence.
ACCESSION BI372699
VERSION BI372699.1 GI:15068727
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 389)
AUTHORS Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S., Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin,G.M.
TITLE BDGP/HHMI RE Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798

```
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic AE003631: arm:2L [10950468,11211850]
            estimated-cyto:32D2-32F1: 05/16/2001
            Plate: RE.597  row: D  column: 6
            High quality sequence stop: 331.
FEATURES              Location/Qualifiers
     source           1. .389
                      /organism="Drosophila melanogaster"
                      /db_xref="taxon:7227"
                      /clone="RE59742"
                      /clone_lib="RE Drosophila melanogaster normalized Embryo
                      pFlc-1"
                      /sex="male and female"
                      /dev_stage="0-24 hours mixed stage embryonic"
                      /lab_host="DH5-alpha TonA"
                      /note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2:
                      BamHI; Library was kindly generated by Piero Carninci at
                      the RIKEN. The library  was normalized and excised using
                      Cre recombinase. Plasmid cDNA library."
BASE COUNT       98 a     91 c    130 g     69 t      1 others
ORIGIN

  Query Match             51.7%;  Score 31;  DB 13;  Length 389;
  Best Local Similarity   71.4%;  Pred. No. 4.7;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||||||| ||||| ||||||||  |  || | ||  ||  || || | || || ||
Db        264 TGCAGTGGCGGCGGCGGCGGCTNCAGCACCTCCCCCTCCACTTCACCGTCACC 209


RESULT 2
BI372718/c
LOCUS       BI372718                590 bp    mRNA    linear   EST 01-AUG-2001
DEFINITION  RE59764.5prime RE Drosophila melanogaster normalized Embryo pFlc-1
            Drosophila melanogaster cDNA clone RE59764 5 similar to CG4751:
            FBan0004751 GO:[] located on: 2L 32D4-32D4;: 05/16/2001, mRNA
            sequence.
ACCESSION   BI372718
VERSION     BI372718.1  GI:15068746
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 590)
  AUTHORS   Stapleton,M., Brokstein,P., Hong,L., Tyler,D., Berman,B., Carlson
            ,J., Champe,M., Chavez,C., Dorsett,V., Farfan,D., Frise,E., George
            ,R., Gonzalez,M., Guarin,H., Harris,N., Li,P., Liao,G., Misra,S.,
            Mungall,C.J., Nunoo,J., Pacleb,J., Paragas,V., Park,S.,
            Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin
            ,G.M.
  TITLE     BDGP/HHMI RE Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic AE003631: arm:2L [10950468,11211850]
            estimated-cyto:32D2-32F1: 05/16/2001
            Plate: RE.597  row: F  column: 4
            High quality sequence stop: 466.
FEATURES              Location/Qualifiers
     source           1. .590
                      /organism="Drosophila melanogaster"
                      /db_xref="taxon:7227"
                      /clone="RE59764"
                      /clone_lib="RE Drosophila melanogaster normalized Embryo
                      pFlc-1"
                      /sex="male and female"
                      /dev_stage="0-24 hours mixed stage embryonic"
                      /lab_host="DH5-alpha TonA"
                      /note="Organ: embryo; Vector: pFlc1; Site_1: XhoI; Site_2:
                      BamHI; Library was kindly generated by Piero Carninci at
                      the RIKEN. The library  was normalized and excised using
                      Cre recombinase. Plasmid cDNA library."
BASE COUNT      154 a    139 c    191 g    105 t      1 others
ORIGIN

  Query Match             51.7%;  Score 31;  DB 13;  Length 590;
  Best Local Similarity   71.4%;  Pred. No. 5.3;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||||||| ||||| ||||||||  |  || | ||  ||  || || | || || ||
Db        264 TGCAGTGGCGGCGGCGGCGGCGGNTGCAGCACCTCCCCCTCCACTTCACCGTCACC 209


RESULT 3
AI546686/c
LOCUS       AI546686                475 bp    mRNA    linear   EST 19-APR-2001
DEFINITION  SD10406.5prime SD Drosophila melanogaster Schneider L2 cell culture
            pOT2 Drosophila melanogaster cDNA clone SD10406 5prime, mRNA
            sequence.
ACCESSION   AI546686
VERSION     AI546686.1  GI:4464059
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 475)
  AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic sequence AC005115
            Plate: 104  row: A  column: 6
            High quality sequence stop: 405.
FEATURES              Location/Qualifiers
     source           1. .475
                      /organism="Drosophila melanogaster"
                      /db_xref="taxon:7227"
                      /clone="SD10406"
                      /clone_lib="SD Drosophila melanogaster Schneider L2 cell
                      culture pOT2"
                      /lab_host="DH5-alpha"
                      /note="Vector: pOT2; Site_1: EcoRI; Site_2: Xho1; Sized
                      fractionated cDNAs were directly ligated into pOT2.
                      Plasmid cDNA library."
BASE COUNT      123 a    108 c    160 g     84 t
ORIGIN

  Query Match             50.7%;  Score 30.4;  DB 9;  Length 475;
  Best Local Similarity   71.4%;  Pred. No. 7.8;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              |||||||| ||||| ||||||||  |  || | ||  ||  || || | || || ||
Db        214 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 159


RESULT 4
AI511787/c
LOCUS       AI511787                484 bp    mRNA    linear   EST 19-APR-2001
DEFINITION  LD43310.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
```

melanogaster cDNA clone LD43310 5prime, mRNA sequence.
ACCESSION AI511787
VERSION AI511787.1 GI:4421205
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 484)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
TITLE BDGP/HHMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic sequence AC005115
Plate: 433 row: A column: 10
High quality sequence stop: 424.
FEATURES Location/Qualifiers
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="LD43310"
/clone_lib="LD Drosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. "
BASE COUNT 129 a 113 c 163 g 79 t
ORIGIN

Query Match 50.7%; Score 30.4; DB 9; Length 484;
Best Local Similarity 71.4%; Pred. No. 7.8;
Matches 40; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
||||||||| ||||| |||||||| | || | || || || | || || ||
Db 223 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 168

RESULT 5
AI512758/c
LOCUS AI512758 526 bp mRNA linear EST 23-APR-2001
DEFINITION LD44770.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
melanogaster cDNA clone LD44770 5 similar to CG4751: FBan0004751
located on: 2L 32D4-32D4;: 04/10/2001, mRNA sequence.
ACCESSION AI512758
VERSION AI512758.2 GI:13770030
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 526)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
TITLE BDGP/HHMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT On Mar 16, 1999 this sequence version replaced gi:4422176.
Other_ESTs: LD44770.3prime
Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003631: arm:2L [10950468,11211850]
estimated-cyto:32D2-32F1: 04/10/2001
Plate: LD.447 row: F column: 10
High quality sequence stop: 457
POLYA=No.
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/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="LD44770"
/clone_lib="LD Drosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. "
BASE COUNT 140 a 127 c 172 g 87 t
ORIGIN

Query Match 50.7%; Score 30.4; DB 9; Length 526;
Best Local Similarity 71.4%; Pred. No. 8;
Matches 40; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

Qy 2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
||||||||| ||||| |||||||| | || | || || || | || || ||
Db 244 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 189

RESULT 6
AA949039/c
LOCUS AA949039 544 bp mRNA linear EST 19-APR-2001
DEFINITION LD27781.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
melanogaster cDNA clone LD27781 5prime, mRNA sequence.
ACCESSION AA949039
VERSION AA949039.1 GI:3110948
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 544)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
Lewis,S. and Rubin,G.M.
TITLE BDGP/HHMI Drosophila EST Project
JOURNAL Unpublished (2001)
COMMENT Contact: Stapleton, M.
BDGP
Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 277 row: G column: 9
High quality sequence stop: 455.
FEATURES Location/Qualifiers
source 1. .544
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone="LD27781"
/clone_lib="LD Drosophila melanogaster embryo pOT2"
/sex="male and female"
/dev_stage="0 to 24 hours mixed stage embryonic"
/lab_host="XL1 Blue"
/note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. "
BASE COUNT 141 a 128 c 182 g 92 t 1 others
ORIGIN

Query Match 50.7%; Score 30.4; DB 9; Length 544;
Best Local Similarity 71.4%; Pred. No. 8.1;

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  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              ||||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
Db        220 TGCAGTGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 165


RESULT 7
AI541995/c
LOCUS       AI541995                558 bp    mRNA    linear   EST 19-APR-2001
DEFINITION  SD07995.5prime SD Drosophila melanogaster Schneider L2 cell culture
            pOT2 Drosophila melanogaster cDNA clone SD07995 5prime, mRNA
            sequence.
ACCESSION   AI541995
VERSION     AI541995.1  GI:4459368
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 558)
  AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic sequence AC005115
            Plate: 79  row: H  column: 11
            High quality sequence stop: 418.
FEATURES             Location/Qualifiers
     source          1. .558
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="SD07995"
                     /clone_lib="SD Drosophila melanogaster Schneider L2 cell
                     culture pOT2"
                     /lab_host="DH5-alpha"
                     /note="Vector: pOT2; Site_1: EcoRI; Site_2: Xho1; Sized
                     fractionated cDNAs were directly ligated into pOT2.
                     Plasmid cDNA library."
BASE COUNT      141 a    132 c    187 g     98 t
ORIGIN

  Query Match             50.7%;  Score 30.4;  DB 9;  Length 558;
  Best Local Similarity   71.4%;  Pred. No. 8.2;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              ||||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
Db        214 TGCAGTGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 159


RESULT 8
BI638233/c
LOCUS       BI638233                610 bp    mRNA    linear   EST 10-SEP-2001
DEFINITION  SD20467.5prime SD Drosophila melanogaster Schneider L2 cell culture
            pOT2 Drosophila melanogaster cDNA clone SD20467 5 similar to
            CG4751: FBan0004751 GO:[] located on: 2L 32D4-32D4;: 05/19/2001,
            mRNA sequence.
ACCESSION   BI638233
VERSION     BI638233.1  GI:15540443
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 610)
  AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic AE003631: arm:2L [10950468,11211850]
            estimated-cyto:32D2-32F1: 05/19/2001
            Plate: SD.204  row: F  column: 7
            High quality sequence stop: 609.
FEATURES             Location/Qualifiers
     source          1. .610
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="SD20467"
                     /clone_lib="SD Drosophila melanogaster Schneider L2 cell
                     culture pOT2"
                     /lab_host="DH5-alpha"
                     /note="Vector: pOT2; Site_1: EcoRI; Site_2: Xho1; Sized
                     fractionated cDNAs were directly ligated into pOT2.
                     Plasmid cDNA library."
BASE COUNT      158 a    148 c    198 g    106 t
ORIGIN

  Query Match             50.7%;  Score 30.4;  DB 13;  Length 610;
  Best Local Similarity   71.4%;  Pred. No. 8.4;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              ||||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
Db        214 TGCAGTGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 159


RESULT 9
AA735618/c
LOCUS       AA735618                622 bp    mRNA    linear   EST 23-APR-2001
DEFINITION  LD21627.5prime LD Drosophila melanogaster embryo pOT2 Drosophila
            melanogaster cDNA clone LD21627 5 similar to CG4751: FBan0004751
            located on: 2L 32D4-32D4;: 04/10/2001, mRNA sequence.
ACCESSION   AA735618
VERSION     AA735618.2  GI:13767408
KEYWORDS    EST.
SOURCE      fruit fly.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 622)
  AUTHORS   Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G.,
            Lewis,S. and Rubin,G.M.
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     On Jan 9, 1998 this sequence version replaced gi:2761548.
            Other_ESTs: LD21627.3prime
            Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            hit genomic AE003631: arm:2L [10950468,11211850]
            estimated-cyto:32D2-32F1: 04/10/2001
            Plate: LD.216  row: C  column: 3
            High quality sequence stop: 554
            POLYA=No.
FEATURES             Location/Qualifiers
     source          1. .622
                     /organism="Drosophila melanogaster"
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                     /db_xref="taxon:7227"
                     /clone="LD21627"
                     /clone_lib="LD Drosophila melanogaster embryo pOT2"
                     /sex="male and female"
                     /dev_stage="0 to 24 hours mixed stage embryonic"
                     /lab_host="XL1 Blue"
                     /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
                     XhoI; Sized fractionated cDNAs were directly ligated into
                     pOT2. "
BASE COUNT       161 a    151 c    200 g    110 t
ORIGIN

  Query Match             50.7%;  Score 30.4;  DB 9;  Length 622;
  Best Local Similarity   71.4%;  Pred. No. 8.4;
  Matches   40;  Conservative    0;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              ||||||||| ||||| |||||||| |  || | ||  ||  || || | || || ||
Db        223 TGCAGTGGCGGCGGCGGCGGCGGCTGCAGCACCTCCCCCTCCACTTCACCGTCACC 168


RESULT 10
AA049894/c
LOCUS       AA049894                 442 bp    mRNA    linear   EST 30-DEC-1996
DEFINITION  mj11d08.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA
            clone IMAGE:475791 5', mRNA sequence.
ACCESSION   AA049894
VERSION     AA049894.1  GI:1755226
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 442)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     On Dec 30, 1996 this sequence version replaced gi:1529566.
            Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:286535
            Seq primer: -28M13 rev2 from Amersham
            High quality sequence stop: 405.
FEATURES             Location/Qualifiers
     source          1. .442
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:475791"
                     /clone_lib="Soares mouse embryo NbME13.5 14.5"
                     /sex="unknown"
                     /tissue_type="embryo"
                     /dev_stage="13.5-14.5dpc total fetus"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGGAAATTTTTTTTTTTTTTTTTTTTTTT
                     T 3'], on equal amounts of mRNA from 2 13.5dpc and 2
                     14.5dpc embryos [total RNA provided by  Minoru Ko, Wayne
                     State Univ., from 2 ]; double-stranded cDNA was ligated to
                     Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector. Library went through one round of
                     normalization, and was constructed by Bento Soares and
                     M.Fatima Bonaldo.  "
BASE COUNT       79 a    142 c    122 g     99 t
ORIGIN

  Query Match             48.7%;  Score 29.2;  DB 9;  Length 442;
  Best Local Similarity   69.0%;  Pred. No. 19;
  Matches   40;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              |||| ||||||| |||| |||||||    | | |||| ||| ||  || | | | ||
Db        107 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 50


RESULT 11
AZ758753
LOCUS       AZ758753                 499 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0550L21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0550L21 R, DNA sequence.
ACCESSION   AZ758753
VERSION     AZ758753.1  GI:12864893
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 499)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
            ,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0550  row: L  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 499.
FEATURES             Location/Qualifiers
     source          1. .499
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0550L21"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
```

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 124 a 144 c 125 g 106 t
ORIGIN

Query Match 48.7%; Score 29.2; DB 17; Length 499;
Best Local Similarity 69.0%; Pred. No. 20;
Matches 40; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
Db 122 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 179

RESULT 12
BI987608/c
LOCUS BI987608 600 bp mRNA linear EST 20-DEC-2001
DEFINITION 3203-65 Mouse E14.5 retina lambda ZAP II Library Mus musculus cDNA, mRNA sequence.
ACCESSION BI987608
VERSION BI987608.1 GI:17958576
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 600)
AUTHORS Mu,X., Zhao,S., Pershad,R., Hsieh,T.-F., Scarpa,A., Wang,S.W., White,R.A., Beremand,P.D., Thomas,T.L., Gan,L. and Klein,W.H.
TITLE Gene expression in the developing mouse retina by EST sequencing and microarray analysis
JOURNAL Nucleic Acids Res. 29 (24), 4983-4993 (2001)
MEDLINE 21671825
COMMENT Contact: Klein WH
Department of Biochemistry and Molecular Biology
University of Texas M.D. Anderson Cancer Center
Box 117, 1515 Holcombe Blvd., Houston, TX 77030, USA
Tel: 713 792 3646
Fax: 713 790 0329.
FEATURES Location/Qualifiers
source 1. .600
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="Mouse E14.5 retina lambda ZAP II Library"
/tissue_type="neural retina"
/dev_stage="embryonic day 14.5 post-fertilization"
/note="Vector: pAMP10 (Gibco); Cloned unidirectionally. Primer: Oligo dT. RNA Isolation: cytoplasmic RNA preps (Manniatis); Cloning Technique: CUA Cloning (CloneAmp, Life Technologies); Average insert size: 1.8 Kb; Insertion site: TACGTCCACTGAATTCTGAGTG--->. Other information regarding entire library may be found at http://pga.swmed.edu/Data/Libraries/microarray_cdna_libraries.htm."
BASE COUNT 133 a 188 c 156 g 123 t
ORIGIN

Query Match 48.7%; Score 29.2; DB 13; Length 600;
Best Local Similarity 69.0%; Pred. No. 21;
Matches 40; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

Qy 3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
Db 443 GCAGAGGTGGCGCTGGCAGCGGATCCCTGAGCATGCCTCCCCGTAGGCCTTGCGCAGG 386

RESULT 13
BG583687
LOCUS BG583687 750 bp mRNA linear EST 11-APR-2001
DEFINITION EST485440 GVN Medicago truncatula cDNA clone pGVN-74M19 5' end, mRNA sequence.
ACCESSION BG583687
VERSION BG583687.1 GI:13598751
KEYWORDS EST.
SOURCE barrel medic.
ORGANISM Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
REFERENCE 1 (bases 1 to 750)
AUTHORS Fedorova,M., Pierson,B.L., Samac,D.A., Vance,C.P., Gantt,G.S., Town,C.D., Van Aken,S., Utterback,T., Cho,J. and Fraser,C.M.
TITLE ESTs from one month old nitrogen-fixing root nodules of Medicago truncatula, 2001
JOURNAL Unpublished (2001)
COMMENT Contact: Carroll P. Vance
Department of Agronomy and Plant Genetics
University of Minnesota
411 Borlaug Hall, 1991 Upper Buford Circle, St.Paul, MN 55108 USA
Tel: 612 625 5715
Fax: 651-649-5058
Email: vance004@maroon.tc.umn.edu
University of Minnesota name: M384766e TIGR sequence name: MTCEM82TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
FEATURES Location/Qualifiers
source 1. .750
/organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pGVN-74M19"
/clone_lib="GVN"
/tissue_type="N2-fixing root nodules"
/dev_stage="effective root nodules harvested one month post inoculation with Sinorhizobium meliloti"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from effective root nodules harvested one month post inoculation with Sinorhizobium meliloti. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells."
BASE COUNT 169 a 139 c 203 g 239 t
ORIGIN

Query Match 46.7%; Score 28; DB 12; Length 750;
Best Local Similarity 66.7%; Pred. No. 55;
Matches 40; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
Db 424 CTCCGGTGGTGGCGGTGGCGGCAATAATAATAACAATCCATTTCCTGATCCATCTTCTGG 483

RESULT 14
AA940899/c
LOCUS AA940899 260 bp mRNA linear EST 19-APR-2001
DEFINITION LD23227.5prime LD Drosophila melanogaster embryo pOT2 Drosophila melanogaster cDNA clone LD23227 5prime, mRNA sequence.
ACCESSION AA940899
VERSION AA940899.1 GI:3100812
KEYWORDS EST.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 260)
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.

```
  TITLE     BDGP/HHMI Drosophila EST Project
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Stapleton, M.
            BDGP
            Lawrence Berkeley National Lab
            One Cyclotron Rd, Berkeley, CA 94720, USA
            Fax: 510 486 6798
            Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
            Plate: 232  row: C  column: 3
            High quality sequence stop: 159.
FEATURES             Location/Qualifiers
     source          1. .260
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone="LD23227"
                     /clone_lib="LD Drosophila melanogaster embryo pOT2"
                     /sex="male and female"
                     /dev_stage="0 to 24 hours mixed stage embryonic"
                     /lab_host="XL1 Blue"
                     /note="Organ: embryo; Vector: pOT2; Site_1: EcoRI; Site_2:
                     XhoI; Sized fractionated cDNAs were directly ligated into
                     pOT2. "
BASE COUNT       71 a     52 c     83 g     54 t
ORIGIN

  Query Match             46.3%;  Score 27.8;  DB 9;  Length 260;
  Best Local Similarity   69.1%;  Pred. No. 47;
  Matches   38;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              ||||||| ||||| |||||||| |  || |  |  ||  || || | || || ||
Db        228 GCAGTGGCGGCGGCGGCGGCGGCTGCAGCACTTCCCCCTCCACTTCACCGTCACC 174


RESULT 15
CNS00HE3
LOCUS       CNS00HE3               1101 bp    DNA     linear   GSS 03-JUN-1999
DEFINITION  Drosophila melanogaster genome survey sequence TET3 end of BAC:
            BACR34G01 of RPCI-98 library from Drosophila melanogaster (fruit
            fly), genomic survey sequence.
ACCESSION   AL073368
VERSION     AL073368.1  GI:4953148
KEYWORDS    GSS.
SOURCE      Drosophila melanogaster.
  ORGANISM  Drosophila melanogaster
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
            Ephydroidea; Drosophilidae; Drosophila.
REFERENCE   1  (bases 1 to 1101)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT     Determination of this BAC-end sequence was carried out as part of a
            collaboration with the Berkeley Drosophila Genome Project (BDGP).
            The BDGP is constructing a physical map of the Drosophila
            melanogaster genome using these BACs. For further information
            please see  http://www.fruitfly.org The BDGP Drosophila
            melanogaster BAC library was prepared by Kazutoyo Osoegawa and
            Aaron Mammoser in Pieter de Jong's laboratory in the Department of
            Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
            NY. The library is named RPCI-98 and was constructed by partial
            EcoRI digestion of Drosophila DNA provided by the BDGP from the
            isogenic strain y2; cn bw sp, the same strain used for the BDGP's
            P1 and EST libraries. A more detailed description of the library
            and how to order individual BAC clones, the entire library, or
            filters for hybridization from the BACPAC Resource Center can be
            found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES             Location/Qualifiers
     source          1. .1101
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                     /db_xref="taxon:7227"
                     /clone="BACR34G01"
                     /clone_lib="RPCI-98"
                     /note="end : TET3"
BASE COUNT      175 a    323 c    288 g    229 t     86 others
ORIGIN

  Query Match             46.3%;  Score 27.8;  DB 17;  Length 1101;
  Best Local Similarity   66.0%;  Pred. No. 71;
  Matches   35;  Conservative    3;  Mismatches   15;  Indels    0;  Gaps    0;

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Job time : 112.731 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 06:24:59 ; Search time 3.30846 Seconds
(without alignments)
5561.687 Million cell updates/sec

Title: US-09-917-265-83
Perfect score: 60
Sequence: 1 ctgcagtggtggcggtggcg.....accctactccatccccggg 60

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	25.4	42.3	69	2	US-08-373-190-12	Sequence 12, Appl
2	25.4	42.3	69	3	US-08-350-215-11	Sequence 11, Appl
3	25.4	42.3	70	2	US-08-438-190A-11	Sequence 11, Appl
4	25.4	42.3	70	3	US-09-287-145A-11	Sequence 11, Appl
5	25.4	42.3	70	4	US-09-556-111-11	Sequence 11, Appl
6	24.6	41.0	748	1	US-08-235-838-10	Sequence 10, Appl
7	24.6	41.0	748	2	US-08-465-473B-10	Sequence 10, Appl
8	24.6	41.0	2012	1	US-08-235-838-15	Sequence 15, Appl
9	24.6	41.0	2012	2	US-08-465-473B-15	Sequence 15, Appl
10	23.6	39.3	830	3	US-09-165-240-1	Sequence 1, Appli
11	23.6	39.3	830	4	US-09-568-059-1	Sequence 1, Appli
12	23.6	39.3	833	3	US-09-165-240-2	Sequence 2, Appli
13	23.6	39.3	833	4	US-09-568-059-2	Sequence 2, Appli
14	23.6	39.3	843	4	US-09-423-439-43	Sequence 43, Appl
15	23.6	39.3	877	4	US-09-605-785-769	Sequence 769, App
16	23.6	39.3	1998	4	US-09-423-439-50	Sequence 50, Appl
17	23.4	39.0	378	3	US-08-513-974B-33	Sequence 33, Appl
18	23.4	39.0	378	4	US-08-776-971-28	Sequence 28, Appl
19	23.4	39.0	434	3	US-08-513-974B-365	Sequence 365, App
20	23.4	39.0	434	4	US-08-776-971-105	Sequence 105, App
21	23.4	39.0	1113	4	US-09-172-353-1	Sequence 1, Appli
22	23.4	39.0	1116	4	US-08-776-971-139	Sequence 139, App
23	23.4	39.0	1228	1	US-08-401-908-35	Sequence 35, Appl
24	23.4	39.0	1605	2	US-08-356-786-9	Sequence 9, Appli
25	23.4	39.0	1848	1	US-08-447-422-15	Sequence 15, Appl
26	23.2	38.7	89	2	US-08-373-190-51	Sequence 51, Appl
27	23.2	38.7	89	2	US-08-438-190A-51	Sequence 51, Appl
28	23.2	38.7	89	3	US-09-287-145A-51	Sequence 51, Appl
29	23.2	38.7	89	4	US-09-556-111-51	Sequence 51, Appl
30	23.2	38.7	1560	2	US-08-751-767A-11	Sequence 11, Appl
31	23.2	38.7	1623	2	US-08-751-767A-9	Sequence 9, Appli
32	23.2	38.7	6139	2	US-08-751-767A-7	Sequence 7, Appli
33	23	38.3	96	2	US-08-385-335A-33	Sequence 33, Appl
34	22.8	38.0	57	1	US-08-323-084A-20	Sequence 20, Appl
35	22.8	38.0	57	1	US-08-674-008-20	Sequence 20, Appl
36	22.6	37.7	720	2	US-08-800-198-7	Sequence 7, Appli
37	22.6	37.7	720	3	US-09-296-595-7	Sequence 7, Appli
38	22.6	37.7	777	3	US-08-469-318-55	Sequence 55, Appl
39	22.6	37.7	777	3	US-08-468-609A-55	Sequence 55, Appl
40	22.6	37.7	777	4	US-08-446-872A-55	Sequence 55, Appl
41	22.6	37.7	777	4	US-08-762-227A-55	Sequence 55, Appl
42	22.6	37.7	777	5	PCT-US95-01185-55	Sequence 55, Appl
43	22.4	37.3	5020	3	US-08-938-291A-3	Sequence 3, Appli
44	22.2	37.0	156	4	US-09-605-785-771	Sequence 771, App
45	22.2	37.0	874	4	US-09-605-785-770	Sequence 770, App

ALIGNMENTS

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RESULT 1
US-08-373-190-12
; Sequence 12, Application US/08373190
; Patent No. 5851829
;  GENERAL INFORMATION:
;    APPLICANT:  MARASCO, WAYNE
;    APPLICANT:  HASELTINE, WILLIAM
;    TITLE OF INVENTION:  METHOD OF INTRACELLULAR BINDING OF PROTEINS
;    NUMBER OF SEQUENCES:  79
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/373,190
;      FILING DATE:  17-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/06735
;      FILING DATE:  16-JUL-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  RESNICK, DAVID S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  41956-PCT-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  STRE UR 2002
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  69 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-373-190-12

  Query Match             42.3%;  Score 25.4;  DB 2;  Length 69;
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Db         23 GTGGGAGCGGTGGCGGCGGATCTGAGCTCSWGMTGACCCAGTCTCCA 69


RESULT 2
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; Sequence 11, Application US/08350215
; Patent No. 6004940
;  GENERAL INFORMATION:
;    APPLICANT:  MARASCO, WAYNE A.
;    APPLICANT:  RICHARDSON, JENNIFER
;    TITLE OF INVENTION:  INTRACELLULAR TARGETING OF ENDOGENOUS
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  58
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/350,215
;      FILING DATE:  12-DEC-1994
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  EISENSTEIN, RONALD I.
;      REGISTRATION NUMBER:  30628
;      REFERENCE/DOCKET NUMBER:  41956-CP3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 523-3400
;      TELEFAX:  (617) 523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  69 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-350-215-11

  Query Match             42.3%;  Score 25.4;  DB 3;  Length 69;
  Best Local Similarity   68.1%;  Pred. No. 0.99;
  Matches   32;  Conservative    2;  Mismatches   13;  Indels    0;  Gaps    0;

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RESULT 3
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; Sequence 11, Application US/08438190A
; Patent No. 5965371
;  GENERAL INFORMATION:
;    APPLICANT:  MARASCO, WAYNE
;    APPLICANT:  HASELTINE, WILLIAM
;    TITLE OF INVENTION:  METHOD OF INTRACELLULAR BINDING OF
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  78
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/438,190A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  EISENSTEIN, RONALD I.
;      REGISTRATION NUMBER:  30628
;      REFERENCE/DOCKET NUMBER:  41956
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 523-3400
;      TELEFAX:  (617) 523-6440
;      TELEX:  200291 STRE UR
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  70 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-438-190A-11

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  Best Local Similarity   68.1%;  Pred. No. 0.99;
  Matches   32;  Conservative    2;  Mismatches   13;  Indels    0;  Gaps    0;

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RESULT 4
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; Sequence 11, Application US/09287145A
; Patent No. 6072036
;  GENERAL INFORMATION:
;    APPLICANT:  MARASCO, WAYNE
;    APPLICANT:  HASELTINE, WILLIAM
;    TITLE OF INVENTION:  METHOD OF INTRACELLULAR BINDING OF
;    TITLE OF INVENTION:  PROTEINS
;    NUMBER OF SEQUENCES:  78
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;      ADDRESSEE:  CUSHMAN
;      STREET:  130 WATER STREET
;      CITY:  BOSTON
;      STATE:  MASSACHUSETTS
;      COUNTRY:  US
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/287,145A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/438,190
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  EISENSTEIN, RONALD I.
;      REGISTRATION NUMBER:  30628
;      REFERENCE/DOCKET NUMBER:  41956
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;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (617) 523-3400
;       TELEFAX:  (617) 523-6440
;       TELEX:  200291 STRE UR
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  70 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-09-287-145A-11

  Query Match             42.3%;  Score 25.4;  DB 3;  Length 70;
  Best Local Similarity   68.1%;  Pred. No. 0.99;
  Matches   32;  Conservative    2;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          6 GTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCA 52
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Db         24 GTGGGAGCGGTGGCGGCGGATCTGAGCTCSWGMTGACCCAGTCTCCA 70


RESULT 5
US-09-556-111-11
; Sequence 11, Application US/09556111
; Patent No. 6329173
;   GENERAL INFORMATION:
;        APPLICANT: MARASCO, WAYNE
;                   HASELTINE, WILLIAM
;        TITLE OF INVENTION: METHOD OF INTRACELLULAR BINDING OF
;                            PROTEINS
;        NUMBER OF SEQUENCES: 78
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
;                        CUSHMAN
;             STREET: 130 WATER STREET
;             CITY: BOSTON
;             STATE: MASSACHUSETTS
;             COUNTRY: US
;             ZIP: 02109
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/556,111
;             FILING DATE: 21-Apr-2000
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/438,190
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: EISENSTEIN, RONALD I.
;             REGISTRATION NUMBER: 30628
;             REFERENCE/DOCKET NUMBER: 41956
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (617) 523-3400
;             TELEFAX: (617) 523-6440
;             TELEX: 200291 STRE UR
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 70 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-556-111-11

  Query Match             42.3%;  Score 25.4;  DB 4;  Length 70;
  Best Local Similarity   68.1%;  Pred. No. 0.99;
  Matches   32;  Conservative    2;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          6 GTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCA 52
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RESULT 6
US-08-235-838-10
; Sequence 10, Application US/08235838
; Patent No. 5571894
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5571894man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/235,838
;      FILING DATE:  TBA
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elmer, James Scott
;      REGISTRATION NUMBER:  36,129
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8614
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  748 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Mouse
;      INDIVIDUAL ISOLATE:  E. coli
;    IMMEDIATE SOURCE:
;      CLONE:  pWW15-Fv51
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  6..728
;      OTHER INFORMATION:  /note= "1-8 synthetic spacer;9-368
;      OTHER INFORMATION:  FWP51 Heavy ChainVar.Dom.;99-113 CDR1H;156-206
;      OTHER INFORMATION:  CDR2H;303-335 CDR3H;369-413 Syn.Spcr;414-728 FWP51
;      OTHER INFORMATION:  Light ChainVar.Dom;483-515 CDR1L;561-581 CDR2L;
;      OTHER INFORMATION:  729-748 Syn.Spcr.
US-08-235-838-10

  Query Match             41.0%;  Score 24.6;  DB 1;  Length 748;
  Best Local Similarity   65.5%;  Pred. No. 3.4;
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  Matches   36;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

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RESULT 7
US-08-465-473B-10
; Sequence 10, Application US/08465473B
; Patent No. 5939531
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5939531man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NOVARTIS Corporation
;      STREET:  564 Morris Avenue
;      CITY:  Summit
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07901-6940
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,473B
;      FILING DATE:  5 June 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pfeiffer, Hesna J.
;      REGISTRATION NUMBER:  22,640
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)522 6940
;      TELEFAX:  (908)522 6955
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  748 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Mouse
;      INDIVIDUAL ISOLATE:  E. coli
;    IMMEDIATE SOURCE:
;      CLONE:  pWW15-Fv51
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  6..728
;      OTHER INFORMATION:  /note= "1-8 synthetic spacer;9-368
;      OTHER INFORMATION:  FWP51 Heavy ChainVar.Dom.;99-113 CDR1H;156-206
;      OTHER INFORMATION:  CDR2H;303-335 CDR3H;369-413 Syn.Spcr;414-728 FWP51
;      OTHER INFORMATION:  Light ChainVar.Dom;483-515 CDR1L;561-581 CDR2L;
;      OTHER INFORMATION:  729-748 Syn.Spcr.
US-08-465-473B-10

  Query Match             41.0%;  Score 24.6;  DB 2;  Length 748;
  Best Local Similarity   65.5%;  Pred. No. 3.4;
  Matches   36;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
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Db        388 GCGGTGGCTCCGGCGGTGGCGGTTCTGACATCCAGCTGACCCAGTCTCCATCCTC 442


RESULT 8
US-08-235-838-15
; Sequence 15, Application US/08235838
; Patent No. 5571894
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5571894man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CIBA-GEIGY Corporation
;      STREET:  7 Skyline Drive
;      CITY:  Hawthorne
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10532
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/235,838
;      FILING DATE:  TBA
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elmer, James Scott
;      REGISTRATION NUMBER:  36,129
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (919)541-8614
;      TELEFAX:  (919)541-8689
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2012 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Mouse/Pseudomonas aeruginosa
;      INDIVIDUAL ISOLATE:  E. coli
;    IMMEDIATE SOURCE:
;      CLONE:  pWW215-51
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1911
;      OTHER INFORMATION:  /note= "64-87 FLAG peptide and
;      OTHER INFORMATION:  enterokinase cleavage site;97-456 FWP51 heavy
;      OTHER INFORMATION:  chain variable domain;457-501 15 aa linker
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;       OTHER INFORMATION:  sequence;502-822 FWP51 light chain variable
;       OTHER INFORMATION:  domain
;     FEATURE:
;       NAME/KEY:  sig_peptide
;       LOCATION:  1..63
;       OTHER INFORMATION:  /note= "ompA signal peptide"
;     FEATURE:
;       NAME/KEY:  mat_peptide
;       LOCATION:  94..1911
;     FEATURE:
;       NAME/KEY:  3'UTR
;       LOCATION:  1912..2012
;       OTHER INFORMATION:  /function= "3' non-coding region of
;       OTHER INFORMATION:  the exotoxin A gene"
;     FEATURE:
;       NAME/KEY:  misc_feature
;       LOCATION:  826..1911
;       OTHER INFORMATION:  /note= "Exotoxin A gene coding
;       OTHER INFORMATION:  region (coding for amino acids 252 to 613 of the
;       OTHER INFORMATION:  mature exotoxin A)"
US-08-235-838-15

  Query Match             41.0%;  Score 24.6;  DB 1;  Length 2012;
  Best Local Similarity   65.5%;  Pred. No. 4.3;
  Matches   36;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
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Db        476 GCGGTGGCTCCGGCGGTGGCGGTTCTGACATCCAGCTGACCCAGTCTCCATCCTC 530


RESULT 9
US-08-465-473B-15
; Sequence 15, Application US/08465473B
; Patent No. 5939531
;  GENERAL INFORMATION:
;    APPLICANT:  Wels, Winfried S.
;    APPLICANT:  Hynes, Nancy E.
;    APPLICANT:  Harwerth, Ina-Maria
;    APPLICANT:  Groner, Bernd
;    APPLICANT:  Hardman, No. 5939531man
;    APPLICANT:  Zwickl, Markus
;    TITLE OF INVENTION:  Recombinant Antibodies Specific for a
;    TITLE OF INVENTION:  Growth Factor Receptor
;    NUMBER OF SEQUENCES:  34
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NOVARTIS Corporation
;      STREET:  564 Morris Avenue
;      CITY:  Summit
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07901-6940
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,473B
;      FILING DATE:  5 June 1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/828,832
;      FILING DATE:  31-JAN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 91-810079.3
;      FILING DATE:  05-FEB-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Pfeiffer, Hesna J.
;      REGISTRATION NUMBER:  22,640
;      REFERENCE/DOCKET NUMBER:  4-18518/A/CIP/CONT2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (908)522 6940
;      TELEFAX:  (908)522 6955
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2012 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Mouse/Pseudomonas aeruginosa
;      INDIVIDUAL ISOLATE:  E. coli
;    IMMEDIATE SOURCE:
;      CLONE:  pWW215-51
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1911
;      OTHER INFORMATION:  /note= "64-87 FLAG peptide and
;      OTHER INFORMATION:  enterokinase cleavage site;97-456 FWP51 heavy
;      OTHER INFORMATION:  chain variable domain;457-501 15 aa linker
;      OTHER INFORMATION:  sequence;502-822 FWP51 light chain variable
;      OTHER INFORMATION:  domain
;    FEATURE:
;      NAME/KEY:  sig_peptide
;      LOCATION:  1..63
;      OTHER INFORMATION:  /note= "ompA signal peptide"
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  94..1911
;    FEATURE:
;      NAME/KEY:  3'UTR
;      LOCATION:  1912..2012
;      OTHER INFORMATION:  /function= "3' non-coding region of
;      OTHER INFORMATION:  the exotoxin A gene"
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  826..1911
;      OTHER INFORMATION:  /note= "Exotoxin A gene coding
;      OTHER INFORMATION:  region (coding for amino acids 252 to 613 of the
;      OTHER INFORMATION:  mature exotoxin A)"
US-08-465-473B-15

  Query Match             41.0%;  Score 24.6;  DB 2;  Length 2012;
  Best Local Similarity   65.5%;  Pred. No. 4.3;
  Matches   36;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              || ||||   ||| || ||||| |||   | |  ||  ||||   |||||||| |
Db        476 GCGGTGGCTCCGGCGGTGGCGGTTCTGACATCCAGCTGACCCAGTCTCCATCCTC 530


RESULT 10
US-09-165-240-1
; Sequence 1, Application US/09165240A
; Patent No. 6087164
; GENERAL INFORMATION:
;  APPLICANT: Hochberg, Abraham
;  APPLICANT: Ayesh, Suhail
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE: 9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/165,240A
;  CURRENT FILING DATE: 1998-10-01
;  EARLIER APPLICATION NUMBER: US 08/943,608
;  EARLIER FILING DATE: 1997-10-03
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 830
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-165-240-1
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  Query Match             39.3%;  Score 23.6;  DB 3;  Length 830;
  Best Local Similarity   69.6%;  Pred. No. 8.1;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy         12 GCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
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Db         59 GGGGTGGCTGGGGGAGTCGAAACTCGCCAGTCTCCACTCCACTCCC 104


RESULT 11
US-09-568-059-1
; Sequence 1, Application US/09568059
; Patent No. 6306833
; GENERAL INFORMATION:
;  APPLICANT:  Hochberg, Abraham
;  APPLICANT:  Ayesh, Suhail
;  TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION:  TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE:  9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/568,059
;  CURRENT FILING DATE:  2000-05-10
;  PRIOR APPLICATION NUMBER:   09/165,240
;  PRIOR FILING DATE:   1998-10-01
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 830
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-568-059-1

  Query Match             39.3%;  Score 23.6;  DB 4;  Length 830;
  Best Local Similarity   69.6%;  Pred. No. 8.1;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy         12 GCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
              | |||||| | ||   | |||||| |||| | | ||||||  |||
Db         59 GGGGTGGCTGGGGGAGTCGAAACTCGCCAGTCTCCACTCCACTCCC 104


RESULT 12
US-09-165-240-2
; Sequence 2, Application US/09165240A
; Patent No. 6087164
; GENERAL INFORMATION:
;  APPLICANT: Hochberg, Abraham
;  APPLICANT: Ayesh, Suhail
;  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION: TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE: 9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/165,240A
;  CURRENT FILING DATE: 1998-10-01
;  EARLIER APPLICATION NUMBER: US 08/943,608
;  EARLIER FILING DATE: 1997-10-03
;  NUMBER OF SEQ ID NOS: 11
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 833
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-165-240-2

  Query Match             39.3%;  Score 23.6;  DB 3;  Length 833;
  Best Local Similarity   69.6%;  Pred. No. 8.1;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy         12 GCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
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Db         47 GGGGTGGCTGGGGGAGTCGAAACTCGCCAGTCTCCACTCCACTCCC 92


RESULT 13
US-09-568-059-2
; Sequence 2, Application US/09568059
; Patent No. 6306833
; GENERAL INFORMATION:
;  APPLICANT:  Hochberg, Abraham
;  APPLICANT:  Ayesh, Suhail
;  TITLE OF INVENTION:  METHODS AND COMPOSITIONS FOR INDUCING
;  TITLE OF INVENTION:  TUMOR-SPECIFIC CYTOTOXICITY
;  FILE REFERENCE:  9457-0014-999
;  CURRENT APPLICATION NUMBER: US/09/568,059
;  CURRENT FILING DATE:  2000-05-10
;  PRIOR APPLICATION NUMBER:   09/165,240
;  PRIOR FILING DATE:   1998-10-01
;  NUMBER OF SEQ ID NOS:  11
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 2
;   LENGTH: 833
;   TYPE: DNA
;   ORGANISM: Homo Sapien
US-09-568-059-2

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  Best Local Similarity   69.6%;  Pred. No. 8.1;
  Matches   32;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy         12 GCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCC 57
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Db         47 GGGGTGGCTGGGGGAGTCGAAACTCGCCAGTCTCCACTCCACTCCC 92


RESULT 14
US-09-423-439-43
; Sequence 43, Application US/09423439
; Patent No. 6339070
;  GENERAL INFORMATION:
;       APPLICANT: EMERY, Stephen Charles
;                  BLAKEY, David Charles
;       TITLE OF INVENTION: CHEMICAL COMPOUNDS
;       NUMBER OF SEQUENCES: 60
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Pillsbury Winthrop, L.L.P.
;            STREET: 1100 New York Ave., N.W.
;            CITY: Washington
;            STATE: D.C.
;            COUNTRY: U.S.A.
;            ZIP: 20005
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: MS Word
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/423,439
;            FILING DATE: 09-No. 6339070-1999
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: PCT/GB98/01294
;            FILING DATE: 05-MAY-1998
;            APPLICATION NUMBER: GB 9709421.3
;            FILING DATE: 10-MAY-1997
;  INFORMATION FOR SEQ ID NO: 43:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 843 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: other nucleic acid
;       SEQUENCE DESCRIPTION: SEQ ID NO: 43:
US-09-423-439-43

  Query Match             39.3%;  Score 23.6;  DB 4;  Length 843;
  Best Local Similarity   64.8%;  Pred. No. 8.1;
  Matches   35;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;
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Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATC 54
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Db        444 CGGTGGTGGGTCGGGTGGCGGCGGATCTCAGATTGTGCTCACCCAGTCTCCAGC 497


RESULT 15
US-09-605-785-769
; Sequence 769, Application US/09605785
; Patent No. 6321716
; GENERAL INFORMATION:
;  APPLICANT: Xu, Jiangchun
;  APPLICANT:  Dillon, Davin C.
;  APPLICANT:  Mitcham, Jennifer L.
;  APPLICANT:  Harlocker, Susan L.
;  APPLICANT:  Jiang, Yuqui
;  APPLICANT:  Henderson, Robert A.
;  APPLICANT:  Kalos, Michael D.
;  APPLICANT:  Fanger, Gary R.
;  APPLICANT:  Retter, Marc W.
;  APPLICANT:  Stolk, John A.
;  APPLICANT:  Day, Craig H.
;  APPLICANT:  Vedvick, Thomas S.
;  APPLICANT:  Carter, Darrick
;  APPLICANT:  Li, Samuel
;  APPLICANT:  Wang, Aijun
;  APPLICANT:  Skeiky, Yasir A.W.
;  APPLICANT:  Hepler, William
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;  TITLE OF INVENTION:  DIAGNOSIS OF PROSTATE CANCER
;  FILE REFERENCE: 210121.427C16
;  CURRENT APPLICATION NUMBER: US/09/605,785
;  CURRENT FILING DATE:  2000-06-27
;  NUMBER OF SEQ ID NOS: 835
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 769
;   LENGTH: 877
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(877)
;   OTHER INFORMATION: n=A,T,C or G
US-09-605-785-769

  Query Match             39.3%;  Score 23.6;  DB 4;  Length 877;
  Best Local Similarity   65.3%;  Pred. No. 8.2;
  Matches   32;  Conservative    0;  Mismatches   17;  Indels    0;  Gaps    0;

Qy         12 GCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
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Db         17 GCGGTGGCGGCCGCTCTAGAACTAGTGGATCCACTAGTCCANNGNGGGG 65


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Title: US-09-917-265-83
Perfect score: 60
Sequence: 1 ctgcagtggtggcggtggcg.....acccctactccatccccggg 60

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1114047 seqs, 798260406 residues

Total number of hits satisfying chosen parameters: 2228094

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
6: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 2		60	100.0	60	10	US-09-917-265-84	Sequence 84, Appl
3		60	100.0	1533	10	US-09-917-265-43	Sequence 43, Appl
c 4		60	100.0	1533	10	US-09-917-265-45	Sequence 45, Appl
5		60	100.0	1599	10	US-09-917-265-38	Sequence 38, Appl
c 6		60	100.0	1599	10	US-09-917-265-40	Sequence 40, Appl
7		59	98.3	1533	10	US-09-917-265-66	Sequence 66, Appl
c 8		59	98.3	1533	10	US-09-917-265-68	Sequence 68, Appl
9		59	98.3	1599	10	US-09-917-265-61	Sequence 61, Appl
c 10		59	98.3	1599	10	US-09-917-265-63	Sequence 63, Appl
11		27.6	46.0	8608	10	US-09-828-825-7	Sequence 7, Appli
12		27.6	46.0	8623	10	US-09-828-825-5	Sequence 5, Appli
13		27.6	46.0	8629	10	US-09-828-825-15	Sequence 15, Appl
14		27.6	46.0	8638	10	US-09-828-825-9	Sequence 9, Appli
15		27.6	46.0	8644	10	US-09-828-825-13	Sequence 13, Appl
16		27.6	46.0	8659	10	US-09-828-825-11	Sequence 11, Appl
17		26	43.3	771	9	US-10-198-846-4404	Sequence 4404, Ap
18		25.2	42.0	1148	10	US-09-764-864-529	Sequence 529, App
19		25.2	42.0	1179	10	US-09-764-864-76	Sequence 76, Appl
20		25.2	42.0	6485	12	US-10-044-090-290	Sequence 290, App
21		25	41.7	816	10	US-09-766-543-9	Sequence 9, Appli
22		25	41.7	840	10	US-09-766-543-11	Sequence 11, Appl
c 23		24.8	41.3	1785	10	US-09-732-357A-1	Sequence 1, Appli
c 24		24.8	41.3	1807	9	US-10-205-823-384	Sequence 384, App
c 25		24.8	41.3	1847	9	US-09-978-295A-235	Sequence 235, App
c 26		24.8	41.3	1847	9	US-09-938-418-3	Sequence 3, Appli
c 27		24.8	41.3	1847	9	US-09-978-697-235	Sequence 235, App
c 28		24.8	41.3	1847	9	US-09-978-192A-235	Sequence 235, App
c 29		24.8	41.3	1847	9	US-09-999-832A-235	Sequence 235, App
c 30		24.8	41.3	1847	9	US-09-978-189-235	Sequence 235, App
c 31		24.8	41.3	1847	9	US-09-978-608A-235	Sequence 235, App
c 32		24.8	41.3	1847	9	US-09-978-191A-235	Sequence 235, App
c 33		24.8	41.3	1847	9	US-09-978-403A-235	Sequence 235, App
c 34		24.8	41.3	1847	9	US-09-978-564A-235	Sequence 235, App
c 35		24.8	41.3	1847	9	US-09-978-585A-235	Sequence 235, App
c 36		24.8	41.3	1847	9	US-10-017-081A-235	Sequence 235, App
c 37		24.8	41.3	1847	9	US-09-978-824-235	Sequence 235, App
c 38		24.8	41.3	1847	9	US-09-981-915A-235	Sequence 235, App
c 39		24.8	41.3	1847	9	US-09-999-833A-235	Sequence 235, App
c 40		24.8	41.3	1847	9	US-10-167-749-235	Sequence 235, App
c 41		24.8	41.3	1847	9	US-09-918-585A-235	Sequence 235, App
c 42		24.8	41.3	1847	9	US-09-978-423A-235	Sequence 235, App
c 43		24.8	41.3	1847	9	US-10-013-921A-235	Sequence 235, App
c 44		24.8	41.3	1847	9	US-09-978-193A-235	Sequence 235, App
c 45		24.8	41.3	1847	9	US-10-013-929A-235	Sequence 235, App

ALIGNMENTS

RESULT 1
US-09-917-265-83
; Sequence 83, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 83
; LENGTH: 60
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Primer
US-09-917-265-83

Query Match 100.0%; Score 60; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 1.5e-13;
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60

RESULT 2
US-09-917-265-84/c
; Sequence 84, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265

```
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 84
;    LENGTH: 60
;    TYPE: DNA
;    ORGANISM: Artificial sequence
;    FEATURE:
;    OTHER INFORMATION: Synthetic Primer
US-09-917-265-84

  Query Match             100.0%;  Score 60;  DB 10;  Length 60;
  Best Local Similarity   100.0%;  Pred. No. 1.5e-13;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         60 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1


RESULT 3
US-09-917-265-43
; Sequence 43, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
;    LENGTH: 1533
;    TYPE: DNA
;    ORGANISM: Felis catus
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1)..(1533)
;    OTHER INFORMATION:
US-09-917-265-43

  Query Match             100.0%;  Score 60;  DB 10;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-13;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        915 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974


RESULT 4
US-09-917-265-45/c
; Sequence 45, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
;    LENGTH: 1533
;    TYPE: DNA
;    ORGANISM: Felis catus
US-09-917-265-45

  Query Match             100.0%;  Score 60;  DB 10;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-13;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


RESULT 5
US-09-917-265-38
; Sequence 38, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
;    LENGTH: 1599
;    TYPE: DNA
;    ORGANISM: Felis catus
;    FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1)..(1599)
;    OTHER INFORMATION:
US-09-917-265-38

  Query Match             100.0%;  Score 60;  DB 10;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-13;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        981 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1040


RESULT 6
US-09-917-265-40/c
; Sequence 40, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
;    LENGTH: 1599
;    TYPE: DNA
;    ORGANISM: Felis catus
US-09-917-265-40

  Query Match             100.0%;  Score 60;  DB 10;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 2.1e-13;
  Matches   60;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
```

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        619 CTGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


RESULT 7
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match             98.3%;  Score 59;  DB 10;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-13;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        916 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 974


RESULT 8
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

  Query Match             98.3%;  Score 59;  DB 10;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 4.9e-13;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


RESULT 9
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

  Query Match             98.3%;  Score 59;  DB 10;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 5e-13;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        982 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 1040


RESULT 10
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match             98.3%;  Score 59;  DB 10;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 5e-13;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 TGCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 560


RESULT 11
US-09-828-825-7
; Sequence 7, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
```

```
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 8608
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4263)
;   OTHER INFORMATION: Human IL12.2 sequence (2460-4253 is coding
;   OTHER INFORMATION: sequence, 13 amino acid flexible linker at
;   OTHER INFORMATION: 3606-3676)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4253)
;   OTHER INFORMATION: IL12.2 coding sequence (13 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4362)..(4383)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4393)..(4614)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4709)..(5164)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5228)..(6595)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7006)..(7866)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-7

  Query Match            46.0%;  Score 27.6;  DB 10;  Length 8608;
  Best Local Similarity   67.2%;  Pred. No. 0.48;
  Matches   39;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              | || |||||||||||  ||  ||  |||||| | ||     | ||||||  ||| ||
Db       3634 GAAGCGGTGGCGGTGGAAGCCCATGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGG 3691


RESULT 12
US-09-828-825-5
; Sequence 5, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 8623
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1956 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4278)
;   OTHER INFORMATION: Human IL12.3 - 2640-4268 is coding sequence,
;   OTHER INFORMATION: flexible linker from 3606-3690
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4268)
;   OTHER INFORMATION: IL 12.3 coding sequence - has 28 amino acid linker
;   OTHER INFORMATION: sequence
;   NAME/KEY: promoter
;   LOCATION: (4398)..(4407)
;   OTHER INFORMATION: T3 RNA polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4408)..(4629)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4724)..(5179)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5243)..(6610)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7021)..(7881)
;   OTHER INFORMATION: Ampicillin resistance
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
US-09-828-825-5

  Query Match            46.0%;  Score 27.6;  DB 10;  Length 8623;
  Best Local Similarity   67.2%;  Pred. No. 0.48;
  Matches   39;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              | || |||||||||||  ||  ||  |||||| | ||     | ||||||  ||| ||
Db       3649 GAAGCGGTGGCGGTGGAAGCCCATGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGG 3706


RESULT 13
US-09-828-825-15
; Sequence 15, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 8629
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
```

```
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2726)
;   OTHER INFORMATION: Human IL12.2 (coding sequence is 1103-2716, 10
;   OTHER INFORMATION: amino acid linker at 2087-2116)
;   NAME/KEY: CDS
;   LOCATION: (1103)..(2716)
;   OTHER INFORMATION: Human IL12.2 (10 amino acid linker)
;   NAME/KEY: RBS
;   LOCATION: (2752)..(3332)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (3369)..(4263)
;   OTHER INFORMATION: Human B7.1 sequence
;   NAME/KEY: promoter
;   LOCATION: (4383)..(4404)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4414)..(4635)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4730)..(5185)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5249)..(6616)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7027)..(7887)
;   OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-15

  Query Match             46.0%;  Score 27.6;  DB 10;  Length 8629;
  Best Local Similarity   67.2%;  Pred. No. 0.48;
  Matches   39;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              | || ||||||||||||  ||  ||  |||||| | ||     | ||||||  ||| ||
Db       2097 GAAGCGGTGGCGGTGGAAGCCCATGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGG 2154


RESULT 14
US-09-828-825-9
; Sequence 9, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
;   LENGTH: 8638
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: misc_feature
;   LOCATION: (890)..(1002)
;   OTHER INFORMATION: Intervening sequence
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(1984)
;   OTHER INFORMATION: Human B7.1 (1090-1954 is coding sequence)
;   NAME/KEY: RBS
;   LOCATION: (2013)..(2593)
;   OTHER INFORMATION: IRES sequence
;   NAME/KEY: misc_feature
;   LOCATION: (2627)..(4293)
;   OTHER INFORMATION: Human IL12.4 (coding sequence is 2640-4283, 33
;   OTHER INFORMATION: amino acid linker at 3606-3706)
;   NAME/KEY: CDS
;   LOCATION: (2640)..(4283)
;   OTHER INFORMATION: IL12.4 coding sequence (33 amino acid linker)
;   NAME/KEY: promoter
;   LOCATION: (4392)..(4413)
;   OTHER INFORMATION: T3 RNA Polymerase promoter
;   NAME/KEY: polyA_signal
;   LOCATION: (4423)..(4644)
;   OTHER INFORMATION: SV40 fragment containing polyadenylation signal
;   NAME/KEY: rep_origin
;   LOCATION: (4739)..(5194)
;   OTHER INFORMATION: f1 origin of replication
;   NAME/KEY: misc_feature
;   LOCATION: (5258)..(6625)
;   OTHER INFORMATION: Neo r expression cassette
;   NAME/KEY: misc_feature
;   LOCATION: (7036)..(7896)
;   OTHER INFORMATION: Ampicillin resistance
US-09-828-825-9

  Query Match             46.0%;  Score 27.6;  DB 10;  Length 8638;
  Best Local Similarity   67.2%;  Pred. No. 0.48;
  Matches   39;  Conservative    0;  Mismatches   19;  Indels    0;  Gaps    0;

Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              | || ||||||||||||  ||  ||  |||||| | ||     | ||||||  ||| ||
Db       3664 GAAGCGGTGGCGGTGGAAGCCCATGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGG 3721


RESULT 15
US-09-828-825-13
; Sequence 13, Application US/09828825
; Patent No. US20020018767A1
; GENERAL INFORMATION:
;  APPLICANT: Lee, Seewoo
;  APPLICANT:  Kim, Han-soo
;  TITLE OF INVENTION: Anti-cancer Cellular Vaccine
;  FILE REFERENCE: 84906-102
;  CURRENT APPLICATION NUMBER: US/09/828,825
;  CURRENT FILING DATE:  2001-04-10
;  PRIOR APPLICATION NUMBER: KR00-43498
;  PRIOR FILING DATE: 2000-07-27
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;   LENGTH: 8644
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: plasmid
;   NAME/KEY: misc_feature
;   LOCATION: (1)..(750)
;   OTHER INFORMATION: CMV enhancer and promoter
;   NAME/KEY: promoter
;   LOCATION: (1067)..(1085)
;   OTHER INFORMATION: T7 RNA polymerase promoter
;   NAME/KEY: misc_feature
;   LOCATION: (1090)..(2731)
;   OTHER INFORMATION: Human IL12.3 (1103-2731 is coding sequence, 15
;   OTHER INFORMATION: amino acid linker at 2087-2131)
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; NAME/KEY: CDS
; LOCATION: (1103)..(2731)
; OTHER INFORMATION: IL12.3 (15 amino acid linker)
; NAME/KEY: RBS
; LOCATION: (2767)..(3347)
; OTHER INFORMATION: IRES sequence
; NAME/KEY: misc_feature
; LOCATION: (3384)..(4278)
; OTHER INFORMATION: Human B7.1 sequence
; NAME/KEY: promoter
; LOCATION: (4398)..(4419)
; OTHER INFORMATION: T3 RNA polymerase promoter
; NAME/KEY: polyA_signal
; LOCATION: (4429)..(4650)
; OTHER INFORMATION: SV40 fragment containing polyadenylation signal
; NAME/KEY: rep_origin
; LOCATION: (4745)..(5200)
; OTHER INFORMATION: f1 origin of replication
; NAME/KEY: misc_feature
; LOCATION: (5264)..(5681)
; OTHER INFORMATION: Neo r expression cassette
; NAME/KEY: misc_feature
; LOCATION: (7042)..(7902)
; OTHER INFORMATION: Ampicillin resistance gene
US-09-828-825-13

Query Match 46.0%; Score 27.6; DB 10; Length 8644;
Best Local Similarity 67.2%; Pred. No. 0.48;
Matches 39; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

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Qy          3 GCAGTGGTGGCGGTGGCGGCGGATCTAGAAACTTGCCAACCCCTACTCCATCCCCGGG 60
              | || |||||||||||  ||  ||  |||||| | ||     | ||||||  ||| ||
Db       2112 GAAGCGGTGGCGGTGGAAGCCCATGGAGAAACCTCCCCGTGGCCACTCCAGACCCAGG 2169
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Search completed: July 16, 2003, 13:16:31
Job time : 11.7413 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:00:49 ; Search time 1850.51 Seconds
(without alignments)
10474.108 Million cell updates/sec

Title: US-09-917-265-46
Perfect score: 666
Sequence: 1 atgtgcccgccgcgcggcct.....tgagttatctgaattcttcc 666

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
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17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
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25: em_pl:*
26: em_ro:*
27: em_sts:*
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32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	615	92.3	669	6	AR151072	AR151072 Sequence
2	615	92.3	669	6	E15018	E15018 Canine mRNA
3	501	75.2	669	6	AR151062	AR151062 Sequence
4	419	62.9	669	4	CFU49085	U49085 Canis famil
5	81	12.2	285	4	AF054605	AF054605 Felis cat
6	81	12.2	669	4	FCU83185	U83185 Felis catus
7	81	12.2	669	4	FCIL12P35	Y07761 F.catus mRN
8	75	11.3	666	6	AX154613	AX154613 Sequence
9	66	9.9	666	6	AX154612	AX154612 Sequence
10	62	9.3	660	6	AX154615	AX154615 Sequence
11	62	9.3	660	6	AX154616	AX154616 Sequence
12	59	8.9	660	6	AR008951	AR008951 Sequence
13	59	8.9	660	6	AX154614	AX154614 Sequence
14	59	8.9	660	6	AX154617	AX154617 Sequence
15	59	8.9	660	6	AX154618	AX154618 Sequence
16	59	8.9	660	6	AX154619	AX154619 Sequence
17	59	8.9	660	6	AX154621	AX154621 Sequence
18	59	8.9	660	6	AX154634	AX154634 Sequence
19	59	8.9	660	6	BD007071	BD007071 IL-12 gen
20	59	8.9	660	6	BD007079	BD007079 Gene expr
21	59	8.9	660	6	I28592	I28592 Sequence 3
22	59	8.9	721	6	AR052862	AR052862 Sequence
23	59	8.9	762	9	AF101062	AF101062 Homo sapi
24	59	8.9	780	9	MMU19842	U19842 Macaca mula
25	59	8.9	823	9	AF180562	AF180562 Homo sapi
26	59	8.9	1026	6	AR091390	AR091390 Sequence
27	59	8.9	1026	9	HUMCLMF35	M65271 Human cytot
28	59	8.9	1287	6	AX084108	AX084108 Sequence
29	59	8.9	1316	6	AR050785	AR050785 Sequence
30	59	8.9	1316	6	AR212036	AR212036 Sequence
31	59	8.9	1316	9	HUMNKSFP35	M65291 Human natur
32	59	8.9	1364	6	AR082685	AR082685 Sequence
33	59	8.9	1364	6	AR122961	AR122961 Sequence
34	59	8.9	1364	6	I28326	I28326 Sequence 3
35	59	8.9	1364	6	I89771	I89771 Sequence 3
36	59	8.9	1560	6	AR091395	AR091395 Sequence
37	59	8.9	1623	6	AR091394	AR091394 Sequence
38	59	8.9	1645	6	A92078	A92078 Sequence 2
39	59	8.9	6139	6	AR091393	AR091393 Sequence
40	59	8.9	11792	9	AF404773	AF404773 Homo sapi
41	59	8.9	157079	9	AC010370	AC010370 Homo sapi
42	59	8.9	176108	9	AC026118	AC026118 Homo sapi
c 43	59	8.9	275547	2	AC129109	AC129109 Homo sapi
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45	56	8.4	669	6	AX076483	AX076483 Sequence

ALIGNMENTS

RESULT 1
AR151072
LOCUS AR151072 669 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 12 from patent US 6231850.
ACCESSION AR151072
VERSION AR151072.1 GI:15117122
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 669)
AUTHORS Okano,F., Satoh,M. and Yamada,K.
TITLE Canine interleukin 12
JOURNAL Patent: US 6231850-A 12 15-MAY-2001;
FEATURES Location/Qualifiers

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     source          1. .669
                     /organism="unknown"
BASE COUNT      185 a    177 c    144 g    163 t
ORIGIN

  Query Match             92.3%;  Score 615;  DB 6;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  665;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
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Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
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Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 2
E15018
LOCUS       E15018                  669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
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            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
            FT                   /product='interleukin12 35kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /db_xref="taxon:9616"
BASE COUNT      185 a    177 c    144 g    163 t
ORIGIN

  Query Match             92.3%;  Score 615;  DB 6;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 0;
  Matches  665;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
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Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
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Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
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Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
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Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

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Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
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Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
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Qy        661 TCTTCC 666
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Db        661 TCTTCC 666


RESULT 3
AR151062
LOCUS       AR151062                669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6231850.
ACCESSION   AR151062
VERSION     AR151062.1  GI:15117112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
BASE COUNT      183 a    178 c    146 g    162 t
ORIGIN

  Query Match            75.2%;  Score 501;  DB 6;  Length 669;
  Best Local Similarity  99.7%;  Pred. No. 6.1e-277;
  Matches  601;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         36 CCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTC 95
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Qy         96 ACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155

Qy        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215
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Db        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215

Qy        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275
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Db        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275

Qy        276 ATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAG 335
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Qy        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395
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Db        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395

Qy        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455
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Db        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455

Qy        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGC 515
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCTATCGATGAGCTGTTACAGGC 515

Qy        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575

Qy        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635

Qy        636 CGA 638
              |||
Db        636 CGA 638


RESULT 4
CFU49085
LOCUS       CFU49085                669 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U49085
VERSION     U49085.1  GI:1223905
KEYWORDS    .
SOURCE      Canis familiaris.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis familiaris"
                     /db_xref="taxon:9615"
     CDS             1. .669
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                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAA92058.1"
                     /db_xref="GI:1223906"
                     /translation="MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHS
                     QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                     LNSS"
BASE COUNT      183 a    177 c    145 g    164 t
ORIGIN

  Query Match            62.9%;  Score 419;  DB 4;  Length 669;
  Best Local Similarity  99.8%;  Pred. No. 1.2e-229;
  Matches  469;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        197 CCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGG 256
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 CCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGG 256

Qy        257 AGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCT 316
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 AGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCT 316

Qy        317 CTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGT 376
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 CTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGT 376

Qy        377 GCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACG 436
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 GCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACG 436

Qy        437 CAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTA 496
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        437 CAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGTTGACAGCTA 496

Qy        497 TCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCC 556
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 TCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCC 556

Qy        557 TTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCA 616
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 TTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCA 616

Qy        617 GAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
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Db        617 GAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 5
AF054605
LOCUS       AF054605                285 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p35 subunit mRNA, partial cds.
ACCESSION   AF054605
VERSION     AF054605.1  GI:3126818
KEYWORDS    .
SOURCE      Felis catus.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
  MEDLINE   99322318
   PUBMED   10391845
REFERENCE   2  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
            Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
                     /cell_line="FL4"
                     /cell_type="T cell"
                     /note="persistant FIV infection"
     CDS             <1. .>285
                     /codon_start=3
                     /product="interleukin 12 p35 subunit"
                     /protein_id="AAC15978.1"
                     /db_xref="GI:3126819"
                     /translation="LLRAISNTLHKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLP
                     LELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVE"
BASE COUNT       84 a     70 c     64 g     67 t
ORIGIN

  Query Match             12.2%;  Score 81;  DB 4;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-35;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 161

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        162 CTGGCTTCCAGAGAGATCTCT 182


RESULT 6
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
  MEDLINE   98182592
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
     CDS             1. .669
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAB93836.1"
                     /db_xref="GI:2735053"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNSS"
BASE COUNT       191 a    179 c    137 g    162 t
ORIGIN

  Query Match             12.2%;  Score 81;  DB 4;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-35;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 7
FCIL12P35
LOCUS       FCIL12P35               669 bp    mRNA    linear   MAM 13-MAY-1997
DEFINITION  F.catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      cat.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
  MEDLINE   97246745
   PUBMED   9089110
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .669
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                     /gene="IL-12.p35"
     CDS             1. .669
                     /gene="IL-12.p35"
                     /function="heterodimer with IL-12 p40 chain"
                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
                     /db_xref="SWISS-PROT:O02743"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNAS"
BASE COUNT      190 a    178 c    139 g    162 t
ORIGIN

  Query Match             12.2%;  Score 81;  DB 4;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-35;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 8
AX154613
LOCUS       AX154613                 666 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 17 from Patent WO0140257.
ACCESSION   AX154613
VERSION     AX154613.1  GI:14536188
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 17 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      186 a    179 c    141 g    160 t
ORIGIN

  Query Match             11.3%;  Score 75;  DB 6;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-31;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        372 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCAT 431
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCAT 428

Qy        432 GAACGCAAAGCTTTT 446
              |||||||||||||||
Db        429 GAACGCAAAGCTTTT 443


RESULT 9
AX154612
LOCUS       AX154612                 666 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 16 from Patent WO0140257.
ACCESSION   AX154612
VERSION     AX154612.1  GI:14536187
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 16 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      186 a    181 c    141 g    158 t
ORIGIN

  Query Match             9.9%;  Score 66;  DB 6;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-26;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        381 TAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAA 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 TAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAA 437

Qy        441 GCTTTT 446
              ||||||
Db        438 GCTTTT 443


RESULT 10
AX154615
LOCUS       AX154615                 660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 19 from Patent WO0140257.
ACCESSION   AX154615
VERSION     AX154615.1  GI:14536190
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 19 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      182 a    178 c    142 g    158 t
ORIGIN

  Query Match             9.3%;  Score 62;  DB 6;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-24;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGT 624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGT 615

Qy        625 GC 626
              ||
Db        616 GC 617


RESULT 11
AX154616
LOCUS       AX154616                 660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 20 from Patent WO0140257.
ACCESSION   AX154616
VERSION     AX154616.1  GI:14536191
KEYWORDS    .
SOURCE      synthetic construct.
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  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 20 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      190 a    171 c    137 g    162 t
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 7.8e-24;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGT 624
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGT 615

Qy        625 GC 626
              ||
Db        616 GC 617


RESULT 12
AR008951
LOCUS       AR008951                660 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5756085.
ACCESSION   AR008951
VERSION     AR008951.1  GI:3967756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5756085-A 3 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unknown"
BASE COUNT      188 a    164 c    139 g    169 t
ORIGIN

  Query Match             8.9%;  Score 59;  DB 6;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-22;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 614


RESULT 13
AX154614
LOCUS       AX154614                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 18 from Patent WO0140257.
ACCESSION   AX154614
VERSION     AX154614.1  GI:14536189
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 18 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    172 c    136 g    163 t
ORIGIN

  Query Match             8.9%;  Score 59;  DB 6;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-22;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 614


RESULT 14
AX154617
LOCUS       AX154617                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 21 from Patent WO0140257.
ACCESSION   AX154617
VERSION     AX154617.1  GI:14536192
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 21 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      184 a    172 c    141 g    163 t
ORIGIN

  Query Match             8.9%;  Score 59;  DB 6;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-22;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 614


RESULT 15
AX154618
LOCUS       AX154618                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 22 from Patent WO0140257.
ACCESSION   AX154618
VERSION     AX154618.1  GI:14536193
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    173 c    136 g    162 t
ORIGIN

  Query Match             8.9%;  Score 59;  DB 6;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 4.2e-22;
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Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 614
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14: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1995.DAT:*
17: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1996.DAT:*
18: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:*
19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
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21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	666	100.0	669	20	AAX35626	Nucleic acid encod
2	666	100.0	669	20	AAX03163	Nucleic acid encod
3	666	100.0	669	22	AAI64389	Canine coding sequ
4	666	100.0	1282	20	AAX18178	Canine full length
5	615	92.3	669	19	AAV13819	Canine IL-12 P35 s
6	591	88.7	591	20	AAX18179	Canine mature CLAF
7	501	75.2	669	19	AAV13818	Canine IL-12 P35 s
8	501	75.2	669	20	AAX35616	Nucleic acid encod
9	501	75.2	669	20	AAX03153	Nucleic acid encod
10	501	75.2	669	22	AAI64379	Canine coding sequ
11	81	12.2	591	19	AAV56629	Feline FLAFp35 cDN
12	81	12.2	679	22	AAF26097	Feline fil12p35a D
13	81	12.2	1441	19	AAV56628	Feline FLAFp35 cDN
14	75	11.3	666	22	AAD15212	Modified human cyt
15	66	9.9	666	22	AAD15211	Modified human cyt
16	62	9.3	660	22	AAD15214	Modified human cyt
17	62	9.3	660	22	AAD15215	Modified human cyt
18	59	8.9	660	16	AAQ97485	Human interleukin-
19	59	8.9	660	19	AAV07274	Human Interleukin-
20	59	8.9	660	19	AAV07218	DNA encoding human
21	59	8.9	660	20	AAZ40407	Human interleukin
22	59	8.9	660	22	AAD15213	Modified human cyt
23	59	8.9	660	22	AAD15216	Modified human cyt
24	59	8.9	660	22	AAD15217	Modified human cyt
25	59	8.9	660	22	AAD15218	Modified human cyt
26	59	8.9	660	22	AAD15220	Modified human cyt
27	59	8.9	660	22	AAD15221	Human cytokine p35
28	59	8.9	689	19	AAV56641	Feline FLAFp35 DNA
29	59	8.9	721	15	AAQ67880	EPV 42 kD promoter
30	59	8.9	721	20	AAZ08515	Vaccinia E3L/human
31	59	8.9	762	20	AAV83207	Interleukin (IL)-1
32	59	8.9	762	21	AAF21323	Human low adenosin
33	59	8.9	762	21	AAA35201	Human adenosine re
34	59	8.9	856	12	AAQ12150	Cytotoxic lymphocy
35	59	8.9	856	18	AAT77850	35 kDa subunit of
36	59	8.9	856	18	AAV00402	35 kDa subunit of
37	59	8.9	856	18	AAT97970	35 kDa subunit of
38	59	8.9	856	19	AAV37772	Cytotoxic lymphocy
39	59	8.9	1026	21	AAZ40020	Human p35 coding s
40	59	8.9	1287	22	AAF76882	DNA encoding fusio
41	59	8.9	1316	18	AAT63621	Interleukin-12 p35
42	59	8.9	1364	17	AAT48099	Human interleukin-
43	59	8.9	1364	19	AAV42536	Human interleukin-
44	59	8.9	1364	19	AAV15228	Heterodimeric huma
45	59	8.9	1364	21	AAZ28863	Human interleukin-

ALIGNMENTS

RESULT 1
AAX35626
ID AAX35626 standard; cDNA to mRNA; 669 BP.
XX
AC AAX35626;
XX
DT 09-JUL-1999 (first entry)
XX
DE Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1..669
FT /*tag= a
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-308068/26.
DR P-PSDB; AAY02343.

```
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 15-16; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

  Query Match             100.0%;  Score 666;  DB 20;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 2
AAX03163
ID   AAX03163 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03163;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84374.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

  Query Match             100.0%;  Score 666;  DB 20;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
```

```
Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666
```

RESULT 3
AAI64389
ID AAI64389 standard; DNA; 669 BP.
XX
AC AAI64389;
XX
DT 23-NOV-2001 (first entry)
XX
DE Canine coding sequence #4.
XX
KW Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS Canis familiaris.
XX

FH	Key	Location/Qualifiers
FT	CDS	1..669
FT		/*tag= a
FT		/product= "Canine protein #4"
FT	sig_peptide	1..75
FT		/*tag= b
FT	mat_peptide	76..666
FT		/*tag= c

XX
PN JP2001161378-A.
XX
PD 19-JUN-2001.
XX
PF 26-SEP-2000; 2000JP-0292946.
XX
PR 01-OCT-1999; 99JP-0281234.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 2001-592466/67.
DR P-PSDB; AAG66483.
XX
PT Preparation of a highly pure protein, interleukin 12, a protein
PT inhibiting the activity of interleukin 12, and a treating agent and a
PT treating method for immunopathy of mammalian -
XX
PS Claim 6; Page 18; 21pp; Japanese.
XX
CC The present invention relates to a method for the preparation of a highly
CC pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC IL12. The protein is used as a preventive agent for dog immunopathy. The
CC present sequence was used in the method of the present invention.
XX
SQ Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

Query Match 100.0%; Score 666; DB 22; Length 669;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666
```

RESULT 4
AAX18178
ID AAX18178 standard; cDNA; 1282 BP.
XX

```
AC   AAX18178;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74324.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 33-34; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 other;

  Query Match             100.0%;  Score 666;  DB 20;  Length 1282;
  Best Local Similarity   100.0%;  Pred. No. 0;
  Matches  666;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 125

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 185

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 245

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 305

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 365

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 425

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 485

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 545

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 605

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 665

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 725

Qy        661 TCTTCC 666
              ||||||
Db        726 TCTTCC 731


RESULT 5
AAV13819
ID   AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13819;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41793.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 11; Pages 11-12; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
```

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XX
SQ   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 other;

  Query Match            92.3%;  Score 615;  DB 19;  Length 669;
  Best Local Similarity  99.8%;  Pred. No. 7.3e-293;
  Matches  665;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
              ||||||
Db        661 TCTTCC 666


RESULT 6
AAX18179
ID   AAX18179 standard; cDNA; 591 BP.
XX
AC   AAX18179;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine mature CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74325.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 34-35; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 other;

  Query Match            88.7%;  Score 591;  DB 20;  Length 591;
  Best Local Similarity  100.0%;  Pred. No. 4.9e-281;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300

Qy        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360

Qy        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480

Qy        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
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Db        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591


RESULT 7
AAV13818
ID   AAV13818 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13818;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41792.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 9; Page 9; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             75.2%;  Score 501;  DB 19;  Length 669;
  Best Local Similarity   99.7%;  Pred. No. 1.1e-236;
  Matches  601;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         36 CCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTC 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 CCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTC 95

Qy         96 ACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155

Qy        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215

Qy        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275

Qy        276 ATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAG 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAG 335

Qy        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395

Qy        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455

Qy        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGC 515
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCTATCGATGAGCTGTTACAGGC 515

Qy        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575

Qy        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635

Qy        636 CGA 638
              |||
Db        636 CGA 638


RESULT 8
AAX35616
ID   AAX35616 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35616;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02340.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 13; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
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CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match           75.2%;  Score 501;  DB 20;  Length 669;
  Best Local Similarity   99.7%;  Pred. No. 1.1e-236;
  Matches  601;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         36 CCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTC 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 CCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTC 95

Qy         96 ACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155

Qy        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215

Qy        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275

Qy        276 ATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAG 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAG 335

Qy        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395

Qy        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455

Qy        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGC 515
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCTATCGATGAGCTGTTACAGGC 515

Qy        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575

Qy        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635

Qy        636 CGA 638
              |||
Db        636 CGA 638


RESULT 9
AAX03153
ID   AAX03153 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03153;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84372.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 26-27; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match           75.2%;  Score 501;  DB 20;  Length 669;
  Best Local Similarity   99.7%;  Pred. No. 1.1e-236;
  Matches  601;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         36 CCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTC 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 CCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTC 95

Qy         96 ACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155

Qy        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215

Qy        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275

Qy        276 ATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAG 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAG 335

Qy        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395

Qy        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455
```

```
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Db        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455

Qy        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGC 515
                |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCTATCGATGAGCTGTTACAGGC 515

Qy        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575

Qy        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635

Qy        636 CGA 638
                |||
Db        636 CGA 638


RESULT 10
AAI64379
ID   AAI64379 standard; DNA; 669 BP.
XX
AC   AAI64379;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= "Canine protein #2"
FT   sig_peptide     1..75
FT                   /*tag=  b
FT   mat_peptide     76..666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66481.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Claim 6; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             75.2%;  Score 501;  DB 22;  Length 669;
  Best Local Similarity   99.7%;  Pred. No. 1.1e-236;
  Matches  601;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         36 CCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTC 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 CCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTC 95

Qy         96 ACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155

Qy        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215

Qy        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275

Qy        276 ATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAG 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAG 335

Qy        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395

Qy        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455

Qy        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGC 515
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCTATCGATGAGCTGTTACAGGC 515

Qy        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575

Qy        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635

Qy        636 CGA 638
              |||
Db        636 CGA 638


RESULT 11
AAV56629
ID   AAV56629 standard; cDNA; 591 BP.
XX
AC   AAV56629;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA mature transcript.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
```

```
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76176.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 23; Page 59; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp35.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus.
XX
SQ   Sequence 591 BP; 179 A; 151 C; 120 G; 141 T; 0 other;

  Query Match             12.2%;  Score 81;  DB 19;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 12
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02263.
XX
PR   08-JUL-1999;   99CH-0001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs -
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 other;

  Query Match             12.2%;  Score 81;  DB 22;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 13
AAV56628
ID   AAV56628 standard; cDNA; 1441 BP.
XX
AC   AAV56628;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             133..811
FT                   /*tag=  a
FT   sig_peptide     133..217
FT                   /*tag=  b
FT   mat_peptide     218..808
FT                   /*tag=  c
FT                   /product= "FLAFp35"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
```

```
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 other;

  Query Match             12.2%;  Score 81;  DB 19;  Length 1441;
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Db        380 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 439

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        440 CTGGCTTCCAGAGAGATCTCT 460


RESULT 14
AAD15212
ID   AAD15212 standard; DNA; 666 BP.
XX
AC   AAD15212;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-146.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1..75
FT                   /*tag= b
FT   mat_peptide     76..663
FT                   /*tag= c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08605.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 87; Page 139; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA.
XX
SQ   Sequence 666 BP; 186 A; 179 C; 141 G; 160 T; 0 other;

  Query Match             11.3%;  Score 75;  DB 22;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 8e-27;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        372 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCAT 431
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCAT 428

Qy        432 GAACGCAAAGCTTTT 446
              |||||||||||||||
Db        429 GAACGCAAAGCTTTT 443


RESULT 15
AAD15211
ID   AAD15211 standard; DNA; 666 BP.
XX
AC   AAD15211;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-42.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
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FT   sig_peptide     1..75
FT                   /*tag= b
FT   mat_peptide     76..663
FT                   /*tag= c
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XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08604.
```

XX
PT Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT p40 and p35 polypeptides), useful for treating various diseases e.g.
PT diabetic retinopathy and cancer -
XX
PS Claim 87; Page 139; 223pp; English.
XX
CC The invention relates to nucleic acids encoding modified cytokine
CC polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC gamma induction activities. The polypeptides and polynucleotides of the
CC invention are useful for treating various diseases e.g. bacterial
CC infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC vaccinated host's cell-mediated immunity for protective response to a
CC pathogen. The present sequence is a modified human p35 protein encoding
CC DNA.
XX
SQ Sequence 666 BP; 186 A; 181 C; 141 G; 158 T; 0 other;

Query Match 9.9%; Score 66; DB 22; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.2e-22;
Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        381 TAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAA 440
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 TAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAA 437

Qy        441 GCTTTT 446
              ||||||
Db        438 GCTTTT 443
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17: gb_gss:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	13	21	3.2	853	17	BH246749	BH246749 BOGAA09TR
c	14	20	3.0	241	17	AZ891891	AZ891891 RPCI-24-2
	15	20	3.0	340	17	AQ373901	AQ373901 RPCI11-14
c	16	20	3.0	385	12	BE703854	BE703854 MR2-NN111
c	17	20	3.0	405	10	AW114770	AW114770 rs59b05.y
	18	20	3.0	421	17	AQ673149	AQ673149 HS_5496_A
	19	20	3.0	511	9	AA135692	AA135692 z111c04.r
c	20	20	3.0	516	17	AQ478437	AQ478437 RPCI-11-2
	21	20	3.0	581	14	BQ508151	BQ508151 EST615566
c	22	20	3.0	604	14	W63576	W63576 zc55h09.r1
	23	20	3.0	673	13	BM427122	BM427122 pgf2n.pk0
	24	20	3.0	711	14	BQ509384	BQ509384 EST616799
	25	20	3.0	742	13	BI175859	BI175859 EST516942
	26	20	3.0	757	13	BI177417	BI177417 EST518362
	27	20	3.0	859	12	BE737982	BE737982 601572557
	28	20	3.0	921	14	BQ883361	BQ883361 AGENCOURT
	29	20	3.0	995	13	BM416238	BM416238 OP21326 M
c	30	19	2.9	172	12	BE932909	BE932909 CM2-HT087
	31	19	2.9	234	9	AA078213	AA078213 7H16D07 C
	32	19	2.9	246	14	BQ322232	BQ322232 RC4-CT084
c	33	19	2.9	247	10	BB425487	BB425487 BB425487
	34	19	2.9	255	9	AA078183	AA078183 7H16B12 C
	35	19	2.9	259	10	BE604331	BE604331 WHE1405-1
	36	19	2.9	284	10	BB150477	BB150477 BB150477
	37	19	2.9	286	14	BQ392367	BQ392367 NISC_mq24
c	38	19	2.9	287	9	AL777805	AL777805 AL777805
c	39	19	2.9	300	12	BF757569	BF757569 CM4-CT057
	40	19	2.9	314	9	AL643008	AL643008 AL643008
	41	19	2.9	317	14	BQ392345	BQ392345 NISC_mq23
c	42	19	2.9	318	9	AL640225	AL640225 AL640225
	43	19	2.9	334	14	BQ392422	BQ392422 NISC_mq24
	44	19	2.9	371	9	AA772037	AA772037 ai39g07.s
c	45	19	2.9	380	9	AA826164	AA826164 od85h04.s

ALIGNMENTS

RESULT 1
BI824638
LOCUS BI824638 447 bp mRNA linear EST 04-OCT-2001
DEFINITION 603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5', mRNA sequence.
ACCESSION BI824638
VERSION BI824638.1 GI:15936188
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 447)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11435 row: o column: 19
High quality sequence start: 3
High quality sequence stop: 445.
FEATURES Location/Qualifiers

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     source          1. .447
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5175018"
                     /clone_lib="NIH_MGC_115"
                     /lab_host="DH10B"
                     /note="Organ: pooled brain, lung, testis; Vector:
                     pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                     source anonymous pool of 6 male brains, age range 23-27; 1
                     male lung, age 27; and 1 male testis, age 69.  Library is
                     oligo-dT primed and directionally cloned (EcoRV site is
                     destroyed upon  cloning).  Average insert size 1.8 kb,
                     insert size range 1-3 kb. Library is normalized and
                     enriched for full-length clones and was  constructed by C.
                     Gruber (Invitrogen).  Research Genetics tracking  code
                     021. Note: this is a NIH_MGC Library."
BASE COUNT      149 a     63 c     87 g    148 t
ORIGIN

  Query Match             6.2%;  Score 41;  DB 13;  Length 447;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-11;
  Matches   41;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        583 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              |||||||||||||||||||||||||||||||||||||||||
Db          1 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 41


RESULT 2
BI523344/c
LOCUS       BI523344                1099 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3',
            mRNA sequence.
ACCESSION   BI523344
VERSION     BI523344.1  GI:15348136
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1099)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 40
            High quality sequence stop: 727.
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      359 a    244 c    218 g    276 t      2 others
ORIGIN

  Query Match             6.0%;  Score 40;  DB 13;  Length 1099;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-10;
  Matches   40;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        584 AAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              ||||||||||||||||||||||||||||||||||||||||
Db        524 AAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 485


RESULT 3
AI050362
LOCUS       AI050362                589 bp    mRNA    linear   EST 09-JUL-1998
DEFINITION  ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN
            PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35
            subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:3299479
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
     source          1. .589
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:1379220"
                     /clone_lib="Soares_thymus_2NbMT"
                     /sex="male"
                     /tissue_type="Thymus"
                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      162 a    159 c    142 g    126 t
ORIGIN

  Query Match             4.7%;  Score 31;  DB 9;  Length 589;
  Best Local Similarity   100.0%;  Pred. No. 1e-05;
  Matches   31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

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Qy        385 AGCATCTATGAGGACTTGAAGATGTACCAGA 415
              |||||||||||||||||||||||||||||||
Db        324 AGCATCTATGAGGACTTGAAGATGTACCAGA 354


RESULT 4
BF552757
LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /clone_lib="UI-R-C0"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0
                     library is a subtracted library derived from the UI-R-A1
                     and UI-R-E1 libraries. The UI-R-A1 library consisted of a
                     mixture of individually tagged normalized libraries
                     constructed from rat  placenta, adult lung, brain, liver,
                     kidney, heart, spleen, ovary,  and muscle. The UI-R-E1
                     library  consisted of a mixture of individually tagged
                     normalized libraries constructed from 8, 12 and 18-day
                     embryo. The tag is a string of 3-5 nucleotides present
                     between the Not I  site and the oligo-dT track which
                     allows identification of the library of origin of a clone
                     within the mixture. The subtracted library (UI-R-C0) was
                     constructed as follows: PCR amplified cDNA inserts from a
                     pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had
                     been derived was used as a driver in a hybridization with
                     the pooled UI-R-A1 and UI-R-E1 library in the form of
                     single-stranded circles.  The remaining single-stranded
                     circles (subtracted library) was purified by
                     hydroxyapatite column chromatography, converted to
                     double-stranded circles and electroporated into DH10B
                     bacteria (Life Technologies) to generate the UI-R-C0
                     library. This procedure has been previously described
                     (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                     1996)"
BASE COUNT      106 a     93 c     89 g     85 t
ORIGIN

  Query Match             4.5%;  Score 30;  DB 12;  Length 373;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-05;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        385 AGCATCTATGAGGACTTGAAGATGTACCAG 414
              ||||||||||||||||||||||||||||||
Db         98 AGCATCTATGAGGACTTGAAGATGTACCAG 127


RESULT 5
BI523569
LOCUS       BI523569                832 bp    mRNA    linear   EST 29-AUG-2001
DEFINITION  603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5',
            mRNA sequence.
ACCESSION   BI523569
VERSION     BI523569.1  GI:15348361
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 832)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11605  row: l  column: 09
            High quality sequence start: 23
            High quality sequence stop: 821.
FEATURES             Location/Qualifiers
     source          1. .832
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      220 a    233 c    200 g    179 t
ORIGIN

  Query Match             4.4%;  Score 29;  DB 13;  Length 832;
  Best Local Similarity   100.0%;  Pred. No. 0.00015;
  Matches   29;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        208 GAAGAGATTGATCATGAAGATATCACAAA 236
              |||||||||||||||||||||||||||||
Db        520 GAAGAGATTGATCATGAAGATATCACAAA 548


RESULT 6
BM257856
LOCUS       BM257856                342 bp    mRNA    linear   EST 17-DEC-2001
DEFINITION  521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BM257856
VERSION     BM257856.1  GI:17893455
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KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 125  row: E  column: 18
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .342
                      /organism="Bos taurus"
                      /db_xref="taxon:9913"
                      /clone_lib="MARC 3BOV"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                      Library made from pooled tissue from marrow, alveolar
                      macrophage, ovary, fetal semitendonosus muscle, and fetal
                      longissimus muscle."
BASE COUNT       67 a    135 c     74 g     66 t
ORIGIN

  Query Match             3.9%;  Score 26;  DB 13;  Length 342;
  Best Local Similarity   100.0%;  Pred. No. 0.0053;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 CAGAAGGCCAGACAAACTCTAGAATT 191
              ||||||||||||||||||||||||||
Db        294 CAGAAGGCCAGACAAACTCTAGAATT 319


RESULT 7
BG702253
LOCUS       BG702253                812 bp    mRNA    linear   EST 07-MAY-2001
DEFINITION  602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5',
            mRNA sequence.
ACCESSION   BG702253
VERSION     BG702253.1  GI:13973409
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 812)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10714  row: e  column: 15
            High quality sequence stop: 804.
FEATURES              Location/Qualifiers
     source           1. .812
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4816118"
                      /clone_lib="NIH_MGC_95"
                      /tissue_type="hippocampus"
                      /lab_host="DH10B"
                      /note="Organ: brain; Vector: pBluescriptR (modified
                      pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                      ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                      size-selected for  average insert size 2.5 kb and
                      normalized to ROT 5. This is a primary library enriched
                      for  full-length clones and constructed using the
                      Cap-trapper method (Carninci, in preparation).  Library
                      constructed by M. Brownstein (NIMH/NHGRI, National
                      Institutes of Health).  Note: this is a NIH_MGC Library."
BASE COUNT      188 a    249 c    226 g    149 t
ORIGIN

  Query Match             3.9%;  Score 26;  DB 12;  Length 812;
  Best Local Similarity   100.0%;  Pred. No. 0.0071;
  Matches   26;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        166 CAGAAGGCCAGACAAACTCTAGAATT 191
              ||||||||||||||||||||||||||
Db        573 CAGAAGGCCAGACAAACTCTAGAATT 598


RESULT 8
BF203063
LOCUS       BF203063                255 bp    mRNA    linear   EST 06-NOV-2000
DEFINITION  WHE1768_H05_O10ZS Wheat pre-anthesis spike cDNA library Triticum
            aestivum cDNA clone WHE1768_H05_O10, mRNA sequence.
ACCESSION   BF203063
VERSION     BF203063.1  GI:11117805
KEYWORDS    EST.
SOURCE      bread wheat.
  ORGANISM  Triticum aestivum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
            ; Triticeae; Triticum.
REFERENCE   1  (bases 1 to 255)
  AUTHORS   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
            ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
            Seaton,C.L. and Tong,J.C.
  TITLE     The structure and function of the expressed portion of the wheat
            genomes - Pre-anthesis spike cDNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oandersn@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: Stratagene SK primer.
FEATURES              Location/Qualifiers
     source           1. .255
                      /organism="Triticum aestivum"
                      /cultivar="Chinese Spring"
                      /db_xref="taxon:4565"
                      /clone="WHE1768_H05_O10"
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```
                     /clone_lib="Wheat pre-anthesis spike cDNA library"
                     /tissue_type="Spike before anthesis"
                     /dev_stage="Adult plant"
                     /lab_host="E. coli SOLR"
                     /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
                     Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
                     greenhouse.  Whole spike with awns trimmed,  white, green
                     and yellow anther were collected and total RNA, and
                     poly(A) RNA were prepared, a cDNA library was made, and
                     the cDNA  clones were in vivo excised to give pBluescript
                     phagemids in the TJ  Close lab (Choi, Close, Fenton) at
                     the University of California,  Riverside.  Plasmid DNA
                     preparations and DNA sequencing were performed  in the OD
                     Anderson lab (all other authors)."
BASE COUNT       25 a    120 c     75 g     35 t
ORIGIN

  Query Match             3.3%;  Score 22;  DB 12;  Length 255;
  Best Local Similarity   100.0%;  Pred. No. 0.83;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          5 GCCCGCCGCGCGGCCTCCTCCT 26
              ||||||||||||||||||||||
Db         14 GCCCGCCGCGCGGCCTCCTCCT 35


RESULT 9
AQ393691/c
LOCUS       AQ393691                489 bp    DNA     linear   GSS 06-MAR-1999
DEFINITION  CITBI-E1-2544N3.TF CITBI-E1 Homo sapiens genomic clone 2544N3, DNA
            sequence.
ACCESSION   AQ393691
VERSION     AQ393691.1  GI:4364714
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 489)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
            Venter,J.C.
  TITLE     Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: CITBI-E1-2544N3.TR
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are available from Research Genetics (info@resgen.com). BAC
            end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: M13-21
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .489
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="2544N3"
                     /clone_lib="CITBI-E1"
                     /sex="male"
                     /cell_type="sperm"
                     /note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
                     CalTech Human BAC Library D"
BASE COUNT      148 a     97 c    103 g    140 t      1 others
ORIGIN

  Query Match             3.2%;  Score 21;  DB 17;  Length 489;
  Best Local Similarity   100.0%;  Pred. No. 3.7;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        287 ATGAGAGTTGCCTGGCTTCCA 307
              |||||||||||||||||||||
Db        441 ATGAGAGTTGCCTGGCTTCCA 421


RESULT 10
BU002107
LOCUS       BU002107                679 bp    mRNA    linear   EST 22-AUG-2002
DEFINITION  QGG30D21.yg.ab1 QG_EFGHJ lettuce serriola Lactuca sativa cDNA clone
            QGG30D21, mRNA sequence.
ACCESSION   BU002107
VERSION     BU002107.1  GI:22436502
KEYWORDS    EST.
SOURCE      Lactuca sativa.
  ORGANISM  Lactuca sativa
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Asteridae; euasterids II; Asterales; Asteraceae; Lactuceae;
            Lactuca.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.,
            Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison
            ,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
            Church,S., Jackson,L. and Bradford,K.
  TITLE     Lettuce and Sunflower ESTs from the Compositae Genome Project
            http://compgenomics.ucdavis.edu/
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alexander Kozik [R.W.Michelmore]
            Department of Vegetable Crops, R.W.Michelmore Lab
            University of California at Davis (UCD)
            Asmundson Hall, UCD, Davis, CA 95616, USA
            Tel: 1-(530)-742-1742
            Fax: 1-(530)-752-9659
            Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
            singleton, see http://cgpdb.ucdavis.edu/ for details.
            Plate: QGG30  row: D  column: 21.
FEATURES             Location/Qualifiers
     source          1. .679
                     /organism="Lactuca sativa"
                     /cultivar="L.serriola"
                     /db_xref="taxon:4236"
                     /clone="QGG30D21"
                     /clone_lib="QG_EFGHJ lettuce serriola"
                     /lab_host="E.coli"
                     /note="Vector: pBRcDNASfiAB; The library was constructed
                     from 10 different sources of RNA from a single genotype.
                     Separate cDNAs were generated using primers that
                     incorporated unique 5' and 3' tags to distinguish each
                     source of RNA. cDNAs were then pooled, size-fractionated,
                     directionally cloned into a custom medium-copy vector and
                     transformations made with four size classes to minimize
                     size bias. Details of each source of RNA and library
                     construction can be obtained at http://cgpdb.ucdavis.edu/
                     TAG_LIB=QG_EFGHJ lettuce serriola
                     TAG_TISSUE=flowers pre-fertilized
                     TAG_SEQ=GCTTGACGGG"
BASE COUNT      175 a    163 c    113 g    228 t
ORIGIN

  Query Match             3.2%;  Score 21;  DB 14;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 4.2;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        273 GGAATTAACCATGAATGAGAG 293
              |||||||||||||||||||||
Db          8 GGAATTAACCATGAATGAGAG 28


RESULT 11
BH728255
LOCUS       BH728255                726 bp    DNA     linear   GSS 20-FEB-2002
DEFINITION  BOMIG81TR BO_2_3_KB Brassica oleracea genomic clone BOMIG81, DNA
```

```
            sequence.
ACCESSION   BH728255
VERSION     BH728255.1  GI:18833650
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 726)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOMIG81TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .726
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOMIG81"
                     /clone_lib="BO_2_3_KB"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      171 a    194 c    172 g    189 t
ORIGIN

  Query Match             3.2%;  Score 21;  DB 17;  Length 726;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        120 CCTCAACCACTCCCAAAACCT 140
              |||||||||||||||||||||
Db        663 CCTCAACCACTCCCAAAACCT 683


RESULT 12
AQ631366/c
LOCUS       AQ631366                733 bp    DNA     linear   GSS 17-JUN-1999
DEFINITION  RPCI-11-482B16.TV RPCI-11 Homo sapiens genomic clone RPCI-11-482B16
            , DNA sequence.
ACCESSION   AQ631366
VERSION     AQ631366.1  GI:5094001
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 733)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
            ,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genet cs (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .733
                     /organism="Homo sapiens"
                     /db_xref="GDB:7684743"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-482B16"
                     /clone_lib="RPCI-11"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
BASE COUNT      223 a    127 c    133 g    250 t
ORIGIN

  Query Match             3.2%;  Score 21;  DB 17;  Length 733;
  Best Local Similarity   100.0%;  Pred. No. 4.3;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        569 ATTTTTATAAAACTAAAATCA 589
              |||||||||||||||||||||
Db        145 ATTTTTATAAAACTAAAATCA 125


RESULT 13
BH246749
LOCUS       BH246749                853 bp    DNA     linear   GSS 26-NOV-2001
DEFINITION  BOGAA09TR BOGA Brassica oleracea genomic clone BOGAA09, DNA
            sequence.
ACCESSION   BH246749
VERSION     BH246749.1  GI:17067298
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 853)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOGAA09TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .853
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOGAA09"
                     /clone_lib="BOGA"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      204 a    228 c    206 g    215 t
ORIGIN

  Query Match             3.2%;  Score 21;  DB 17;  Length 853;
  Best Local Similarity   100.0%;  Pred. No. 4.5;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        120 CCTCAACCACTCCCAAAACCT 140
              |||||||||||||||||||||
Db        690 CCTCAACCACTCCCAAAACCT 710
```

```
RESULT 14
AZ891891/c
LOCUS       AZ891891                 241 bp    DNA     linear   GSS 05-MAR-2001
DEFINITION  RPCI-24-201J11.TV RPCI-24 Mus musculus genomic clone RPCI-24-201J11
            , DNA sequence.
ACCESSION   AZ891891
VERSION     AZ891891.1  GI:13210836
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 241)
  AUTHORS   Zhao,S., Nierman,W., Malek,J., Shatsman,S., Akinret,B., Levins,M.,
            Tseqaye,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregeorgis,E.,
            Russell,D., de Jong,P. and Fraser,C.M.
  TITLE     Mouse BAC End Sequences from Library RPCI-24
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Shaying Zhao
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: szhao@tigr.org
            Clones are derived from the mouse BAC library RPCI-24. For BAC
            library availability, please contact Pieter de Jong
            (pdejong@mail.cho.org). Clones may be purchased from BACPAC
            Resources (http://www.chori.org/bacpac/orderingframe.htm). BAC end
            page: http://ww .tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
            Plate: 201  row: J  column: 11
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .241
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="RPCI-24-201J11"
                     /clone_lib="RPCI-24"
                     /sex="Male"
                     /cell_type="Spleen/Brain"
                     /note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
                     RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
                     library was  cloned in the pTARBAC1 cloning vector at the
                     BamH1 sites using MboI  partially digested male C57BL/6J
                     DNA."
BASE COUNT       57 a     39 c     35 g    110 t
ORIGIN

  Query Match             3.0%;  Score 20;  DB 17;  Length 241;
  Best Local Similarity   100.0%;  Pred. No. 11;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        569 ATTTTTATAAAACTAAAATC 588
              ||||||||||||||||||||
Db         20 ATTTTTATAAAACTAAAATC 1


RESULT 15
AQ373901
LOCUS       AQ373901                 340 bp    DNA     linear   GSS 20-MAY-1999
DEFINITION  RPCI11-145D9.TV RPCI-11 Homo sapiens genomic clone RPCI-11-145D9,
            DNA sequence.
ACCESSION   AQ373901
VERSION     AQ373901.1  GI:4344924
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 340)
  AUTHORS   Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter
            ,J.C.
  TITLE     Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
            Map Building
  JOURNAL   Unpublished (1997)
COMMENT     Other_GSSs: RPCI11-145D9.TJ
            Contact: Shaying Zhao, William Nierman, Mark Adams
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850
            Tel: 301 838 0200
            Fax: 301 838 0208
            Email: hbe@tigr.org
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
            Research Genetics (info@resgen.com). BAC end search page:
            http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
            Seq primer: T7
            Class: BAC ends.
FEATURES             Location/Qualifiers
     source          1. .340
                     /organism="Homo sapiens"
                     /db_xref="GDB:7555376"
                     /db_xref="taxon:9606"
                     /clone="RPCI-11-145D9"
                     /clone_lib="RPCI-11"
                     /sex="Male"
                     /cell_type="Lymphocytes"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     RPCI11 Human Male BAC Library"
BASE COUNT      122 a     61 c     41 g    116 t
ORIGIN

  Query Match             3.0%;  Score 20;  DB 17;  Length 340;
  Best Local Similarity   100.0%;  Pred. No. 12;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        224 AAGATATCACAAAGGATAAA 243
              ||||||||||||||||||||
Db         24 AAGATATCACAAAGGATAAA 43


Search completed: July 16, 2003, 15:58:19
Job time : 1148.39 secs
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:16:38 ; Search time 35.369 Seconds
(without alignments)
5774.736 Million cell updates/sec

Title: US-09-917-265-46
Perfect score: 666
Sequence: 1 atgtgcccgccgcgcggcct.....tgagttatctgaattcttcc 666

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 441362 seqs, 153338381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA:*
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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	615	92.3	669	4	US-09-079-984A-12	Sequence 12, Appl
	2	501	75.2	669	4	US-09-079-984A-2	Sequence 2, Appli
	3	59	8.9	660	1	US-08-186-529-3	Sequence 3, Appli
	4	59	8.9	660	1	US-08-640-386A-3	Sequence 3, Appli
	5	59	8.9	721	2	US-08-184-009-199	Sequence 199, App
	6	59	8.9	721	2	US-08-458-356-199	Sequence 199, App
	7	59	8.9	721	4	US-08-460-736-199	Sequence 199, App
	8	59	8.9	762	4	US-08-848-760B-21	Sequence 21, Appl
	9	59	8.9	1026	2	US-08-751-767A-1	Sequence 1, Appli
	10	59	8.9	1316	2	US-08-684-687-3	Sequence 3, Appli
	11	59	8.9	1316	4	US-09-851-520-3	Sequence 3, Appli
	12	59	8.9	1364	1	US-08-265-087-3	Sequence 3, Appli
	13	59	8.9	1364	1	US-08-621-493-3	Sequence 3, Appli
	14	59	8.9	1364	2	US-08-965-688-3	Sequence 3, Appli
	15	59	8.9	1364	4	US-09-260-173-3	Sequence 3, Appli
	16	59	8.9	1560	2	US-08-751-767A-11	Sequence 11, Appl
	17	59	8.9	1623	2	US-08-751-767A-9	Sequence 9, Appli
	18	59	8.9	1645	4	US-09-310-842-2	Sequence 2, Appli
	19	59	8.9	6139	2	US-08-751-767A-7	Sequence 7, Appli
	20	31	4.7	713	2	US-08-385-335A-10	Sequence 10, Appl
	21	31	4.7	6295	2	US-08-659-206A-4	Sequence 4, Appli
	22	31	4.7	7287	2	US-08-659-206A-1	Sequence 1, Appli
	23	30	4.5	39	4	US-09-079-984A-15	Sequence 15, Appl
c	24	27	4.1	39	4	US-09-079-984A-16	Sequence 16, Appl
c	25	20	3.0	20	3	US-08-621-841-52	Sequence 52, Appl
c	26	20	3.0	20	4	US-09-851-520-28	Sequence 28, Appl
c	27	20	3.0	20	4	US-09-851-520-31	Sequence 31, Appl
c	28	20	3.0	20	4	US-09-851-520-58	Sequence 58, Appl
c	29	19	2.9	20	4	US-09-851-520-59	Sequence 59, Appl
c	30	18	2.7	20	4	US-09-851-520-57	Sequence 57, Appl
c	31	18	2.7	409	4	US-09-189-060B-13	Sequence 13, Appl
	32	18	2.7	415	4	US-09-189-060B-15	Sequence 15, Appl
	33	18	2.7	4456	4	US-09-095-443-1	Sequence 1, Appli
	34	18	2.7	4403765	4	US-09-103-840A-2	Sequence 2, Appli
	35	18	2.7	4411529	4	US-09-103-840A-1	Sequence 1, Appli
	36	17	2.6	20	1	US-08-012-543-13	Sequence 13, Appl
c	37	17	2.6	20	4	US-09-851-520-32	Sequence 32, Appl
c	38	17	2.6	20	4	US-09-851-520-39	Sequence 39, Appl
c	39	17	2.6	20	4	US-09-851-520-50	Sequence 50, Appl
c	40	17	2.6	20	4	US-09-851-520-56	Sequence 56, Appl
	41	17	2.6	21	1	US-08-012-543-20	Sequence 20, Appl
	42	17	2.6	423	1	US-08-470-179-180	Sequence 180, App
c	43	17	2.6	826	1	US-08-631-200-10	Sequence 10, Appl
c	44	17	2.6	826	1	US-08-829-553-10	Sequence 10, Appl
c	45	17	2.6	826	2	US-08-922-267A-10	Sequence 10, Appl

ALIGNMENTS

```
RESULT 1
US-09-079-984A-12
; Sequence 12, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-12

  Query Match             92.3%;  Score 615;  DB 4;  Length 669;
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  Best Local Similarity   99.8%;  Pred. No. 1.9e-310;
  Matches  665;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
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Db        661 TCTTCC 666


RESULT 2
US-09-079-984A-2
; Sequence 2, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

  Query Match             75.2%;  Score 501;  DB 4;  Length 669;
  Best Local Similarity   99.7%;  Pred. No. 3.8e-251;
  Matches  601;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         36 CCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTC 95
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         36 CCTGGTCCTGCTAAGCCACCTGGACCACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTC 95

Qy         96 ACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 ACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAG 155

Qy        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 CAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGAT 215

Qy        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 TGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGA 275

Qy        276 ATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAG 335
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 ATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAG 335

Qy        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 TTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGA 395

Qy        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        396 GGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCC 455

Qy        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGC 515
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        456 CAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCTATCGATGAGCTGTTACAGGC 515

Qy        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTA 575

Qy        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        576 TAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCAT 635

Qy        636 CGA 638
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Db        636 CGA 638


RESULT 3
US-08-186-529-3
; Sequence 3, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-186-529-3

  Query Match             8.9%;  Score 59;  DB 1;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-21;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 614


RESULT 4
US-08-640-386A-3
; Sequence 3, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-640-386A-3

  Query Match             8.9%;  Score 59;  DB 1;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-21;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 614


RESULT 5
US-08-184-009-199
; Sequence 199, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
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;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-199

  Query Match             8.9%;  Score 59;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-21;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 675


RESULT 6
US-08-458-356-199
; Sequence 199, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-199

  Query Match             8.9%;  Score 59;  DB 2;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-21;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 675


RESULT 7
US-08-460-736-199
; Sequence 199, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-199

  Query Match             8.9%;  Score 59;  DB 4;  Length 721;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-21;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        617 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 675


RESULT 8
US-08-848-760B-21
; Sequence 21, Application US/08848760B
; Patent No. 6248721
;  GENERAL INFORMATION:
;       APPLICANT: Chang, Lung-Ji
;       TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;       NUMBER OF SEQUENCES: 33
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
```

```
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
;             STATE: Florida
;             COUNTRY: United States of America
;             ZIP: 32606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/848,760B
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: 09-APR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: PACE, DORAN R.
;             REGISTRATION NUMBER: 38,261
;             REFERENCE/DOCKET NUMBER: CNG-100C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (352) 375-8100
;             TELEFAX: (352) 372-5800
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-848-760B-21

  Query Match             8.9%;  Score 59;  DB 4;  Length 762;
  Best Local Similarity   100.0%;  Pred. No. 3.2e-21;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 716


RESULT 9
US-08-751-767A-1
; Sequence 1, Application US/08751767A
; Patent No. 5994104
;  GENERAL INFORMATION:
;    APPLICANT:  ANDERSON, ROBERT J.
;    APPLICANT:  GRANT, HUGH
;    APPLICANT:  MACDONALD, IAN D.
;    TITLE OF INVENTION:  INTERLUKIN-12 FUSION PROTEIN
;    NUMBER OF SEQUENCES:  80
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VA
;      COUNTRY:  USA
;      ZIP:  22201
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/751,767A
;      FILING DATE:  08-NOV-1996
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SADOFF, B.J.
;      REGISTRATION NUMBER:  36,663
;      REFERENCE/DOCKET NUMBER:  117-221
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  7038164091
;      TELEFAX:  7038164100
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1026 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  170..826
US-08-751-767A-1

  Query Match             8.9%;  Score 59;  DB 2;  Length 1026;
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  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Db        725 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 783


RESULT 10
US-08-684-687-3
; Sequence 3, Application US/08684687
; Patent No. 5830451
;  GENERAL INFORMATION:
;    APPLICANT:  KIEFF, ELLIOTT D.
;    APPLICANT:  DEVERGNE, ODILE
;    TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
;      STREET:  600 ATLANTIC AVENUE
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,687
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,092
;      FILING DATE:  11-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GATES, EDWARD R.
;      REGISTRATION NUMBER:  31,616
;      REFERENCE/DOCKET NUMBER:  B0801/7051
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1316 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    FEATURE:
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;       NAME/KEY:  CDS
;       LOCATION:  102..863
US-08-684-687-3

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  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 11
US-09-851-520-3
; Sequence 3, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-09-851-520-3

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RESULT 12
US-08-265-087-3
; Sequence 3, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-265-087-3

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  Best Local Similarity   100.0%;  Pred. No. 3.1e-21;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
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Db        758 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 816


RESULT 13
US-08-621-493-3
; Sequence 3, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
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;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-621-493-3

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RESULT 14
US-08-965-688-3
; Sequence 3, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
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;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-965-688-3

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  Best Local Similarity   100.0%;  Pred. No. 3.1e-21;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        565 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 623
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Db        758 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 816


RESULT 15
US-09-260-173-3
; Sequence 3, Application US/09260173
; Patent No. 6168923
;  GENERAL INFORMATION:
;       APPLICANT: Scott, Phillip
;                  Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
;            STATE: Pennsylvania
;            COUNTRY: USA
;            ZIP: 19477
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.25
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/260,173
;            FILING DATE: 01-Mar-1999
;            CLASSIFICATION: <Unknown>
;                            17-JUN-1994
;                            18-APR-1994
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: 08/965,688
;            FILING DATE: <Unknown>
;            APPLICATION NUMBER: 08/265,087
;            FILING DATE: 17-JUN-1994
;            APPLICATION NUMBER: US 08/229,282
;            FILING DATE: 18-APR-1994
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Bak, Mary E.
;            REGISTRATION NUMBER: 31,215
;            REFERENCE/DOCKET NUMBER: WST51AUSA
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: 215-540-9206
;            TELEFAX: 215-540-5818
;  INFORMATION FOR SEQ ID NO: 3:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 1364 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: double
;            TOPOLOGY: unknown
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;            NAME/KEY:  CDS
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US-09-260-173-3

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:21:13 ; Search time 126.098 Seconds
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Title: US-09-917-265-46
Perfect score: 666
Sequence: 1 atgtgcccgccgcgcggcct.....tgagttatctgaattcttcc 666

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	666	100.0	666	10	US-09-917-265-46	Sequence 46, Appl
c 2	666	100.0	666	10	US-09-917-265-48	Sequence 48, Appl
3	666	100.0	1455	10	US-09-917-265-104	Sequence 104, App
c 4	666	100.0	1455	10	US-09-917-265-106	Sequence 106, App
5	591	88.7	591	10	US-09-917-265-49	Sequence 49, Appl
c 6	591	88.7	591	10	US-09-917-265-51	Sequence 51, Appl
7	494	74.2	1533	10	US-09-917-265-66	Sequence 66, Appl
c 8	494	74.2	1533	10	US-09-917-265-68	Sequence 68, Appl
9	494	74.2	1599	10	US-09-917-265-61	Sequence 61, Appl
c 10	494	74.2	1599	10	US-09-917-265-63	Sequence 63, Appl
11	81	12.2	561	10	US-09-917-265-101	Sequence 101, App
c 12	81	12.2	561	10	US-09-917-265-103	Sequence 103, App
13	81	12.2	591	10	US-09-917-265-35	Sequence 35, Appl
c 14	81	12.2	591	10	US-09-917-265-37	Sequence 37, Appl
15	81	12.2	591	12	US-10-079-616-9	Sequence 9, Appli
16	81	12.2	666	10	US-09-917-265-32	Sequence 32, Appl
c 17	81	12.2	666	10	US-09-917-265-34	Sequence 34, Appl
18	81	12.2	1441	12	US-10-079-616-8	Sequence 8, Appli
19	81	12.2	1533	10	US-09-917-265-43	Sequence 43, Appl
c 20	81	12.2	1533	10	US-09-917-265-45	Sequence 45, Appl
21	81	12.2	1599	10	US-09-917-265-38	Sequence 38, Appl
c 22	81	12.2	1599	10	US-09-917-265-40	Sequence 40, Appl
23	59	8.9	660	10	US-09-754-014-6	Sequence 6, Appli
24	59	8.9	660	10	US-09-836-866-4	Sequence 4, Appli
25	59	8.9	689	12	US-10-079-616-26	Sequence 26, Appl
26	59	8.9	762	9	US-09-826-025-21	Sequence 21, Appl
27	59	8.9	1026	9	US-10-172-399-5	Sequence 5, Appli
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29	59	8.9	1645	9	US-10-228-811-2	Sequence 2, Appli
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32	59	8.9	8608	10	US-09-828-825-7	Sequence 7, Appli
33	59	8.9	8623	10	US-09-828-825-5	Sequence 5, Appli
34	59	8.9	8629	10	US-09-828-825-15	Sequence 15, Appl
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36	59	8.9	8644	10	US-09-828-825-13	Sequence 13, Appl
37	59	8.9	8659	10	US-09-828-825-11	Sequence 11, Appl
38	31	4.7	1265	9	US-10-172-399-1	Sequence 1, Appli
39	27	4.1	79	12	US-10-079-616-24	Sequence 24, Appl
40	24	3.6	39	10	US-09-917-265-91	Sequence 91, Appl
c 41	22	3.3	22	10	US-09-917-265-94	Sequence 94, Appl
42	20	3.0	20	10	US-09-917-265-93	Sequence 93, Appl
43	20	3.0	95	12	US-10-079-616-22	Sequence 22, Appl
c 44	20	3.0	558	9	US-10-198-846-12574	Sequence 12574, A
c 45	20	3.0	828	9	US-10-198-846-5002	Sequence 5002, Ap

ALIGNMENTS

RESULT 1
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(666)
; OTHER INFORMATION:
US-09-917-265-46

Query Match 100.0%; Score 666; DB 10; Length 666;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
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Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        661 TCTTCC 666
                ||||||
Db        661 TCTTCC 666
```

RESULT 2
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-48

Query Match 100.0%; Score 666; DB 10; Length 666;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 607

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 547

Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 427

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 307

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 247

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 187

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 127

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 7

Qy        661 TCTTCC 666
                ||||||
Db          6 TCTTCC 1
```

RESULT 3
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (232)..(897)
; OTHER INFORMATION:
US-09-917-265-104

Query Match 100.0%; Score 666; DB 10; Length 1455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        232 ATGTGCCCGCCGCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 291

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 351
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Qy        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 411

Qy        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 471

Qy        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 531

Qy        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 591

Qy        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 651

Qy        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 711

Qy        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 771

Qy        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        772 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 831

Qy        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        832 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 891

Qy        661 TCTTCC 666
              ||||||
Db        892 TCTTCC 897
```

RESULT 4
US-09-917-265-106/c
; Sequence 106, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-106

Query Match 100.0%; Score 666; DB 10; Length 1455;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1224 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 1165

Qy         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1164 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 1105

Qy         121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 1045

Qy         181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 985

Qy         241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         984 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 925

Qy         301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         924 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 865

Qy         361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         864 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 805

Qy         421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         804 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 745

Qy         481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         744 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 685

Qy         541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         684 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 625

Qy         601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         624 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 565

Qy         661 TCTTCC 666
               ||||||
Db         564 TCTTCC 559
```

RESULT 5
US-09-917-265-49
; Sequence 49, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
; OTHER INFORMATION:
US-09-917-265-49

Query Match 88.7%; Score 591; DB 10; Length 591;
Best Local Similarity 100.0%; Pred. No. 3.5e-313;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60

Qy        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300

Qy        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360

Qy        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480

Qy        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591


RESULT 6
US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-51

  Query Match             88.7%;  Score 591;  DB 10;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-313;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 532

Qy        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 472

Qy        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 412

Qy        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 292

Qy        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 232

Qy        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 112

Qy        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
                ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 1


RESULT 7
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

  Query Match             74.2%;  Score 494;  DB 10;  Length 1533;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-260;
  Matches  494;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        143 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 202
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1010 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 1069

Qy        203 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 262
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1070 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 1129

Qy        263 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 322
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1130 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 1189
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Qy        323 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1190 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 1249

Qy        383 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1250 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 1309

Qy        443 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1310 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 1369

Qy        503 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1370 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 1429

Qy        563 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1430 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 1489

Qy        623 GTGCGGTGACCATC 636
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Db       1490 GTGCGGTGACCATC 1503
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RESULT 8
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
; LENGTH: 1533
; TYPE: DNA
; ORGANISM: Canis familiaris
US-09-917-265-68

Query Match 74.2%; Score 494; DB 10; Length 1533;
Best Local Similarity 100.0%; Pred. No. 4.7e-260;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        143 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 202
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        524 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 465

Qy        203 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 405

Qy        263 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 345

Qy        323 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 382
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Db        344 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 285

Qy        383 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 442
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Db        284 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 225

Qy        443 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 502
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Db        224 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 165

Qy        503 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 562
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Db        164 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 105

Qy        563 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 622
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Db        104 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 45

Qy        623 GTGCGGTGACCATC 636
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Db         44 GTGCGGTGACCATC 31
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RESULT 9
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
; APPLICANT: Wonderling, Ramani S.
; APPLICANT: Boroughs, Karen L.
; TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
; FILE REFERENCE: IM-5
; CURRENT APPLICATION NUMBER: US/09/917,265
; CURRENT FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: 60/223,016
; PRIOR FILING DATE: 2000-08-04
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 1599
; TYPE: DNA
; ORGANISM: Canis familiaris
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1599)
; OTHER INFORMATION:
US-09-917-265-61

Query Match 74.2%; Score 494; DB 10; Length 1599;
Best Local Similarity 100.0%; Pred. No. 4.7e-260;
Matches 494; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        143 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 202
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Db       1076 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 1135

Qy        203 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1136 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 1195

Qy        263 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 322
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Qy        323 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 382
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Db       1256 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 1315

Qy        383 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 442
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Db       1316 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 1375

Qy        443 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 502
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Db       1376 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 1435

Qy        503 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 562
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1436 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 1495

Qy        563 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 622
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Db       1496 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 1555

Qy        623 GTGCGGTGACCATC 636
              ||||||||||||||
Db       1556 GTGCGGTGACCATC 1569


RESULT 10
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

  Query Match             74.2%;  Score 494;  DB 10;  Length 1599;
  Best Local Similarity   100.0%;  Pred. No. 4.7e-260;
  Matches  494;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        143 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 202
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Db        524 TGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCA 465

Qy        203 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 262
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 CTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCT 405

Qy        263 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 322
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 GCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGA 345

Qy        323 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 382
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        344 TAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTA 285

Qy        383 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 442
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        284 GCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGC 225

Qy        443 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 502
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 TTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATG 165

Qy        503 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 562
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Db        164 AGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAG 105

Qy        563 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 622
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        104 AGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTC 45

Qy        623 GTGCGGTGACCATC 636
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Db         44 GTGCGGTGACCATC 31


RESULT 11
US-09-917-265-101
; Sequence 101, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(561)
;   OTHER INFORMATION:
US-09-917-265-101

  Query Match             12.2%;  Score 81;  DB 10;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 192

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        193 CTGGCTTCCAGAGAGATCTCT 213


RESULT 12
US-09-917-265-103/c
; Sequence 103, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 103
;   LENGTH: 561
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-103

  Query Match             12.2%;  Score 81;  DB 10;  Length 561;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 13
US-09-917-265-35
; Sequence 35, Application US/09917265
; Patent No. US20020052030A1
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; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-35

  Query Match             12.2%;  Score 81;  DB 10;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
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Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 14
US-09-917-265-37/c
; Sequence 37, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-37

  Query Match             12.2%;  Score 81;  DB 10;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 370

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
              |||||||||||||||||||||
Db        369 CTGGCTTCCAGAGAGATCTCT 349


RESULT 15
US-10-079-616-9
; Sequence 9, Application US/10079616
; Patent No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 591 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-079-616-9

  Query Match             12.2%;  Score 81;  DB 12;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
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Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        298 CTGGCTTCCAGAGAGATCTCT 318
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Db        223 CTGGCTTCCAGAGAGATCTCT 243


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OM protein - nucleic search, using frame_plus_p2n model

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Perfect score: 1128
Sequence: 1 MCPPRGLLLVTILVLLSHLD.....HAFRIRAVTIDRMMSYLNSS 222

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Delop 6.0 , Delext 7.0

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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3: gb_in:*
4: gb_om:*
5: gb_ov:*
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7: gb_ph:*
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12: gb_sy:*
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14: gb_vi:*
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16: em_fun:*
17: em_hum:*
18: em_in:*
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40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1128	100.0	669	6	AR151072	AR151072 Sequence
2	1128	100.0	669	6	E15018	E15018 Canine mRNA
3	1107	98.1	669	4	CFU49085	U49085 Canis famil
4	1099	97.4	669	6	AR151062	AR151062 Sequence
5	1043	92.5	669	4	FCIL12P35	Y07761 F.catus mRN
6	1041	92.3	669	4	FCU83185	U83185 Felis catus
7	1034	91.7	669	6	AX076201	AX076201 Sequence
8	1034	91.7	669	6	AX076483	AX076483 Sequence
9	1034	91.7	4201	6	AX076477	AX076477 Sequence
10	967.5	85.8	660	6	AX154614	AX154614 Sequence
11	967.5	85.8	660	6	AX154621	AX154621 Sequence
12	967	85.7	669	4	ECIL12P35	Y11130 Equus cabal
13	962.5	85.3	660	6	AX154618	AX154618 Sequence
14	960	85.1	1426	4	PIGIL12PSU	L35765 Sus scrofa
15	958.5	85.0	660	6	AX154617	AX154617 Sequence
16	957.5	84.9	660	6	AX154619	AX154619 Sequence
17	948.5	84.1	660	6	AX154620	AX154620 Sequence
18	940.5	83.4	660	6	AR008951	AR008951 Sequence
19	940.5	83.4	660	6	I28592	I28592 Sequence 3
20	940.5	83.4	762	9	AF101062	AF101062 Homo sapi
21	940.5	83.4	823	9	AF180562	AF180562 Homo sapi
22	940.5	83.4	1316	6	AR050785	AR050785 Sequence
23	940.5	83.4	1316	6	AR212036	AR212036 Sequence
24	940.5	83.4	1316	9	HUMNKSFP35	M65291 Human natur
25	940.5	83.4	1364	6	AR082685	AR082685 Sequence
26	940.5	83.4	1364	6	AR122961	AR122961 Sequence
27	940.5	83.4	1364	6	I28326	I28326 Sequence 3
28	940.5	83.4	1364	6	I89771	I89771 Sequence 3
29	940.5	83.4	1645	6	A92078	A92078 Sequence 2
30	938.5	83.2	660	6	BD007071	BD007071 IL-12 gen
31	938.5	83.2	660	6	BD007079	BD007079 Gene expr
32	936.5	83.0	660	6	AX154616	AX154616 Sequence
33	934.5	82.8	660	6	AX154634	AX154634 Sequence
34	934.5	82.8	721	6	AR052862	AR052862 Sequence
35	934.5	82.8	1026	6	AR091390	AR091390 Sequence
36	934.5	82.8	1026	9	HUMCLMF35	M65271 Human cytot
37	933.5	82.8	660	6	AX154615	AX154615 Sequence
38	926.5	82.1	666	6	AX154612	AX154612 Sequence
39	914.5	81.1	666	6	AX154613	AX154613 Sequence
40	912.5	80.9	660	6	BD007080	BD007080 Gene expr
41	911.5	80.8	666	4	CEU57751	U57751 Cervus elap
42	910.5	80.7	666	4	AF173557	AF173557 Ovis arie
43	909.5	80.6	660	6	BD007081	BD007081 Gene expr
44	908.5	80.5	690	4	BTU14416	U14416 Bos taurus
45	903.5	80.1	703	6	E35793	E35793 Process for

ALIGNMENTS

RESULT 1

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AR151072
LOCUS       AR151072                669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 12 from patent US 6231850.
ACCESSION   AR151072
VERSION     AR151072.1  GI:15117122
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 12 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
BASE COUNT      185 a    177 c    144 g    163 t
ORIGIN

Alignment Scores:
Pred. No.:                5.46e-108      Length:          669
Score:                    1128.00        Matches:         222
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-917-265-47 (1-222) x AR151072 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
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Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
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Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
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Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
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Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
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Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 2
E15018
LOCUS       E15018                  669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
            FT                   /product='interleukin12 35kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /db_xref="taxon:9616"
BASE COUNT      185 a    177 c    144 g    163 t
ORIGIN

Alignment Scores:
Pred. No.:                5.46e-108      Length:          669
Score:                    1128.00        Matches:         222
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-917-265-47 (1-222) x E15018 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
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Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
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Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
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Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
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Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
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Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
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Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666
```

```
RESULT 3
CFU49085
LOCUS       CFU49085                669 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U49085
VERSION     U49085.1  GI:1223905
KEYWORDS    .
SOURCE      Canis familiaris.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis familiaris"
                     /db_xref="taxon:9615"
     CDS             1. .669
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAA92058.1"
                     /db_xref="GI:1223906"
                     /translation="MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHS
                     QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
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                     LNSS"
BASE COUNT      183 a    177 c    145 g    164 t
ORIGIN
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```
Alignment Scores:
Pred. No.:              8.25e-106       Length:         669
Score:                  1107.00         Matches:        218
Percent Similarity:     98.65%          Conservative:   1
Best Local Similarity:  98.20%          Mismatches:     3
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Query Match:            98.14%          Indels:         0
DB:                     4               Gaps:           0

US-09-917-265-47 (1-222) x CFU49085 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
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Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||:::          ||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGATTATATTCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
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Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
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Db        481 AACATGTTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666
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```
RESULT 4
AR151062
LOCUS       AR151062                669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6231850.
ACCESSION   AR151062
VERSION     AR151062.1  GI:15117112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
BASE COUNT      183 a    178 c    146 g    162 t
ORIGIN
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Alignment Scores:
Pred. No.:              5.58e-105       Length:         669
Score:                  1099.00         Matches:        217
Percent Similarity:     98.20%          Conservative:   1
Best Local Similarity:  97.75%          Mismatches:     4
Query Match:            97.43%          Indels:         0
DB:                     6               Gaps:           0

US-09-917-265-47 (1-222) x AR151062 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      ||||||||||||||||||||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        221 SerSer 222
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Db        661 TCTTCC 666

RESULT 5
FCIL12P35
LOCUS       FCIL12P35               669 bp    mRNA    linear   MAM 13-MAY-1997
DEFINITION  F.catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      cat.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
  MEDLINE   97246745
   PUBMED   9089110
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .669
                     /gene="IL-12.p35"
     CDS             1. .669
                     /gene="IL-12.p35"
     .               /function="heterodimer with IL-12 p40 chain"
                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
                     /db_xref="SWISS-PROT:O02743"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNAS"
BASE COUNT      190 a    178 c    139 g    162 t
ORIGIN

Alignment Scores:
Pred. No.:              3.62e-99        Length:         669
Score:                  1043.00         Matches:        204
Percent Similarity:     95.95%          Conservative:   9
Best Local Similarity:  91.89%          Mismatches:     9
Query Match:            92.46%          Indels:         0
DB:                     4               Gaps:           0

US-09-917-265-47 (1-222) x FCIL12P35 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              |||||||:::   |||||||:::||||||||||   :::|||||||||||||:::|||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||   |||   |||||||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480
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Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 SerSer 222
              :::|||
Db        661 GCTTCC 666

RESULT 6
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
  MEDLINE   98182592
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
     CDS             1. .669
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAB93836.1"
                     /db_xref="GI:2735053"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNSS"
BASE COUNT      191 a    179 c    137 g    162 t
ORIGIN

Alignment Scores:
Pred. No.:              5.84e-99       Length:        669
Score:                  1041.00        Matches:       204
Percent Similarity:     95.50%         Conservative:  8
Best Local Similarity:  91.89%         Mismatches:    10
Query Match:            92.29%         Indels:        0
DB:                     4              Gaps:          0

US-09-917-265-47 (1-222) x FCU83185 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   |||||:::||||||||   :::|||||||||||||:::||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||   ||||||||||||:::|||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 7
AX076201
LOCUS       AX076201                669 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104155.
ACCESSION   AX076201
VERSION     AX076201.1  GI:12710826
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p35"
BASE COUNT      189 a    179 c    140 g    161 t
ORIGIN

Alignment Scores:
Pred. No.:              3.11e-98       Length:        669
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Score:                 1034.00       Matches:       201
Percent Similarity:    95.05%        Conservative:  10
Best Local Similarity: 90.54%        Mismatches:    11
Query Match:           91.67%        Indels:        0
DB:                    6             Gaps:          0

US-09-917-265-47 (1-222) x AX076201 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              |||||||::   ||||||:::|||||||   :::|||||||||||:::|||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||   ||||||||||||:::|||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||   |||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 SerSer 222
              :::|||
Db        661 GCTTCC 666

RESULT 8
AX076483
LOCUS       AX076483                669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)

FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
BASE COUNT      189 a    179 c    140 g    161 t
ORIGIN

Alignment Scores:
Pred. No.:             3.11e-98      Length:        669
Score:                 1034.00       Matches:       201
Percent Similarity:    95.05%        Conservative:  10
Best Local Similarity: 90.54%        Mismatches:    11
Query Match:           91.67%        Indels:        0
DB:                    6             Gaps:          0

US-09-917-265-47 (1-222) x AX076483 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              |||||||::   ||||||:::|||||||   :::|||||||||||:::|||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||   ||||||||||||:::|||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||   |||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||:::|||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 SerSer 222
              :::|||
Db        661 GCTTCC 666

RESULT 9
AX076477
LOCUS       AX076477                4201 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104280.
ACCESSION   AX076477
VERSION     AX076477.1  GI:12711029
KEYWORDS    .
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SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 4201)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4201
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="IL-12p35 (pMOLfIL-12p35 (e-,_e31-)clone61)"
BASE COUNT     1086 a    1055 c     999 g    1061 t
ORIGIN

Alignment Scores:
Pred. No.:                2.99e-97        Length:         4201
Score:                    1034.00         Matches:        201
Percent Similarity:       95.05%          Conservative:   10
Best Local Similarity:    90.54%          Mismatches:     11
Query Match:              91.67%          Indels:         0
DB:                       6               Gaps:           0

US-09-917-265-47 (1-222) x AX076477 (1-4201)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db       3047 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 3106

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||||:::|||||||||
Db       3107 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 3166

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||:::|||||||||||||||||||||||||||||
Db       3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||||
Db       3227 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 3286

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db       3287 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 3346

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              |||||||||||||||||||||||||||||||||||||||   |||   |||   |||
Db       3347 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 3406

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||:::|||
Db       3407 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 3466

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 3526

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db       3527 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 3586

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3587 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 3646

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db       3647 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 3706

Qy        221 SerSer 222
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Db       3707 GCTTCC 3712

RESULT 10
AX154614
LOCUS       AX154614                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 18 from Patent WO0140257.
ACCESSION   AX154614
VERSION     AX154614.1  GI:14536189
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 18 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    172 c    136 g    163 t
ORIGIN

Alignment Scores:
Pred. No.:                2.44e-91        Length:         660
Score:                    967.50          Matches:        193
Percent Similarity:       90.54%          Conservative:   8
Best Local Similarity:    86.94%          Mismatches:     18
Query Match:              85.77%          Indels:         3
DB:                       6               Gaps:           1

US-09-917-265-47 (1-222) x AX154614 (1-660)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||      |||||||||         ||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 51

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGC 111

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAA 171

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 231

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||      ||||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTA 291

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              |||||||||   |||   ||||||||||||||||||||||||||   |||   |||
Db        292 AATTCCAGAGAGACTTCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCT 351

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||:::|||
Db        352 TTTATGACAACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 411

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAA 471

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        472 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
                 ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

Qy        221 SerSer 222
                 ||||||
Db        652 TCTTCC 657

RESULT 11
AX154621
LOCUS       AX154621                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 25 from Patent WO0140257.
ACCESSION   AX154621
VERSION     AX154621.1  GI:14536196
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 25 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    172 c    136 g    163 t
ORIGIN

Alignment Scores:
Pred. No.:              2.44e-91       Length:         660
Score:                  967.50         Matches:        193
Percent Similarity:     90.54%         Conservative:   8
Best Local Similarity:  86.94%         Mismatches:     18
Query Match:            85.77%         Indels:         3
DB:                     6              Gaps:           1

US-09-917-265-47 (1-222) x AX154621 (1-660)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||      |||||||||          ||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 51

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGC 111

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAA 171

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 231

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||      ||||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTA 291

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   |||||||||||||||||||||||||   |||   |||
Db        292 AATTCCAGAGAGACTTCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCT 351

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        352 TTTATGACAACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 411

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
                 ||||||   ||||||||||||||||||||:::||||||||||||||||||||||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAA 471

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
                 ||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        472 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
                 ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

Qy        221 SerSer 222
                 ||||||
Db        652 TCTTCC 657

RESULT 12
ECIL12P35
LOCUS       ECIL12P35               669 bp    mRNA    linear   MAM 17-NOV-1999
DEFINITION  Equus caballus mRNA for interleukin 12 p35 subunit.
ACCESSION   Y11130
VERSION     Y11130.1  GI:5441624
KEYWORDS    interleukin-12 subunit p35.
SOURCE      Equus caballus.
  ORGANISM  Equus caballus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Nicolson,L., Penha-Goncalves,M.N., Keanie,J.L., Logan,N.A.,
            Argyle,D.J. and Onions,D.E.
  TITLE     Cloning and sequencing of horse interleukin-12 and interleukin-18
            cDNAs
  JOURNAL   Immunogenetics 50 (1-2), 94-97 (1999)
  MEDLINE   20009534
   PUBMED   10541814
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Nicolson,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-FEB-1997) L. Nicolson, Dept. of Vet. Pathology,
            University of Glasgow Vet. School, Bearsden Rd., Glasgow G61 1QH,
            UK
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Equus caballus"
                     /db_xref="taxon:9796"
                     /cell_line="LPS-stimulated alveolar macrophages"
                     /cell_type="alveolar macrophages"
     gene            1. .669
                     /gene="IL-12 p35"
     CDS             1. .669
                     /gene="IL-12 p35"
                     /codon_start=1
                     /product="interleukin 12 p35 subunit"
                     /protein_id="CAA72012.1"
                     /db_xref="GI:5441625"
                     /translation="MCPPRGLLLVAILVLLNHLDHLSLARNLPTATPGPGMFQCLNHS
                     QNLLRTVSNTLQKARQTLEFYSCTSEEIDHEDITKDKSSTVAACLPLELAPNESCLAS
                     REISFITNGSCLTPGKASSMMTLCLSSIYEDLKMYQVEFKAMNAKLLIDPQRQIFLDE
                     NMLTAIDKLMQALNFNSETVPQKPSLEGLDFYKTKVKLCILLHAFRIRAVTINRMMGY
                     LNAS"
     sig_peptide     1. .69
                     /gene="IL-12 p35"
     misc_feature    1. .16
                     /gene="IL-12 p35"
                     /note="primer-derived sequence"
     misc_feature    651. .669
                     /gene="IL-12 p35"
                     /note="primer-derived sequence"
BASE COUNT      172 a    200 c    153 g    144 t
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Alignment Scores:
Pred. No.:              2.8e-91         Length:         669
Score:                  967.00          Matches:        188
Percent Similarity:     91.44%          Conservative:   15
Best Local Similarity:  84.68%          Mismatches:     19
Query Match:            85.73%          Indels:         0
DB:                     4               Gaps:           0

US-09-917-265-47 (1-222) x ECIL12P35 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||||||||||||||||||||||||   ||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGGCCATCCTGGTCCTCCTAAACCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   |||||||:::|||||||||||||:::|||   ||||||:::|||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACAGCCACACCAGGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||||||||||||||||||||||||   |||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGGACCGTCAGCAACACGCTTCAGAAGGCCAGGCAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACCCTAGAATTCTACTCCTGCACTTCTGAAGAGATCGATCATGAGGATATCACAAAAGAC 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              |||:::|||||||||   ||||||||||||||||||      ||||||||||||||
Db        241 AAGAGCAGCACCGTGGCGGCCTGCCTCCCCCTGGAACTCGCCCCGAACGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||   ||||||||||||||||||||      ||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTCATAACTAATGGGAGTTGCCTGACCCCCGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||       ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TCTATGATGACGCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATCTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||:::|||||||:::|||||||||||||||||:::
Db        421 TTCAAGGCCATGAATGCCAAGCTGTTGATAGATCCTCAGAGGCAGATCTTTCTGGATGAG 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||:::|||:::|||||||||||||||||||   ||||||
Db        481 AACATGCTGACAGCCATTGACAAGCTGATGCAGGCCCTGAACTTCAACAGTGAGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              |||||||||   |||||||||      ||||||||||||||||||:::||||||||||||
Db        541 CCACAAAAGCCCTCCCTTGAAGGACTGGATTTTTATAAAACTAAAGTCAAGCTCTGCATC 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||   |||||||||
Db        601 CTTCTTCATGCCTTCAGAATCCGCGCAGTGACCATCAACAGGATGATGGGCTATCTGAAT 660

Qy        221 SerSer 222
              :::|||
Db        661 GCTTCC 666

RESULT 13
AX154618
LOCUS       AX154618                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 22 from Patent WO0140257.
ACCESSION   AX154618
VERSION     AX154618.1  GI:14536193
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    173 c    136 g    162 t
ORIGIN

Alignment Scores:
Pred. No.:              8.07e-91        Length:         660
Score:                  962.50          Matches:        192
Percent Similarity:     90.09%          Conservative:   8
Best Local Similarity:  86.49%          Mismatches:     19
Query Match:            85.33%          Indels:         3
DB:                     6               Gaps:           1

US-09-917-265-47 (1-222) x AX154618 (1-660)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||||||||||||||||||||||||       ||||||||         ||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 51

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGC 111

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAA 171

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||   ||||||||||||||||||||||||
Db        172 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGACTGATCATGAAGATATCACAAAAGAT 231

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||      ||||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTA 291

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              |||||||||   |||   ||||||||||||||||||||||||||   |||   |||
Db        292 AATTCCAGAGAGACTTCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCT 351

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||:::|||
Db        352 TTTATGACAACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 411

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||:::||||||||||||||||||||||||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAA 471

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        472 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

Qy        221 SerSer 222
              ||||||
Db        652 TCTTCC 657

RESULT 14
PIGIL12PSU
LOCUS       PIGIL12PSU              1426 bp    mRNA    linear   MAM 09-JUL-2001
DEFINITION  Sus scrofa interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   L35765
VERSION     L35765.1  GI:927204
```

```
KEYWORDS    .
SOURCE      Sus scrofa.
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 1426)
  AUTHORS   Foss,D.L. and Murtaugh,M.P.
  TITLE     Molecular cloning and mRNA expression of porcine interleukin-12
  JOURNAL   Vet. Immunol. Immunopathol. 57 (1-2), 121-134 (1997)
  MEDLINE   97383978
   PUBMED   9239844
COMMENT     On Aug 2, 1995 this sequence version replaced gi:755667.
FEATURES             Location/Qualifiers
     source          1. .1426
                     /organism="Sus scrofa"
                     /db_xref="taxon:9823"
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                     /tissue_type="peripheral blood"
     CDS             108. .878
                     /codon_start=1
                     /product="interleukin 12 p35 subunit"
                     /protein_id="AAA73897.1"
                     /db_xref="GI:927205"
                     /translation="MCSPGFGLQTSDLTCDVHPSASSRRLAVTAAPLSMCPLRNLLLV
                     ATLVLLNHLDHLSLGRSLPATTAGPGMFKCLNHSQNLLKAVSNTLQKAKQTLEFYSCT
                     SEEIDHEDITKDKTSTVEACLPLELATNESCLAARETSLITNGNCLTSGKTSFMTTLC
                     LSSIYEDLKMYHVEFQAMNAKLLMDPKRQIFLDQNMLTAITELMQALNFNSETVPQKP
                     SLEELDFYKTKIKLCILLHAFRIRAVTIDRMMSYLNSS"
     primer_bind     196. .216
     primer_bind     complement(859. .878)
     polyA_site      1426
BASE COUNT      422 a    320 c    293 g    391 t
ORIGIN

Alignment Scores:
Pred. No.:              3.79e-90        Length:         1426
Score:                  960.00          Matches:        188
Percent Similarity:     90.09%          Conservative:   12
Best Local Similarity:  84.68%          Mismatches:     22
Query Match:            85.11%          Indels:         0
DB:                     4               Gaps:           0

US-09-917-265-47 (1-222) x PIGIL12PSU (1-1426)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      ||||||||||||:::|||||||||
Db        210 ATGTGTCCGCTGCGCAACCTCCTCCTTGTGGCCACCCTGGTCCTCCTCAACCACCTGGAC 269

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::     ||||||||||||      :::      ||||||:::|||:::|||
Db        270 CATCTCAGTTTGGGCAGGAGCCTCCCTGCAACCACAGCAGGCCCAGGAATGTTCAAATGC 329

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||:::|||
Db        330 CTCAACCACTCCCAAAATCTGCTGAAGGCCGTCAGCAACACACTTCAGAAGGCCAAACAA 389

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        390 ACCCTAGAATTTTACTCCTGCACTTCAGAAGAGATCGATCATGAAGATATCACCAAAGAT 449

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              |||||||||||||||||||||||||||||||||||||      ||||||||||||||||
Db        450 AAAACCAGCACAGTGGAGGCCTGCTTACCACTTGAACTAGCCACGAATGAGAGTTGCCTG 509

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              |||:::||||||   ||||||||||||||||||:::||||||   |||||||||   |||
Db        510 GCTGCCAGAGAGACCTCTTTAATAACTAATGGAAATTGCCTGACTTCTGGAAAGACCTCT 569

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||   :::|||
Db        570 TTTATGACAACCCTGTGCCTTAGCAGTATCTACGAGGACTTGAAGATGTACCATGTGGAG 629

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              |||:::||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        630 TTCCAGGCCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTGGATCAG 689

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||   ||||||:::|||||||||||||||||||||   ||||||
Db        690 AACATGCTGACAGCTATTACTGAGCTGATGCAGGCTCTGAATTTCAACAGTGAGACTGTG 749

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
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Db        750 CCACAGAAGCCCTCCCTGGAAGAACTGGATTTTTATAAGACTAAAATCAAGCTCTGCATA 809

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        810 CTTCTTCATGCCTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAAT 869

Qy        221 SerSer 222
              ||||||
Db        870 TCTTCC 875

RESULT 15
AX154617
LOCUS       AX154617                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 21 from Patent WO0140257.
ACCESSION   AX154617
VERSION     AX154617.1  GI:14536192
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 21 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      184 a    172 c    141 g    163 t
ORIGIN

Alignment Scores:
Pred. No.:              2.1e-90         Length:         660
Score:                  958.50          Matches:        192
Percent Similarity:     90.09%          Conservative:   8
Best Local Similarity:  86.49%          Mismatches:     19
Query Match:            84.97%          Indels:         3
DB:                     6               Gaps:           1

US-09-917-265-47 (1-222) x AX154617 (1-660)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
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Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 51

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 111

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAA 171

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        172 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 231

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              |||||||||||||||||||||||||||||||||||||      ||||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGTTTACCACTGGAATTAGCCACGAATGAGAGTTGCCTG 291

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
```

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Db        292 GCTTCCAGAGGGATCTCTCTGATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCT 351

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
                ||||||||||   |||||||||   ||||||||||||||||||||||||||||||:::|||
Db        352 TTTATGACGACCCTGTGCCTTGGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 411

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
                ||||||   ||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAA 471

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
                ||||||||||||||||||||||||||||||||||||||||||||||||||   ||||||
Db        472 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
                ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 651

Qy        221 SerSer 222
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Db        652 TCTTCC 657


Search completed: July 17, 2003, 06:40:23
Job time : 1992.57 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 16, 2003, 13:41:48 ; Search time 156.955 Seconds
(without alignments)
3185.273 Million cell updates/sec

Title: US-09-917-265-47
Perfect score: 1128
Sequence: 1 MCPPRGLLLVTILVLLSHLD.....HAFRIRAVTIDRMMSYLNSS 222

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09917265_@CGN_1_1_876_@runat_15072003_092106_1592 -NCPU=6 -ICPU=3
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1128	100.0	669	19	AAV13819	Canine IL-12 P35 s
2	1128	100.0	669	20	AAX35626	Nucleic acid encod
3	1128	100.0	669	20	AAX03163	Nucleic acid encod
4	1128	100.0	669	22	AAI64389	Canine coding sequ
5	1128	100.0	1282	20	AAX18178	Canine full length
6	1099	97.4	669	19	AAV13818	Canine IL-12 P35 s
7	1099	97.4	669	20	AAX35616	Nucleic acid encod
8	1099	97.4	669	20	AAX03153	Nucleic acid encod
9	1099	97.4	669	22	AAI64379	Canine coding sequ
10	1046	92.7	689	19	AAV56641	Feline FLAFp35 DNA
11	1046	92.7	1441	19	AAV56628	Feline FLAFp35 cDN
12	1034	91.7	669	22	AAF26083	Feline IL-12p35 en
13	1034	91.7	669	22	AAF26086	Feline IL-12p35 en
14	1034	91.7	4201	22	AAF26077	Feline IL-12p35 en
15	1023	90.7	679	22	AAF26097	Feline fil12p35a D
16	994	88.1	591	20	AAX18179	Canine mature CLAF
17	967.5	85.8	660	22	AAD15213	Modified human cyt
18	967.5	85.8	660	22	AAD15220	Modified human cyt
19	962.5	85.3	660	22	AAD15217	Modified human cyt
20	958.5	85.0	660	22	AAD15216	Modified human cyt
21	957.5	84.9	660	22	AAD15218	Modified human cyt
22	948.5	84.1	660	22	AAD15219	Modified human cyt
23	940.5	83.4	660	16	AAQ97485	Human interleukin-
24	940.5	83.4	660	19	AAV07218	DNA encoding human
25	940.5	83.4	762	20	AAV83207	Interleukin (IL)-1
26	940.5	83.4	762	21	AAF21323	Human low adenosin
27	940.5	83.4	762	21	AAA35201	Human adenosine re
28	940.5	83.4	1316	18	AAT63621	Interleukin-12 p35
29	940.5	83.4	1364	17	AAT48099	Human interleukin-
30	940.5	83.4	1364	19	AAV42536	Human interleukin-
31	940.5	83.4	1364	19	AAV15228	Heterodimeric huma
32	940.5	83.4	1364	21	AAZ28863	Human interleukin-
33	940.5	83.4	1364	22	AAF56281	IL-12 vaccine adju
34	940.5	83.4	4521	21	AAF21326	Human low adenosin
35	940.5	83.4	4521	21	AAA35204	Human adenosine re
36	938.5	83.2	660	19	AAV07274	Human Interleukin-
37	938.5	83.2	660	20	AAZ40407	Human interleukin
38	936.5	83.0	660	22	AAD15215	Modified human cyt
39	935.5	82.9	1396	13	AAQ24371	Natural killer cel
40	934.5	82.8	660	22	AAD15221	Human cytokine p35
41	934.5	82.8	721	15	AAQ67880	EPV 42 kD promoter
42	934.5	82.8	721	20	AAZ08515	Vaccinia E3L/human
43	934.5	82.8	856	18	AAT77850	35 kDa subunit of
44	934.5	82.8	856	18	AAV00402	35 kDa subunit of
45	934.5	82.8	856	18	AAT97970	35 kDa subunit of

ALIGNMENTS

RESULT 1
AAV13819
ID AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC AAV13819;
XX
DT 14-MAY-1998 (first entry)
XX
DE Canine IL-12 P35 subunit cDNA.
XX
KW Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW antiviral; vaccine adjuvant; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1..669
FT /*tag= a

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FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41793.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 11; Pages 11-12; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 other;

Alignment Scores:
Pred. No.:              9.63e-111       Length:         669
Score:                  1128.00         Matches:        222
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     19              Gaps:           0

US-09-917-265-47 (1-222) x AAV13819 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 2
AAX35626
ID   AAX35626 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35626;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02343.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 15-16; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

Alignment Scores:
Pred. No.:              9.63e-111       Length:         669
Score:                  1128.00         Matches:        222
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     20              Gaps:           0
```

```
US-09-917-265-47 (1-222) x AAX35626 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 3
AAX03163
ID   AAX03163 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03163;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers

FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84374.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

Alignment Scores:
Pred. No.:              9.63e-111       Length:         669
Score:                  1128.00         Matches:        222
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     20              Gaps:           0

US-09-917-265-47 (1-222) x AAX03163 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360
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Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 4
AAI64389
ID   AAI64389 standard; DNA; 669 BP.
XX
AC   AAI64389;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #4.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= "Canine protein #4"
FT   sig_peptide     1..75
FT                   /*tag=  b
FT   mat_peptide     76..666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66483.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Claim 6; Page 18; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

Alignment Scores:
Pred. No.:                9.63e-111      Length:          669
Score:                    1128.00        Matches:         222
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       22             Gaps:            0

US-09-917-265-47 (1-222) x AAI64389 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 5
AAX18178
ID   AAX18178 standard; cDNA; 1282 BP.
XX
AC   AAX18178;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
```

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KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74324.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 33-34; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 other;

Alignment Scores:
Pred. No.:              2.37e-110      Length:         1282
Score:                  1128.00        Matches:        222
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     20             Gaps:           0

US-09-917-265-47 (1-222) x AAX18178 (1-1282)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         66 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 125

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 185

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        186 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 245

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 305

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        306 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 365

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        366 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 425

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 485

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 545

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        546 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 605

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        606 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 665

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        666 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 725

Qy        221 SerSer 222
              ||||||
Db        726 TCTTCC 731

RESULT 6
AAV13818
ID   AAV13818 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13818;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41792.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 9; Page 9; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;
```

```
Alignment Scores:
Pred. No.:              1.18e-107       Length:         669
Score:                  1099.00         Matches:        217
Percent Similarity:     98.20%          Conservative:   1
Best Local Similarity:  97.75%          Mismatches:     4
Query Match:            97.43%          Indels:         0
DB:                     19              Gaps:           0

US-09-917-265-47 (1-222) x AAV13818 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      ||||||||||||||||||||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 7
AAX35616
ID   AAX35616 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35616;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX

FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02340.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 13; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

Alignment Scores:
Pred. No.:              1.18e-107       Length:         669
Score:                  1099.00         Matches:        217
Percent Similarity:     98.20%          Conservative:   1
Best Local Similarity:  97.75%          Mismatches:     4
Query Match:            97.43%          Indels:         0
DB:                     20              Gaps:           0

US-09-917-265-47 (1-222) x AAX35616 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      ||||||||||||||||||||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 8
AAX03153
ID   AAX03153 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03153;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84372.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 26-27; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

Alignment Scores:
Pred. No.:                1.18e-107      Length:          669
Score:                    1099.00        Matches:         217
Percent Similarity:       98.20%         Conservative:    1
Best Local Similarity:    97.75%         Mismatches:      4
Query Match:              97.43%         Indels:          0
DB:                       20             Gaps:            0

US-09-917-265-47 (1-222) x AAX03153 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      ||||||||||||||||||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 9
AAI64379
ID   AAI64379 standard; DNA; 669 BP.
XX
AC   AAI64379;
XX
DT   23-NOV-2001  (first entry)
XX
```

```
DE   Canine coding sequence #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= "Canine protein #2"
FT   sig_peptide     1..75
FT                   /*tag= b
FT   mat_peptide     76..666
FT                   /*tag= c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66481.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian -
XX
PS   Claim 6; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

Alignment Scores:
Pred. No.:              1.18e-107      Length:         669
Score:                  1099.00        Matches:        217
Percent Similarity:     98.20%         Conservative:   1
Best Local Similarity:  97.75%         Mismatches:     4
Query Match:            97.43%         Indels:         0
DB:                     22             Gaps:           0

US-09-917-265-47 (1-222) x AAI64379 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      ||||||||||||||||||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 10
AAV56641
ID   AAV56641 standard; DNA; 689 BP.
XX
AC   AAV56641;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 DNA fragment.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ss.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 24; Page 67; 94pp; Japanese.
XX
CC   This sequence encodes a fragment of a novel feline cytokine protein,
CC   FLAFp35. This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus.
XX
SQ   Sequence 689 BP; 192 A; 193 C; 145 G; 159 T; 0 other;

Alignment Scores:
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Pred. No.:              5.41e-102       Length:         689
Score:                  1046.00         Matches:        205
Percent Similarity:     95.95%          Conservative:   8
Best Local Similarity:  92.34%          Mismatches:     9
Query Match:            92.73%          Indels:         0
DB:                     19              Gaps:           0

US-09-917-265-47 (1-222) x AAV56641 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          7 ATGTGCCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||||:::|||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||:::|||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        221 SerSer 222
              ||||||
Db        667 TCTTCC 672

RESULT 11
AAV56628
ID   AAV56628 standard; cDNA; 1441 BP.
XX
AC   AAV56628;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             133..811
FT                   /*tag=  a
FT   sig_peptide     133..217
FT                   /*tag=  b
FT   mat_peptide     218..808
FT                   /*tag=  c
FT                   /product= "FLAFp35"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 other;

Alignment Scores:
Pred. No.:              1.5e-101        Length:         1441
Score:                  1046.00         Matches:        205
Percent Similarity:     95.95%          Conservative:   8
Best Local Similarity:  92.34%          Mismatches:     9
Query Match:            92.73%          Indels:         0
DB:                     19              Gaps:           0

US-09-917-265-47 (1-222) x AAV56628 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||||:::|||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||:::|||||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502
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Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        221 SerSer 222
              ||||||
Db        803 TCTTCC 808

RESULT 12
AAF26083
ID   AAF26083 standard; DNA; 669 BP.
XX
AC   AAF26083;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 4.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02262.
XX
PR   08-JUL-1999;   99CH-0001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats,
PT   contains nucleic acid sequence encoding viral protein under control of
PT   eukaryotic promoter  -
XX
PS   Claim 14; Page 37; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response.
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 other;

Alignment Scores:
Pred. No.:                9.84e-101      Length:          669
Score:                    1034.00        Matches:         201
Percent Similarity:       95.05%         Conservative:    10
Best Local Similarity:    90.54%         Mismatches:      11
Query Match:              91.67%         Indels:          0
DB:                       22             Gaps:            0

US-09-917-265-47 (1-222) x AAF26083 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||   |||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||::|||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 SerSer 222
              :::|||
Db        661 GCTTCC 666

RESULT 13
AAF26086
ID   AAF26086 standard; DNA; 669 BP.
XX
AC   AAF26086;
XX
DT   24-APR-2001  (first entry)
```

```
XX
DE   Feline IL-12p35 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02263.
XX
PR   08-JUL-1999;   99CH-0001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs -
XX
PS   Claim 3; Page 31; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 other;

Alignment Scores:
Pred. No.:                9.84e-101      Length:          669
Score:                    1034.00        Matches:         201
Percent Similarity:       95.05%         Conservative:    10
Best Local Similarity:    90.54%         Mismatches:      11
Query Match:              91.67%         Indels:          0
DB:                       22             Gaps:            0

US-09-917-265-47 (1-222) x AAF26086 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              |||||||:::   |||||||:::|||||||||   :::||||||||||||:::|||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||||||||||||||   ||||||||||||:::||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||   |||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||:::|||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 SerSer 222
              :::|||
Db        661 GCTTCC 666

RESULT 14
AAF26077
ID   AAF26077 standard; DNA; 4201 BP.
XX
AC   AAF26077;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 3.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02262.
XX
PR   08-JUL-1999;   99CH-0001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C, Schroff M, Wittig B, Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats,
PT   contains nucleic acid sequence encoding viral protein under control of
PT   eukaryotic promoter -
```

```
XX
PS   Disclosure; Page 31-33; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response.
XX
SQ   Sequence 4201 BP; 1086 A; 1055 C; 999 G; 1061 T; 0 other;

Alignment Scores:
Pred. No.:                1.25e-99      Length:          4201
Score:                    1034.00       Matches:         201
Percent Similarity:       95.05%        Conservative:    10
Best Local Similarity:    90.54%        Mismatches:      11
Query Match:              91.67%        Indels:          0
DB:                       22            Gaps:            0

US-09-917-265-47 (1-222) x AAF26077 (1-4201)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db       3047 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 3106

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::  ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db       3107 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 3166

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||  ||||||||||||:::|||||||||||||||||||||||||||||
Db       3167 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 3226

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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Db       3227 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 3286

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Db       3287 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTG 3346

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||  |||  |||  |||
Db       3347 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCT 3406

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||  ||||||||||||||||||||||||||||||||||||||||:::|||
Db       3407 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 3466

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3467 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 3526

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db       3527 AACATGCTGACAGCTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTG 3586

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
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Db       3587 CCACAGAACTCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 3646

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||
Db       3647 CTTCTTCATGCTTTCAGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 3706

Qy        221 SerSer 222
              :::|||
Db       3707 GCTTCC 3712

RESULT 15
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02263.
XX
PR   08-JUL-1999;   99CH-0001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs  -
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 other;

Alignment Scores:
Pred. No.:                1.49e-99      Length:          679
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Score:	1023.00	Matches:	201
Percent Similarity:	95.05%	Conservative:	10
Best Local Similarity:	90.54%	Mismatches:	11
Query Match:	90.69%	Indels:	0
DB:	22	Gaps:	0

US-09-917-265-47 (1-222) x AAF26097 (1-679)

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Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              |||||||:::   ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||   ||||||||||||:::||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACCCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||   ||||||||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGGCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAACCCTCCTTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::::::::||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAAAGTGATGAGCTATCTGAAT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666
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Search completed: July 16, 2003, 20:23:56
Job time : 163.955 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 16, 2003, 19:41:51 ; Search time 1055.95 Seconds
(without alignments)
3404.880 Million cell updates/sec

Title: US-09-917-265-47
Perfect score: 1128
Sequence: 1 MCPPRGLLLVTILVLLSHLD.....HAFRIRAVTIDRMMSYLNSS 222

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09917265/runat_15072003_092107_1610/app_query.fasta_1.3114
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09917265_@CGN_1_1_6304_@runat_15072003_092107_1610 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: em_esthum:*
3: em_estin:*
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5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		460	40.8	812	12	BG702253	BG702253 602683459
2		391	34.7	589	9	AI050362	AI050362 ub30a07.r
3	c	384	34.0	1099	13	BI523344	BI523344 603175938
4		361.5	32.0	832	13	BI523569	BI523569 603175938
5		335	29.7	373	12	BF552757	BF552757 UI-R-C0-i
6		251.5	22.3	342	13	BM257856	BM257856 521721 MA
7		131	11.6	447	13	BI824638	BI824638 603033580
8	c	104	9.2	528	9	AI332701	AI332701 qq19a07.x
9		100.5	8.9	982	17	CNS06H7X	AL398659 T7 end of
10		95	8.4	1041	17	CNS05AR7	AL328876 Tetraodon
11		94	8.3	880	14	BQ420717	BQ420717 AGENCOURT
12		93.5	8.3	1007	14	BM904933	BM904933 AGENCOURT
13	c	93	8.2	928	17	AZ541842	AZ541842 ENTFR19TR
14		92	8.2	786	17	BH249132	BH249132 BOGAT94TR
15		91.5	8.1	916	12	BG242870	BG242870 602355851
16		91	8.1	781	17	BH371486	BH371486 AG-ND-138
17		91	8.1	994	14	BQ222548	BQ222548 AGENCOURT
18		90.5	8.0	811	9	AL557307	AL557307 AL557307
19		90.5	8.0	932	9	AL548620	AL548620 AL548620
20		90.5	8.0	1017	13	BM552614	BM552614 AGENCOURT
21		90.5	8.0	1171	13	BM467146	BM467146 AGENCOURT
22		90.5	8.0	1398	11	BC004543	BC004543 Homo sapi
23		90.5	8.0	1398	11	BC014060	BC014060 Homo sapi
24		90	8.0	367	9	AU156524	AU156524 AU156524
25		90	8.0	563	10	AW657864	AW657864 93490 MAR
26	c	89.5	7.9	347	9	AA067614	AA067614 mm23d05.r
27		89	7.9	369	9	AI183411	AI183411 qd24c03.x
28		89	7.9	504	10	BE336896	BE336896 bb68d10.y
29	c	89	7.9	748	11	BC022266	BC022266 Homo sapi
30		89	7.9	939	14	BQ072253	BQ072253 AGENCOURT
31		89	7.9	1127	13	BM554145	BM554145 AGENCOURT
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35		88	7.8	852	17	BH157950	BH157950 ENTSK73TF
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37		88	7.8	1060	14	BQ068020	BQ068020 AGENCOURT
38	c	88	7.8	1071	17	CNS0768B	AL431073 T7 end of
39	c	87.5	7.8	403	14	BQ201205	BQ201205 UI-R-DQ1-
40		87.5	7.8	684	12	BF047027	BF047027 EST1124 M
41		87.5	7.8	755	12	BE886561	BE886561 601509305
42		87.5	7.8	781	14	BP016915	BP016915 BP016915
43		87.5	7.8	871	13	BI217873	BI217873 602934849
44	c	87	7.7	443	9	AA755726	AA755726 vu72a12.r
45		87	7.7	1004	11	AK013272	AK013272 Mus muscu

ALIGNMENTS

RESULT 1
BG702253
LOCUS BG702253 812 bp mRNA linear EST 07-MAY-2001
DEFINITION 602683459F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4816118 5', mRNA sequence.
ACCESSION BG702253
VERSION BG702253.1 GI:13973409
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 812)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

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  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10714  row: e  column: 15
            High quality sequence stop: 804.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_95"
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                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.5 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for  full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health).  Note: this is a NIH_MGC Library."
BASE COUNT      188 a    249 c    226 g    149 t
ORIGIN

Alignment Scores:
Pred. No.:                3.76e-45        Length:         812
Score:                    460.00          Matches:        105
Percent Similarity:       81.48%          Conservative:   5
Best Local Similarity:    77.78%          Mismatches:     22
Query Match:              40.78%          Indels:         6
DB:                       12              Gaps:           1

US-09-917-265-47 (1-222) x BG702253 (1-812)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||         ||||||
Db        417 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 467

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db        468 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 527

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        528 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 587

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||
Db        588 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATCGATCATGAAGATATCACAAAAGAT 647

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||
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Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
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Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLys 135
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Db        765 TTTATGATGTGCCTGTGCCTTAGTAGTAT-TATGAAGACTTGAAA 808

RESULT 2
AI050362
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LOCUS       AI050362                589 bp    mRNA    linear   EST 09-JUL-1998
DEFINITION  ub30a07.r1 Soares_thymus_2NbMT Mus musculus cDNA clone
            IMAGE:1379220 5' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN
            PRECURSOR (HUMAN); gb:M86672 Mus musculus interleukin 12 p35
            subunit, complete cds (MOUSE);, mRNA sequence.
ACCESSION   AI050362
VERSION     AI050362.1  GI:3299479
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of MedicineP
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:901688
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 60.
FEATURES             Location/Qualifiers
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                     /strain="C57BL/6J"
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                     /clone="IMAGE:1379220"
                     /clone_lib="Soares_thymus_2NbMT"
                     /sex="male"
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                     /dev_stage="4 weeks"
                     /lab_host="DH10B"
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                     was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCGTTTTTTTTTTTTTTTTTTTTTTTT
                     3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Bertrand Jordan. Library went through two
                     rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT      162 a    159 c    142 g    126 t
ORIGIN

Alignment Scores:
Pred. No.:                5.35e-37        Length:         589
Score:                    391.00          Matches:        78
Percent Similarity:       74.80%          Conservative:   17
Best Local Similarity:    61.42%          Mismatches:     32
Query Match:              34.66%          Indels:         0
DB:                       9               Gaps:           0

US-09-917-265-47 (1-222) x AI050362 (1-589)

Qy         57 LysAlaArgGlnThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAsp 76
              :::|||||:::   |||:::   |||||||||||||:::|||:::|||||||||||||||
Db        108 CAGGCCAGAGAAAAACTGAAACATTATTCCTGCACTGCTGAAGACATCGATCATGAAGAC 167

Qy         77 IleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsn 96
              ||||||:::|||:::|||||||||:::::   ||||||||||||||||      |||
Db        168 ATCACACGGGACCAAACCAGCACATTGAAGACCTGTTTACCACTGGAACTACACAAGAAC 227
```

```
Qy         97 GluSerCysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
              ||||||||||||||||:::||||||   |||       |||   ||||||||||||
Db        228 GAGAGTTGCCTGGCTACTAGAGAGACTTCTTCCACAACAAGAGGGAGCTGCCTGCCCCCA 287

Qy        117 GlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMet 136
                 |||   |||   |||       |||||||||   ||||||||||||||||||||||||
Db        288 CAGAAGACGTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATG 347

Qy        137 TyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIle 156
              ||||||   |||||||:::|||:::||||||   |||               :::||||||
Db        348 TACCAGACAGAGTTCCAGGCCATCAACGCAGCACTTCAGAATCACAACCATCAGCAGATC 407

Qy        157 PheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsn 176
                 |||||||::   ||||||      ||||||||||||:::|||:::||||||   |||
Db        408 ATTCTAGACAAGGGCATGCTGGGTGGCATCGATGAGCTGATGCAGTCTCTGAATCATAAT 467

Qy        177 SerValThrValProGlnLys 183
                 |||:::   ||||||
Db        468 GGCGAGACTCTGCGCCAGAAA 488
```

RESULT 3
BI523344/c
LOCUS BI523344 1099 bp mRNA linear EST 29-AUG-2001
DEFINITION 603175938T1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 3', mRNA sequence.
ACCESSION BI523344
VERSION BI523344.1 GI:15348136
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1099)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11605 row: 1 column: 09
High quality sequence start: 40
High quality sequence stop: 727.

```
FEATURES             Location/Qualifiers
     source          1. .1099
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks. Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT      359 a    244 c    218 g    276 t      2 others
ORIGIN

Alignment Scores:
Pred. No.:              1.17e-35        Length:         1099
Score:                  384.00          Matches:        86
Percent Similarity:     90.10%          Conservative:   5
Best Local Similarity:  85.15%          Mismatches:     7
Query Match:            34.04%          Indels:         4
DB:                     13              Gaps:           0

US-09-917-265-47 (1-222) x BI523344 (1-1099)

Qy        125 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMet 144
              ||||||   ||||||||||||||||||   |||||||||||||:::|||||||||   |||
Db        737 CTGTGCTTTAGTAGTATTTATGAAGACTG-AAGATGTACCAGGTGGAGTTCAAGACCATG 679

Qy        145 AsnAlaLysLeu-LeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuTh 164
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        678 AATGCAAAGCTTCCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAAAACATGCTGGC 619

Qy        164 rAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSe 184
                  ||||||||||||:::|||||||||||||||||||||   |||||||||||||||||
Db        618 AGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATC 559

Qy        184 rSerLeuGluGluProAsp--PheTyrLysThrLysIleLysLeuCysIleLeuLeuHis 203
              ||||||||||||||||||  |||   ||||||:::|||||||||||||||||||||||||
Db        558 CTCCCTTGAAGAACCGGATTGTTTATCAAAACTGAAATCAAGCTCTGCATACTTCTTCAT 499

Qy        204 AlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 222
              ||||||||||||||||||||||||||||||:::|||||||||||||||:::|||
Db        498 GCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAATGCTTCC 442

RESULT 4
BI523569
LOCUS BI523569 832 bp mRNA linear EST 29-AUG-2001
DEFINITION 603175938F1 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5240216 5', mRNA sequence.
ACCESSION BI523569
VERSION BI523569.1 GI:15348361
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 832)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11605 row: 1 column: 09
High quality sequence start: 23
High quality sequence stop: 821.

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FEATURES   Location/Qualifiers
     source   1. .832
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5240216"
                     /clone_lib="NIH_MGC_121"
                     /lab_host="DH10B"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks. Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning). Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 017. Note:
                     this is a NIH_MGC Library."
BASE COUNT   220 a   233 c   200 g   179 t
ORIGIN
```
```

```
Alignment Scores:
Pred. No.:              3.9e-33         Length:         832
Score:                  361.50          Matches:        74
Percent Similarity:     83.16%          Conservative:   5
Best Local Similarity:  77.89%          Mismatches:     12
Query Match:            32.05%          Indels:         4
DB:                     13              Gaps:           1

US-09-917-265-47 (1-222) x BI523569 (1-832)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||          ||||||
Db        321 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 371

Qy         21 HisLeuThr-TrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCy 40
              ||||||::: |||      :::||||||   |||:::|||   ||||||:::|||   ||
Db        372 CACCTCAGTTTGGCCATGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATG 431

Qy         40 sLeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGl 60
              ||||:::||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        432 CCTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACA 491

Qy         60 nThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAs 80
              ||||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        492 AACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGA 551

Qy         80 pLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 94
              ||||||||||||||||||||||||||||||||||||||||||||
Db        552 TAAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACC 594

RESULT 5
BF552757
LOCUS       BF552757                373 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  UI-R-C0-iz-d-02-0-UI.r1 UI-R-C0 Rattus norvegicus cDNA clone
            UI-R-C0-iz-d-02-0-UI 5', mRNA sequence.
ACCESSION   BF552757
VERSION     BF552757.1  GI:11662487
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 373)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242, USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            cDNA Library Preparation: M.B. Soares Lab Clone distribution:
            clones will be available through Research Genetics (www.resgen.com)
            This clone is also available through the I.M.A.G.E. Consortium at
            LLNL (info@image.llnl.gov). IMAGE ID= 1782759
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .373
                     /organism="Rattus norvegicus"
                     /strain="Sprague-Dawley"
                     /db_xref="taxon:10116"
                     /clone="UI-R-C0-iz-d-02-0-UI"
                     /clone_lib="UI-R-C0"
                     /dev_stage="adult"
                     /lab_host="DH10B (Life Technologies)"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0
                     library is a subtracted library derived from the UI-R-A1
                     and UI-R-E1 libraries. The UI-R-A1 library consisted of a
                     mixture of individually tagged normalized libraries
                     constructed from rat  placenta, adult lung, brain, liver,
                     kidney, heart, spleen, ovary,  and muscle. The UI-R-E1
                     library  consisted of a mixture of individually tagged
                     normalized libraries constructed from 8, 12 and 18-day
                     embryo. The tag is a string of 3-5 nucleotides present
                     between the Not I  site and the oligo-dT track which
                     allows identification of the library of origin of a clone
                     within the mixture. The subtracted library (UI-R-C0) was
                     constructed as follows: PCR amplified cDNA inserts from a
                     pool of UI-R-A1 and UI-R-E1 clones from which 3' ESTs had
                     been derived was used as a driver in a hybridization with
                     the pooled UI-R-A1 and UI-R-E1 library in the form of
                     single-stranded circles.  The remaining single-stranded
                     circles (subtracted library) was purified by
                     hydroxyapatite column chromatography, converted to
                     double-stranded circles and electroporated into DH10B
                     bacteria (Life Technologies) to generate the UI-R-C0
                     library. This procedure has been previously described
                     (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                     1996)"
BASE COUNT      106 a     93 c     89 g     85 t
ORIGIN

Alignment Scores:
Pred. No.:              1.56e-30        Length:         373
Score:                  335.00          Matches:        68
Percent Similarity:     72.13%          Conservative:   20
Best Local Similarity:  55.74%          Mismatches:     34
Query Match:            29.70%          Indels:         0
DB:                     12              Gaps:           0

US-09-917-265-47 (1-222) x BF552757 (1-373)

Qy         99 CysLeuAlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLys 118
              |||||||||:::::|||   |||   |||      ||||||||||          |||
Db          8 TGCCTGGCTACTAAAGAGACTTCTTCCATAATAAGAGGGAGCTGCCTGCCTCCACAAAAG 67

Qy        119 AlaSerPheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGln 138
              |||   |||      |||||||||   ||||||||||||||||||||||||||||||
Db         68 ACTTCTTTGATGATGACCCTGTGCCTTGGTAGCATCTATGAGGACTTGAAGATGTACCAG 127

Qy        139 MetGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeu 158
              ||||||:::|||:::||||||   |||               :::||||||   |||
Db        128 TCAGAGTTCCAGGCCATAAATGCAGCACTTCAGAGCCACAATCATCAGCAGATCACTCTG 187

Qy        159 AspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerVal 178
              |||:::|||||||||   ||||||||||||||:::::::::||||||   :::
Db        188 GACAGAAACATGCTGATGGCTATTGATGAGCTAATGCGGTCTCTGAATCACAGCGGCGAG 247

Qy        179 ThrValProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeu 198
              :::   |||||||:::   :::   |||   |||   |||:::   |||:::||||||
Db        248 ATTCTGCACCAGAAAGCTCCCATGGGAGAAGCAGATCCTTACAGAGTGAAGATGAAGCTC 307

Qy        199 CysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyr 218
              ||||||||||||||||||||      |||   :::||||||:::|||:::|||:::|||
Db        308 TGTATCCTGCTCCATGCCTTCAGCACACGCGTCATGACTATCAACAGGGTGATGAACTAT 367

Qy        219 LeuAsn 220
              |||:::
Db        368 CTGAGC 373

RESULT 6
BM257856
LOCUS       BM257856                342 bp    mRNA    linear   EST 17-DEC-2001
DEFINITION  521721 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION   BM257856
VERSION     BM257856.1  GI:17893455
KEYWORDS    EST.
SOURCE      cow.
  ORGANISM  Bos taurus
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
            Bovidae; Bovinae; Bos.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
            Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C., Bennett
            ,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A., Chitko-McKown,C.G.,
            Pertea,G., Holt,I., Karamycheva,S., Liang,F., Quackenbush,J. and
            Keele,J.W.
  TITLE     Sequence evaluation of four pooled-tissue normalized bovine cDNA
            libraries and construction of a gene index for cattle
  JOURNAL   Genome Res. 11 (4), 626-630 (2001)
  MEDLINE   21180013
COMMENT     Contact: Smith TPL
            USDA, ARS, US Meat Animal Research Center
            PO Box 166, Clay Center, NE 68933-0166, USA
            Tel: 402 762 4366
            Fax: 402 762 4390
            Email: smith@email.marc.usda.gov
            Single pass sequencing. Bases called and alt_trimmed with phred
            v0.980904.e. Vector identified by cross_match with the -minscore 18
            and -minmatch 12 options.
            PCR PRimers
            FORWARD: AGGAAACAGCTATGACCAT
            BACKWARD: GTTTTCCCAGTCACGACG
            Plate: 125  row: E  column: 18
            Seq primer: ATTTAGGTGACACTATAG.
FEATURES              Location/Qualifiers
     source           1. .342
                      /organism="Bos taurus"
                      /db_xref="taxon:9913"
                      /clone_lib="MARC 3BOV"
                      /tissue_type="pooled"
                      /lab_host="DH10B"
                      /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI;
                      Library made from pooled tissue from marrow, alveolar
                      macrophage, ovary, fetal semitendonosus muscle, and fetal
                      longissimus muscle."
BASE COUNT       67 a    135 c     74 g     66 t
ORIGIN

Alignment Scores:
Pred. No.:                1.97e-20        Length:         342
Score:                    251.50          Matches:        52
Percent Similarity:       81.69%          Conservative:   6
Best Local Similarity:    73.24%          Mismatches:     12
Query Match:              22.30%          Indels:         1
DB:                       13              Gaps:           1

US-09-917-265-47 (1-222) x BM257856 (1-342)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuSerHisLeuAsp 20
              |||||||||   |||   |||||||||::::::   ||||||||||||   ||||||
Db        132 ATGTGCCCGCTTCGCAGCCTCCTCCTCATATCCACCCTGGTTCTCCTCCACCACCTGCCC 191

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::      ||||||||||||||||   :::   |||||||||         |||
Db        192 CACCTCAGTTTGGGCAGGAGCCTCCCCACCACCACAGCAAGCCCAGGA---AGGAGCTGC 248

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||::::::||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CTCGACTACTCCCAAAACCTGCTGAGGGCTGTCAGCAACACGCTACAGAAGGCCAGACAA 308

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGlu 71
              |||||||||   ||||||||||||||||||||
Db        309 ACTCTAGAATTTTACTCCTGCACTTCTGAGGAG 341

RESULT 7
BI824638
LOCUS       BI824638                447 bp    mRNA    linear   EST 04-OCT-2001
DEFINITION  603033580F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175018 5',
            mRNA sequence.
ACCESSION   BI824638
VERSION     BI824638.1  GI:15936188
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 447)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM11435  row: o  column: 19
            High quality sequence start: 3
            High quality sequence stop: 445.
FEATURES              Location/Qualifiers
     source           1. .447
                      /organism="Homo sapiens"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:5175018"
                      /clone_lib="NIH_MGC_115"
                      /lab_host="DH10B"
                      /note="Organ: pooled brain, lung, testis; Vector:
                      pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
                      source anonymous pool of 6 male brains, age range 23-27; 1
                      male lung, age 27; and 1 male testis, age 69.  Library is
                      oligo-dT primed and directionally cloned (EcoRV site is
                      destroyed upon  cloning).  Average insert size 1.8 kb,
                      insert size range 1-3 kb. Library is normalized and
                      enriched for full-length clones and was  constructed by C.
                      Gruber (Invitrogen).  Research Genetics tracking  code
                      021. Note: this is a NIH_MGC Library."
BASE COUNT      149 a     63 c     87 g    148 t
ORIGIN

Alignment Scores:
Pred. No.:                1.52e-05        Length:         447
Score:                    131.00          Matches:        26
Percent Similarity:       100.00%         Conservative:   2
Best Local Similarity:    92.86%          Mismatches:     0
Query Match:              11.61%          Indels:         0
DB:                       13              Gaps:           0

US-09-917-265-47 (1-222) x BI824638 (1-447)

Qy        195 LysIleLysLeuCysIleLeuLeuHisAlaPheArgIleArgAlaValThrIleAspArg 214
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGA 60

Qy        215 MetMetSerTyrLeuAsnSerSer 222
              :::|||||||||||||||:::|||
Db         61 GTGATGAGCTATCTGAATGCTTCC 84

RESULT 8
AI332701/c
LOCUS       AI332701                528 bp    mRNA    linear   EST 13-FEB-1999
DEFINITION  qq19a07.x1 Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:1932948
            3' similar to gb:M65291 INTERLEUKIN-12 ALPHA CHAIN PRECURSOR (HUMAN
            );, mRNA sequence.
ACCESSION   AI332701
VERSION     AI332701.1  GI:4069260
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

```
REFERENCE   1  (bases 1 to 528)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 1469   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 451.
FEATURES             Location/Qualifiers
     source          1. .528
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1932948"
                     /clone_lib="Soares_NhHMPu_S1"
                     /tissue_type="Pooled human melanocyte, fetal heart, and
                     pregnant uterus"
                     /lab_host="DH10B"
                     /note="Organ: mixed (see below); Vector: pT7T3D-Pac
                     (Pharmacia) with a modified polylinker; Site_1: Not I;
                     Site_2: Eco RI; Equal amounts of plasmid DNA from three
                     normalized libraries (melanocyte 2NbHM, pregnant uterus
                     NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
                     were made in vitro. Following HAP purification, this DNA
                     was used as tracer in a subtractive hybridization
                     reaction. The driver was PCR-amplified cDNAs from pools of
                     5,000 clones made from the same 3 libraries. The pools
                     consisted of I.M.A.G.E. clones 260232-265223,
                     340488-345479, and 484488-489479."
BASE COUNT      189 a     93 c     63 g    183 t
ORIGIN

Alignment Scores:
Pred. No.:              0.0398          Length:         528
Score:                  104.00          Matches:        21
Percent Similarity:     100.00%         Conservative:   2
Best Local Similarity:  91.30%          Mismatches:     0
Query Match:            9.22%           Indels:         0
DB:                     9               Gaps:           0

US-09-917-265-47 (1-222) x AI332701 (1-528)

Qy        200 IleLeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeu 219
              ||||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||
Db        528 ATACTTCTCCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTG 469

Qy        220 AsnSerSer 222
              |||:::|||
Db        468 AATGCTTCC 460

RESULT 9
CNS06H7X
LOCUS       CNS06H7X                 982 bp    DNA     linear   GSS 17-JUN-2001
DEFINITION  T7 end of clone AS0AA010E05 of library AS0AA from strain CLIB 533
            of Saccharomyces bayanus, genomic survey sequence.
ACCESSION   AL398659
VERSION     AL398659.1  GI:12152337
KEYWORDS    GSS.
SOURCE      Saccharomyces bayanus.
  ORGANISM  Saccharomyces bayanus
            Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
            Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE   1  (bases 1 to 982)
  AUTHORS   Souciet,J.L., Aigle,M., Artiguenave,F., Blandin,G.,
            Bolotin-Fukuhara,M., Bon,E., Brottier,P., Casaregola,S.,
            de-Montigny,J., Dujon,B., Durrens,P., Lepingle,A., Llorente,B.,
            Malpertuy,A., Neuveglise,C., Ozier-Kalogeropoulos,O., Potier,S.,
            Saurin,W., Tekaia,F., Toffano-Nioche,C., Wesolowski-Louvel,M.,
            Wincker,P. and Weissenbach,J.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 1. A set of
            yeast species for molecular evolution studies
  JOURNAL   FEBS Lett. 487 (1), 3-12 (2000)
  MEDLINE   20584711
   PUBMED   11152876
REFERENCE   2  (bases 1 to 982)
  AUTHORS   Bon,E., Neuveglise,C., Casaregola,S., Artiguenave,F., Wincker,P.,
            Aigle,M. and Durrens,P.
  TITLE     Genomic exploration of the hemiascomycetous yeasts: 5.
            Saccharomyces bayanus var. uvarum
  JOURNAL   FEBS Lett. 487 (1), 37-41 (2000)
  MEDLINE   20584715
   PUBMED   11152880
REFERENCE   3  (bases 1 to 982)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage,
            2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail :
            seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT     This GSS is part of a random genomic sequencing program of thirteen
            yeast species: Saccharomyces bayanus var. uvarum, Saccharomyces
            exiguus, Saccharomyces servazzii, Zygosaccharomyces rouxii,
            Saccharomyces kluyveri, Kluyveromyces thermotolerans, Kluyveromyces
            lactis var. lactis, Kluyveromyces marxianus var. marxianus, Pichia
            angusta, Debaryomyces hansenii var.  hansenii, Pichia sorbitophila,
            Candida tropicalis and Yarrowia lipolytica. Genomic inserts of 3 to
            5 kb were prepared and both extremities were sequenced. See
            keywords for description of this sequence and for the sequence of
            the other extremity of this insert.
FEATURES             Location/Qualifiers
     source          1. .982
                     /organism="Saccharomyces bayanus"
                     /strain="CLIB 533"
                     /variety="uvarum"
                     /db_xref="taxon:4931"
                     /clone="AS0AA010E05"
                     /clone_lib="AS0AA"
                     /note="end : T7"
     misc_feature    <3. .>188
                     /note="similar to Saccharomyces cerevisiae ORF YGL012w [
                     ERG4 ; sterol C-24 reductase ]"
                     /evidence=not_experimental
     misc_feature    complement(<400. .>974)
                     /note="similar to Saccharomyces cerevisiae ORF YGL011c [
                     SCL1 ; 20S proteasome subunit YC7ALPHA/Y8 (alpha1) ]
                     1 putative frameshift(s)"
                     /evidence=not_experimental
BASE COUNT      248 a    192 c    181 g    358 t      3 others
ORIGIN

Alignment Scores:
Pred. No.:              0.324           Length:         982
Score:                  100.50          Matches:        53
Percent Similarity:     36.79%          Conservative:   25
Best Local Similarity:  25.00%          Mismatches:     67
Query Match:            8.91%           Indels:         67
DB:                     17              Gaps:           10

US-09-917-265-47 (1-222) x CNS06H7X (1-982)

Qy         18 HisLeuAspHisLeuThrTrpAlaArg---SerLeuProThrAlaSerProSerProGly 36
              :::|||      :::   |||   :::   |||:::|||         ||||||
Db         11 AATTTGGGCCCTATCTTGTGGTTTCAATTCAGTATTCCCATGGTTTTTCCCAGC------ 64

Qy         37 IlePheGlnCysLeuAsnHisSerGlnAsnLeuLeuArgAla---------------------- 50
              :::      |||      :::||||||||||||   |||:::
Db         65 CTTCTTCCTTGTCGTCTTAATTCACAGAACCTTCAGAGATCAGACTAAGTGTAAGAGAAA 124

Qy         51 ValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGlu------------------------ 63
              |||         |||   :::      |||||||||
Db        125 GTATGGCAAGGATTGGGACGAATATTGCAAACATTGTCCTTACATCTTCATTCCTTACGT 184

Qy         64 ----------------------------------------------------------LeuTyr 65
                                                                        ||||||
```

```
Db        185 TTTTTAAAGTTATTTTTGTCTTTACTTTGTCAATTCCTTTACAAAAGTTTATATCTATAT 244

Qy         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
              |||                  ||||||   :::   |||   :::   |||   :::
Db        245 CTGTGTTTA--------------CACGAAAAAGTTCAAAAAATTCGACTTTCTGTTATT 289

Qy         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGlu---------------------- 97
              :::      |||:::   :::   :::||||||
Db        290 TAATCTATAACACCTATATATATAATCCTAAATGAACTTATTTGTACATACGTTATTGCA 349

Qy         98 ---SerCysLeuAlaSerArgGluIleSerLeuIle------ThrAsnGlySerCysLeu 114
              ||||||                  |||::::::        :::   ||||||
Db        350 TGATCGTGTACGTTATTTGACTCTTTTTCTGTGGTTGGATGGGTAGATTAATCTTGTTCA 409

Qy        115 AlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIleTyrGluAspLeu 134
              |||                  |||      ||||||||||||:::
Db        410 GCA--------------------ATTGTTACTAGTCTTTCTTCAATATTCTCA------ 442

Qy        135 LysMetTyrGlnMetGluPheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArg 154
                           ||||||      |||      |||:::      |||
Db        443 --------------GCATTCAAGGTGAAGAATTTGCCACTGGTTGCAACGCCGACTTCT 487

Qy        155 GlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsn 174
              :::   |||   :::   ::::::      |||            :::   |||
Db        488 AAGTCATTCTTTGAAAATTCAGTACCCAATGCGTCGATCATATGAGTAATGGCA------ 541

Qy        175 PheAsnSerValThrValProGlnLysSerSerLeu 186
              ||||||   |||      |||   |||||||||
Db        542 ---AACTCGACTACTTTTTCCCAAGATTCCTCGTTG 574

RESULT 10
CNS05AR7
LOCUS       CNS05AR7               1041 bp    DNA     linear   GSS 26-MAY-2000
DEFINITION  Tetraodon nigroviridis genome survey sequence T7 end of clone
            015P16 of library A from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION   AL328876
VERSION     AL328876.1  GI:8222498
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
  ORGANISM  Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodon.
REFERENCE   1  (bases 1 to 1041)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
  TITLE     Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 1041)
  AUTHORS   Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
  TITLE     Charaterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
  JOURNAL   Unpublished
REFERENCE   3  (bases 1 to 1041)
  AUTHORS   Genoscope.
  TITLE     Direct Submission
  JOURNAL   Submitted (12-APR-2000)
COMMENT     This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
FEATURES             Location/Qualifiers
     source          1. .1041
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="015P16"
                     /clone_lib="A"
                     /note="Genoscope sequence ID : C0AA015DH08C3-end : T7"
BASE COUNT      243 a    312 c    211 g    257 t     18 others
ORIGIN

Alignment Scores:
Pred. No.:                1.69          Length:          1041
Score:                    95.00         Matches:         45
Percent Similarity:       40.00%        Conservative:    19
Best Local Similarity:    28.12%        Mismatches:      50
Query Match:              8.42%         Indels:          46
DB:                       17            Gaps:            8

US-09-917-265-47 (1-222) x CNS05AR7 (1-1041)

Qy          7 LeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAspHisLeuThrTrpAlaArg 26
              ||||||||||:::   ||||||:::   |||   :::||||||
Db        183 CTTCTCTTGCTTTTTATTTTGTTAAAATTA---TATCTTGATTCTTTCTTACTCTGTCTT 239

Qy         27 SerLeuProThrAlaSerProSerPro-----------GlyIlePheGlnCysLeuAsn 42
              ||||||:::::::::|||||||||           |||||||:::   |||   |||
Db        240 TGTCTTCCATCTTCCACTCCCTCCCCCCACTATTTTTAGGGTATTTACAGCTGCTTCAAT 299

Qy         43 ------------------HisSerGlnAsnLeuLeuArg---------------------- 49
                               |||      |||   :::
Db        300 GGAGTCGAGGACCCCGGCCGTTCATCTGGTTTAGCCAAACCTGACCTGACCTCCAACTAC 359

Qy         50 AlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyrSerCysThrSer 69
              |||   :::|||   |||:::      |||          :::|||   |||      :::
Db        360 GCTCAAGCAAACATGCTGAAAATGCTCCGCACTGCCAAGGACCTGGTGTCCACGGCTAAT 419

Qy         70 GluGluIleAspHisGluAspIleThrLysAspLysThrSerThrValGlu--------- 86
                 |||            :::   ||||||            |||:::|||
Db        420 GTGGAAACTTCTCTGGANAACGCCACCAAG-----------ACCATAGAACACCTGAGT 467

Qy         87 ---------AlaCysLeuProLeuGlu------------------------------- 92
                         ||||||:::
Db        468 CGTCACGGCGGGAGCCTGCCGATCCGGGTCCCACAAGTGGCCATGGAAGCCGTGCCGGGA 527

Qy         93 ---------LeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleThr 109
                      |||         ||||||   |||||||||      :::
Db        528 GGATTTGCTTTACGTCACCGAGAATCACTGCTCGCTTCCCCAGCGCTCTTTAACCCCGCC 587

Qy        110 AsnGlySerCys------------LeuAlaSerGlyLysAlaSerPheMetThrValLeu 125
              :::|||||||||            |||   |||:::   :::      |||   |||
Db        588 TCTGGCAGCTGTTACCTCCCTGAAACAGCACAGGGGCGTGAAGCANGGCCCACGCCACTT 647

RESULT 11
BQ420717
LOCUS       BQ420717               880 bp    mRNA    linear   EST 23-MAY-2002
DEFINITION  AGENCOURT_7771502 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:6019246
            5', mRNA sequence.
ACCESSION   BQ420717
VERSION     BQ420717.1  GI:21116032
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 880)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13221  row: g  column: 23
            High quality sequence stop: 649.
```

```
FEATURES             Location/Qualifiers
     source          1. .880
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6019246"
                     /clone_lib="NIH_MGC_70"
                     /tissue_type="epithelioid carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 1.1 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      276 a    198 c    232 g    174 t
ORIGIN

Alignment Scores:
Pred. No.:                1.65          Length:         880
Score:                    94.00         Matches:        44
Percent Similarity:       44.00%        Conservative:   22
Best Local Similarity:    29.33%        Mismatches:     50
Query Match:              8.33%         Indels:         34
DB:                       14            Gaps:           8

US-09-917-265-47 (1-222) x BQ420717 (1-880)

Qy          41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeu---GlnLysAlaArg 59
               |||               ||||||   ||||||:::      |||   ||||||
Db         342 CTCAAGGACAAGAACCAGCTGTTAGAAGCCGTCAACAAGCAGTTGCACCAGAAGTTGACT 401

Qy          60 GlnThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLys 79
               :::|||                                        :::         |||
Db         402 GAAACT----------------------------------------CAGGGAGAGCTGAAG 422

Qy          80 AspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCys 99
               |||   |||      ||||||           |||           ::::::|||
Db         423 GACCTGACCCAGAAGGTAGAG-----------CTGCTGGAGAAGTTTCGGGACAACTGT 470

Qy         100 LeuAla---------SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               ||||||         |||:::   :::              |||       |||||||||
Db         471 TTGGCAATTTTGGAGAGCAAGGGCCTTGATCCAGCTTTAGGCGGTGAGACCCTGGCATCA 530

Qy         117 GlyLysAlaSer------------PheMetThrValLeuCysLeuSerSerIleTyrGlu 132
                  :::   |||                 ::::::|||   |||   ::::::   |||
Db         531 CGACAAGAATCCACTACTGATCACATGGACTCTATGTTGCTGTTAGAAACTTTGCAAGAG 590

Qy         133 AspLeuLysMetTyr-----------------GlnMet---GluPheLysAlaMetAsn 145
               :::||||||::::::                 ||||||   |||   :::|||:::
Db         591 GAGCTGAAGCTTTTTAACGAAACAGCCAAAAAGCAGATGGAGGAGTTACAGGCCTTAAAG 650

Qy         146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeu------ 163
                  ||||||   |||       :::|||      ||||||:::|||      |||
Db         651 GTAAAGCTGGAGATGAAAGAGGAAAGAGTCCGATTCCTAGAACAGCAAACCTTATGTAAC 710

Qy         164 ThrAlaIleAspGluLeuLeuGlnAlaLeu 173
                     ::::::::::|||   |||   |||
Db         711 AATCAAGTAAATGATTTAACACAGCCCTTA 740

RESULT 12
BM904933
LOCUS       BM904933               1007 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6699344 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5557760
            5', mRNA sequence.
ACCESSION   BM904933
VERSION     BM904933.1  GI:19355312
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1007)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12279  row: k  column: 09
            High quality sequence stop: 638.
FEATURES             Location/Qualifiers
     source          1. .1007
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5557760"
                     /clone_lib="NIH_MGC_72"
                     /tissue_type="melanotic melanoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally.  Primer: Oligo dT.
                     Average insert size 2 kb.   Library constructed by Life
                     Technologies."
BASE COUNT      312 a    231 c    256 g    208 t
ORIGIN

Alignment Scores:
Pred. No.:                2.42          Length:         1007
Score:                    93.50         Matches:        47
Percent Similarity:       41.76%        Conservative:   24
Best Local Similarity:    27.65%        Mismatches:     58
Query Match:              8.29%         Indels:         41
DB:                       14            Gaps:           8

US-09-917-265-47 (1-222) x BM904933 (1-1007)

Qy          41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeu---GlnLysAlaArg 59
               |||               ||||||   ||||||:::      |||   ||||||
Db         349 CTCAAGGACAAGAACCAGCTGTTAGAAGCCGTCAACAAGCAGTTGCACCAGAAGTTGACT 408

Qy          60 GlnThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLys 79
               :::|||                                        :::         |||
Db         409 GAAACT----------------------------------------CAGGGAGAGCTGAAG 429

Qy          80 AspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCys 99
               |||   |||      ||||||           |||           ::::::|||
Db         430 GACCTGACCCAGAAGGTAGAG-----------CTGCTGGAGAAGTTTCGGGACAACTGT 477

Qy         100 LeuAla---------SerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSer 116
               ||||||         |||:::   :::                       |||||||||
Db         478 TTGGCAATTTTGGAGAGCAAGGGCCTTGATCCAGCTTTAGGCAGTGAGACCCTGGCATCA 537

Qy         117 GlyLysAlaSer------------PheMetThrValLeuCysLeuSerSerIleTyrGlu 132
                  :::   |||                 ::::::|||   |||   ::::::   |||
Db         538 CGACAAGAATCCACTACTGATCACATGGACTCTATGTTGCTGTTAGAAACTTTGCAAGAG 597

Qy         133 AspLeuLysMetTyr-----------------GlnMet---GluPheLysAlaMetAsn 145
               :::||||||::::::                 ||||||   |||   :::|||:::
Db         598 GAGCTGAAGCTTTTTAACGAAACAGCCAAAAAGCAGATGGAGGAGTTACAGGCCTTAAAG 657

Qy         146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln--------------- 160
                  ||||||   |||       :::|||      ||||||:::|||
Db         658 GTAAAGCTGGAGATGAAAGAGGAAAGAGTCCGATTCCTAGAACAGCCAAACTTATGTAAC 717

Qy         161 ------------AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsn 176
                          ::::::   ||||||:::   |||:::   |||   |||
Db         718 AATCAAGTAAATGATTTAACAACAGCCCTTAAGGAAATGGAGCAGCTATTAGAAATGGTA 777

Qy         177 SerValThrValProGlnLysSerSerLeu 186
                  :::      |||      ||||||
Db         778 GAAGAAAGCAGTGGCCAGATGGGCTCCCTC 807

RESULT 13
```

```
AZ541842/c
LOCUS       AZ541842                928 bp    DNA     linear   GSS 14-NOV-2000
DEFINITION  ENTFR19TR Entamoeba histolytica Sheared DNA Entamoeba histolytica
            genomic, DNA sequence.
ACCESSION   AZ541842
VERSION     AZ541842.1  GI:11149954
KEYWORDS    GSS.
SOURCE      Entamoeba histolytica.
  ORGANISM  Entamoeba histolytica
            Eukaryota; Entamoebidae; Entamoeba.
REFERENCE   1  (bases 1 to 928)
  AUTHORS   Loftus,B., Van Aken,S. and Fraser,C.
  TITLE     Determination of clone end sequences from Entamoeba histolytica
            HM1:IMSS sheared DNA library
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Brendan J Loftus
            Department of Eukaryotic Genomics
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 0208
            Fax: 301 838 3543
            Email: bjloftus@tigr.org
            Clones are derived from the Entamoeba histolytica HM1:IMSS sheared
            DNA library
            Seq primer: M13-Reverse
            Class: shotgun
            High quality sequence start: 16
            High quality sequence stop: 808.
FEATURES             Location/Qualifiers
     source          1. .928
                     /organism="Entamoeba histolytica"
                     /strain="HM1:IMSS"
                     /db_xref="taxon:5759"
                     /clone_lib="Entamoeba histolytica Sheared DNA"
                     /note="Vector: pHOS1; Site_1: Bst I; Constructed at The
                     Institute for Genomic Research (TIGR), Rockville, MD.
                     Genomic DNA isolated from broth cultures of E. histolytica
                     using a  method described by Clark and Diamond (Clark,
                     C.G., and Diamond, L.S.  (1993) Entamoeba histolytica: a
                     method for isolate identification.  Exp. Parasitol.
                     77:450.). The DNA was mechanically sheared to give a
                     tight size distribution (~2 kb). The v + i method used for
                     the library  construction is described in detail in Smith,
                     H.O. and Venter, J.C.  (Making small insert libraries for
                     whole genome shotgun sequencing  projects. In Genome
                     Sequencing: A Practical Approach, eds. M. Vaudin  and B.
                     Barell, Oxford University Press, 1999)."
BASE COUNT      320 a    120 c    151 g    337 t
ORIGIN

Alignment Scores:
Pred. No.:                2.4          Length:          928
Score:                    93.00        Matches:         47
Percent Similarity:       43.53%       Conservative:    27
Best Local Similarity:    27.65%       Mismatches:      67
Query Match:              8.24%        Indels:          29
DB:                       17           Gaps:            9

US-09-917-265-47 (1-222) x AZ541842 (1-928)

Qy          42 AsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArg------ 59
               ||||||      :::::::|||           |||                 |||
Db         625 AACCATCTATTACATATTTTAACCTTAGAAAAGAACATGTTTTATATCAGAAGATTATAC 566

Qy          60 ---GlnThrLeuGluLeuTyrSerCysThrSer-GluGluIle---------------- 72
                  :::|||:::   |||:::   |||::::::    |||
Db         565 TGTAAAACTATGTGACTTTGGAAGTGCTCAACTATCAGAGACATTTTATTATAGAAAGCC 506

Qy          73 ----AspHisGluAspIleThrLysAspLysThrSerThrVal------GluAlaCysLe 89
                   ||||||:::   |||   :::         :::   |||      |||
Db         505 AAACGATCATCAAATAATCAAAGAGTTTATTAATAATAATGTTAAGCCTGAATATCAATC 446

Qy          89 uProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIleTh 109
                  |||      :::   :::   |||:::         ||||||:::      :::
Db         445 TCCAGAAATGATATTATTATATGAAAATCAACCAATTAGTAGAAAAAGTGATATCTGGGC 386

Qy         109 rAsnGlySerCysLeu---------AlaSerGlyLysAlaSerPheMetThrValLeuCy 126
                  |||      |||         |||   |||         |||         |||||
Db         385 ACTTGGATGTTTATTGTTTGAGACTGCAATTGGAACACCACCATTCTCTGCACCACTTTG 326

Qy         126 sLeuSerSerIleTyrGlu---AspLeuLysMetTyrGlnMetGluPheLysAlaMetAs 145
                  |:::|||   :::   :::   ||||||      |||||||||      |||   |||
Db         325 CATTTCTGATGTAAAACAATTAGATTTAACTGATTACCAAATGTCA---AAACGAATGAA 269

Qy         145 nAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln------------As 161
                  :::   |||           |||      :::      ||||||            ||
Db         268 ATCTTTACTT------------AAAGAAATGCTTGTTTTTGATCAAAATAAACGGCCTAA 221

Qy         161 nMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValPr 181
                  |:::   |||   ::::::         |||   :::   |||||||:::         ||
Db         220 TATATACACTATCCTAGAACATTTTAGTCAAGTTGTTGAGTTTAATAAC---------CC 170

Qy         181 oGlnLysSerSerLeuGluGluProAsp 190
                  |   ||||||   :::::::|||   |||
Db         169 ATATAAATCATTTATGAAAGAAACTGAT 142

RESULT 14
BH249132
LOCUS       BH249132                786 bp    DNA     linear   GSS 26-NOV-2001
DEFINITION  BOGAT94TR BOGA Brassica oleracea genomic clone BOGAT94, DNA
            sequence.
ACCESSION   BH249132
VERSION     BH249132.1  GI:17071370
KEYWORDS    GSS.
SOURCE      Brassica oleracea.
  ORGANISM  Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Rosidae; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE   1  (bases 1 to 786)
  AUTHORS   Town,C.D., Van Aken,S., Utterback,T. and Fraser,C.M.
  TITLE     Whole genome shotgun sequencing of Brassica oleracea
  JOURNAL   Unpublished (2001)
COMMENT     Other_GSSs: BOGAT94TF
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TR
            Class: sheared ends.
FEATURES             Location/Qualifiers
     source          1. .786
                     /organism="Brassica oleracea"
                     /strain="TO1000DH3"
                     /db_xref="taxon:3712"
                     /clone="BOGAT94"
                     /clone_lib="BOGA"
                     /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
                     genomic DNA inserted into pHOS1 using BstXI linkers"
BASE COUNT      181 a    218 c    182 g    205 t
ORIGIN

Alignment Scores:
Pred. No.:                2.36         Length:          786
Score:                    92.00        Matches:         33
Percent Similarity:       42.22%       Conservative:    24
Best Local Similarity:    24.44%       Mismatches:      55
Query Match:              8.16%        Indels:          23
DB:                       17           Gaps:            4

US-09-917-265-47 (1-222) x BH249132 (1-786)

Qy          55 LeuGlnLysAlaArgGlnThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHis 74
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Db        383 ATAGACAAGTTGAGAAGCGCTGTGACAGCGTTCTCCTGCGTAGCTGAGTCTGTTGAGCGA 442

Qy         75 GluAspIleThrLysAspLysThrSerThrValGluAlaCysLeuProLeuGluLeuThr 94

Db        443 AGCAGTTCAACTAACGAG---------ACGATCGCTCCGGAGTTCCCTATCACTATCCTG 493

Qy         95 MetAsnGluSerCysLeuAlaSerArgGluIleSerLeuIle-----------ThrAsn 110

Db        494 TTATCCATGTTGTGCTTAGCCAGCAGCCTTATCTCGGCTGTTGCTCGTCTCTGAACATCT 553

Qy        111 GlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeuCysLeuSerSerIle 130

Db        554 AACAAACTGCTTTTCAACTCCTCCAGGAGTTTCTTGACTTGGCTTTCGACCTCGGCG--- 610

Qy        131 TyrGluAspLeuLysMetTyrGlnMetGluPhe-LysAlaMetAsnAlaLysLeuLeuMe 150

Db        611 ----------AGATCACGCCTCGCCGAGTTCGAAGGCGCTGAGACAATCTTTGAAGAA 658

Qy        150 tAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAlaIleAspGluLeuLe 170

Db        659 CGGCGCCAAA----------ACTGGCTTGCCACGGTTATG 688

Qy        170 uGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSer 184

Db        689 TCTATCCATAAACCTTGGGGGAGTATTCAGACCGAGAAGGAGC 731

RESULT 15
BG242870
LOCUS       BG242870                916 bp    mRNA    linear   EST 13-FEB-2001
DEFINITION  602355851F1 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4483981 5',
            mRNA sequence.
ACCESSION   BG242870
VERSION     BG242870.1  GI:12752789
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 916)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Gilbert Smith, Ph.D.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10323  row: f  column: 14
            High quality sequence stop: 690.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /strain="FVB/N"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:4483981"
                     /clone_lib="NCI_CGAP_Mam1"
                     /tissue_type="tumor, biopsy sample"
                     /dev_stage="10 months, virgin"
                     /lab_host="DH10B"
                     /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI;
                     Site_2: NotI; Cloned unidirectionally.  Primer: Oligo dT.
                     Library constructed by Life Technologies. Investigator
                     providing samples: Gilbert Smith, NIH"
BASE COUNT      237 a    210 c    260 g    209 t
ORIGIN

Alignment Scores:
Pred. No.:              3.57          Length:        916
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Score:                  91.50         Matches:       60
Percent Similarity:     35.84%        Conservative:  21
Best Local Similarity:  26.55%        Mismatches:    71
Query Match:            8.11%         Indels:        74
DB:                     12            Gaps:          12

US-09-917-265-47 (1-222) x BG242870 (1-916)

Qy         24 TrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHis 43

Db         68 TGGAAAGGCAGGCTGCCGACTGCCTGTCGGAAGCCG---------------------- 103

Qy         44 SerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeu-Gl 63

Db        104 --------------CAGGAGTGAGAAAGGGTGTCGCAGAGAGCGCGGCGGTGGCTGAGA 148

Qy         63 uLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSe 83

Db        149 TTTCTTC---TGCTGAAGAGAGGAAATCTCATCCAAGGGC------CACAATGTCACTTC 199

Qy         83 rThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerAr 103

Db        200 CCAATTATCCGAGTGCTGCCTGCTCAAGCTAACACTGCCAGAGTCCTGCTCCCTCGGGAG 259

Qy        103 gGluIleSerLeuIleThrAsnGlySerCys--------------------------Le 114

Db        260 GAGTCAAGCTTACTTGGCATGAGGTTCCTGCTTTCCTGGGGTTGAGAGAAGCACAACTAT 319

Qy        114 uAlaSer--------------------GlyLysAlaSer-------------------- 120

Db        320 GGCATCTCTTGATGACCCAGGGAGGTGAGGGAAGGCTTCCTGTGCCCTTTGTGCCTGAAG 379

Qy        121 ----PheMetThrValLeuCysLeuSerSerIleTyrGlu------------------- 132

Db        380 GACCTTCAAGTCTTTCTATCAACTTCAGTCACATTATGAGGAAGAACACTTGGAAGATCG 439

Qy        133 -AspLeuLys--------------MetTyrGlnMetGluPheLysAlaMetAsnAlaLy 147

Db        440 TGATGTCAAAGGGCAAATTAAAAATCTTGTTCAGAAGGCTAGGAAAGCAAAGAAC---AA 496

Qy        147 sLeuLeuMet--------------------------AspProLysArgGlnIlePheLe 158

Db        497 GTTGTTGAAACGAGAAGGAGATGATCGAGTGGAACCAGGACCCAAG------------- 542

Qy        158 uAspGlnAsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerVa 178

Db        543 -GATATGAATCATTCAGTTATGGTGGGGTTGATCCTTACATGTGGGAAC---------- 590

Qy        178 lThrValProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLe 198

Db        591 -------CCCAAGAGCTTGGTGCTATGAGAAGCCATCTTTCTGACTTCAAAAACATCGTG 643

Qy        198 uCysIleLeuLeuHis 203

Db        644 CTGCAGAATAGAGCAC 659


Search completed: July 17, 2003, 09:26:58
Job time : 1062.95 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 16, 2003, 19:43:49 ; Search time 31.3063 Seconds
(without alignments)
2174.711 Million cell updates/sec

Title: US-09-917-265-47
Perfect score: 1128
Sequence: 1 MCPPRGLLLVTILVLLSHLD.....HAFRIRAVTIDRMMSYLNSS 222

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued_Patents_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1128	100.0	669	4	US-09-079-984A-12	Sequence 12, Appl
2	1099	97.4	669	4	US-09-079-984A-2	Sequence 2, Appli
3	940.5	83.4	660	1	US-08-186-529-3	Sequence 3, Appli
4	940.5	83.4	660	1	US-08-640-386A-3	Sequence 3, Appli
5	940.5	83.4	762	4	US-08-848-760B-21	Sequence 21, Appl
6	940.5	83.4	1316	2	US-08-684-687-3	Sequence 3, Appli
7	940.5	83.4	1316	4	US-09-851-520-3	Sequence 3, Appli
8	940.5	83.4	1364	1	US-08-265-087-3	Sequence 3, Appli
9	940.5	83.4	1364	1	US-08-621-493-3	Sequence 3, Appli
10	940.5	83.4	1364	2	US-08-965-688-3	Sequence 3, Appli
11	940.5	83.4	1364	4	US-09-260-173-3	Sequence 3, Appli
12	940.5	83.4	1645	4	US-09-310-842-2	Sequence 2, Appli
13	934.5	82.8	721	2	US-08-184-009-199	Sequence 199, App
14	934.5	82.8	721	2	US-08-458-356-199	Sequence 199, App
15	934.5	82.8	721	4	US-08-460-736-199	Sequence 199, App
16	934.5	82.8	1026	2	US-08-751-767A-1	Sequence 1, Appli
17	869	77.0	1560	2	US-08-751-767A-11	Sequence 11, Appl
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19	869	77.0	6139	2	US-08-751-767A-7	Sequence 7, Appli
20	579.5	51.4	713	2	US-08-385-335A-10	Sequence 10, Appl
21	556.5	49.3	6295	2	US-08-659-206A-4	Sequence 4, Appli
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25	97	8.6	7616	4	US-09-011-745-2	Sequence 2, Appli
26	88.5	7.8	7577	4	US-08-961-527-46	Sequence 46, Appl
27	86.5	7.7	1853	1	US-07-849-438-2	Sequence 2, Appli
28	85.5	7.6	4868	1	US-08-139-937-12	Sequence 12, Appl
29	85.5	7.6	4868	5	PCT-US93-11310-12	Sequence 12, Appl
30	84.5	7.5	8519	4	US-09-261-907-1	Sequence 1, Appli
31	84.5	7.5	8789	1	US-08-328-254-5	Sequence 5, Appli
32	83.5	7.4	10136	1	US-08-353-700-2	Sequence 2, Appli
33	83.5	7.4	10136	5	PCT-US95-16216-2	Sequence 2, Appli
34	82.5	7.3	8460	1	US-08-469-005A-9	Sequence 9, Appli
c 35	81.5	7.2	5599	2	US-08-477-451-9	Sequence 9, Appli
36	81.5	7.2	5599	2	US-08-477-451-13	Sequence 13, Appl
37	80.5	7.1	675	4	US-08-209-603E-12	Sequence 12, Appl
c 38	80.5	7.1	19932	2	US-08-477-451-25	Sequence 25, Appl
39	77	6.8	14231	4	US-08-961-527-81	Sequence 81, Appl
40	76.5	6.8	9737	2	US-08-944-449-7	Sequence 7, Appli
41	76.5	6.8	9737	4	US-09-353-362-7	Sequence 7, Appli
42	75.5	6.7	681	4	US-09-134-001C-741	Sequence 741, App
43	75.5	6.7	7399	2	US-08-418-848A-9	Sequence 9, Appli
44	75.5	6.7	9709	2	US-08-188-583-5	Sequence 5, Appli
45	75.5	6.7	9709	3	US-08-388-353-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-079-984A-12
; Sequence 12, Application US/09079984A
; Patent No. 6231850
; GENERAL INFORMATION:
; APPLICANT: Okano, Fumiyoshi, Satoh, Massahiro,
; APPLICANT: Yamada, Katsushige
; TITLE OF INVENTION: Canine interleukin 12, a production method
; TITLE OF INVENTION: thereof, an immune disease treatment method and preventive
; TITLE OF INVENTION: method using it
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Miller & Christenbury Intellectual Property
; ADDRESSEE: Department of Schnader, Harrison, Segal and Lewis, LLP
; STREET: 1600 Market Street, 39th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,984A
; FILING DATE: 15-MAY-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Austin R. Miller
; REGISTRATION NUMBER: 16,602
; REFERENCE/DOCKET NUMBER: 1051-98
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-1810
; TELEFAX: (215) 568-6946
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:

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;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-12

Alignment Scores:
Pred. No.:              1.71e-138      Length:         669
Score:                  1128.00        Matches:        222
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     4              Gaps:           0

US-09-917-265-47 (1-222) x US-09-079-984A-12 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
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Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 2
US-09-079-984A-2
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; Sequence 2, Application US/09079984A
; Patent No. 6231850
;  GENERAL INFORMATION:
;    APPLICANT:  Okano, Fumiyoshi, Satoh, Massahiro,
;    APPLICANT:  Yamada, Katsushige
;    TITLE OF INVENTION:  Canine interleukin 12, a production method
;    TITLE OF INVENTION:  thereof, an immune disease treatment method and preventive
;    TITLE OF INVENTION:  method using it
;    NUMBER OF SEQUENCES:  16
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Miller & Christenbury Intellectual Property
;      ADDRESSEE:  Department of Schnader, Harrison, Segal and Lewis, LLP
;      STREET:  1600 Market Street, 39th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy Disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/079,984A
;      FILING DATE:  15-MAY-1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Austin R. Miller
;      REGISTRATION NUMBER:  16,602
;      REFERENCE/DOCKET NUMBER:  1051-98
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 563-1810
;      TELEFAX:  (215) 568-6946
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  669 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Canis familiaris
;    FEATURE:
;      NAME/KEY:  Canine IL12
;      LOCATION:  1 to 666
;      IDENTIFICATION METHOD:  Similarity
US-09-079-984A-2

Alignment Scores:
Pred. No.:              1.09e-134      Length:         669
Score:                  1099.00        Matches:        217
Percent Similarity:     98.20%         Conservative:   1
Best Local Similarity:  97.75%         Mismatches:     4
Query Match:            97.43%         Indels:         0
DB:                     4              Gaps:           0

US-09-917-265-47 (1-222) x US-09-079-984A-2 (1-669)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||  |||   ||||||||||||     |||||||||||||||||||||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240
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Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 AACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGT 660

Qy        221 SerSer 222
              ||||||
Db        661 TCTTCC 666

RESULT 3
US-08-186-529-3
; Sequence 3, Application US/08186529
; Patent No. 5573764
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/186,529
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  McDaniels, Patricia A.
;      REGISTRATION NUMBER:  33,194
;      REFERENCE/DOCKET NUMBER:  GI 5225
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8401
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-186-529-3

Alignment Scores:
Pred. No.:              6.44e-114      Length:          660
Score:                  940.50         Matches:         187
Percent Similarity:     88.29%         Conservative:    9
Best Local Similarity:  84.23%         Mismatches:      23
Query Match:            83.38%         Indels:          3
DB:                     1              Gaps:            1

US-09-917-265-47 (1-222) x US-08-186-529-3 (1-660)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||         ||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 51

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 111

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 171

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||
Db        172 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 231

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 291

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   |||||||||||||||||||||||||||   |||   |||
Db        292 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 351

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      |||||||||||||||||||||||||||||||||||||||||:::|||
Db        352 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 411

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 471

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||:::|||||||||||||||||||   ||||||
Db        472 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 651

Qy        221 SerSer 222
              :::|||
Db        652 GCTTCC 657

RESULT 4
US-08-640-386A-3
; Sequence 3, Application US/08640386A
; Patent No. 5756085
;  GENERAL INFORMATION:
;    APPLICANT:  Sykes, Megan
;    APPLICANT:  Wolf, Stanley F.
```

```
;    TITLE OF INVENTION:  USE OF INTERLEUKIN-12 TO PREVENT
;    TITLE OF INVENTION:  GRAFT-VERSUS-HOST DISEASE
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genetics Institute, Inc., Legal Affairs
;      STREET:  87 CambridgePark Drive
;      CITY:  Cambridge
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02140
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/640,386A
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brown, Scott A.
;      REGISTRATION NUMBER:  32,724
;      REFERENCE/DOCKET NUMBER:  GI 5225A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-498-8224
;      TELEFAX:  617-876-5851
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  660 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      CELL TYPE:  Lymphoblast
;      CELL LINE:  RPMI 8866
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..660
US-08-640-386A-3

Alignment Scores:
Pred. No.:              6.44e-114      Length:         660
Score:                  940.50         Matches:        187
Percent Similarity:     88.29%         Conservative:   9
Best Local Similarity:  84.23%         Mismatches:     23
Query Match:            83.38%         Indels:         3
DB:                     1              Gaps:           1

US-09-917-265-47 (1-222) x US-08-640-386A-3 (1-660)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||         ||||||
Db          1 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 51

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   |||||:::||||||   |||:::|||   |||||:::|||   |||
Db         52 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 111

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        112 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 171

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        172 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 231

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        232 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 291

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              |||||||||   |||   ||||||||||||||||||||||||||||   |||   |||
Db        292 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 351

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||:::|||
Db        352 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 411

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 471

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||       ||||||||||:::|||||||||||||||||||   ||||||
Db        472 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 531

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 591

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        592 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 651

Qy        221 SerSer 222
              :::|||
Db        652 GCTTCC 657

RESULT 5
US-08-848-760B-21
; Sequence 21, Application US/08848760B
; Patent No. 6248721
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Animal Model For Evaluation Of Vaccines
;        NUMBER OF SEQUENCES: 33
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
;             STREET: 2421 N.W. 41st Street, Suite A-1
;             CITY: Gainesville
;             STATE: Florida
;             COUNTRY: United States of America
;             ZIP: 32606
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/848,760B
;             FILING DATE: 25-Jan-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: 09-APR-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: PACE, DORAN R.
;             REGISTRATION NUMBER: 38,261
;             REFERENCE/DOCKET NUMBER: CNG-100C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (352) 375-8100
;             TELEFAX: (352) 372-5800
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-08-848-760B-21

Alignment Scores:
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Pred. No.:              8.15e-114       Length:         762
Score:                  940.50          Matches:        187
Percent Similarity:     88.29%          Conservative:   9
Best Local Similarity:  84.23%          Mismatches:     23
Query Match:            83.38%          Indels:         3
DB:                     4               Gaps:           1

US-09-917-265-47 (1-222) x US-08-848-760B-21 (1-762)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||          ||||||
Db        103 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTC---------CTGGAC 153

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::|||||   |||:::|||   ||||||:::|||   |||
Db        154 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 213

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        214 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 273

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||
Db        274 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 333

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        334 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 393

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   ||||||||||||||||||||||||||   |||   |||
Db        394 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 453

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||:::|||
Db        454 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 513

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 573

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||||:::|||||||||||||||||||   ||||||
Db        574 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 633

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 693

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        694 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 753

Qy        221 SerSer 222
              :::|||
Db        754 GCTTCC 759

RESULT 6
US-08-684-687-3
; Sequence 3, Application US/08684687
; Patent No. 5830451
;  GENERAL INFORMATION:
;    APPLICANT:  KIEFF, ELLIOTT D.
;    APPLICANT:  DEVERGNE, ODILE
;    TITLE OF INVENTION:  A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
;    TITLE OF INVENTION:  THEREFOR
;    NUMBER OF SEQUENCES:  8
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  WOLF, GREENFIELD & SACKS, P.C.
;      STREET:  600 ATLANTIC AVENUE
;      CITY:  BOSTON
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/684,687
;      FILING DATE:
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,092
;      FILING DATE:  11-OCT-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  GATES, EDWARD R.
;      REGISTRATION NUMBER:  31,616
;      REFERENCE/DOCKET NUMBER:  B0801/7051
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1316 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA to mRNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  HOMO SAPIENS
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  102..863
US-08-684-687-3

Alignment Scores:
Pred. No.:              1.99e-113       Length:         1316
Score:                  940.50          Matches:        187
Percent Similarity:     88.29%          Conservative:   9
Best Local Similarity:  84.23%          Mismatches:     23
Query Match:            83.38%          Indels:         3
DB:                     2               Gaps:           1

US-09-917-265-47 (1-222) x US-08-684-687-3 (1-1316)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||          ||||||
Db        204 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTC---------CTGGAC 254

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db        255 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 314

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        315 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 374

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||
Db        375 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 434

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        435 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 494

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   ||||||||||||||||||||||||||   |||   |||
Db        495 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 554

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||:::|||
Db        555 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 614
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Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 674

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||||:::||||||||||||||||||||||   ||||||
Db        675 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 734

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        735 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 794

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        795 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 854

Qy        221 SerSer 222
              :::|||
Db        855 GCTTCC 860

RESULT 7
US-09-851-520-3
; Sequence 3, Application US/09851520
; Patent No. 6399379
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INTERLEUKIN 12 P35 SUBUNIT EXPRESSION
;  FILE REFERENCE: RTS-0241
;  CURRENT APPLICATION NUMBER: US/09/851,520
;  CURRENT FILING DATE:  2001-05-07
;  NUMBER OF SEQ ID NOS: 88
; SEQ ID NO 3
;   LENGTH: 1316
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (102)...(863)
US-09-851-520-3

Alignment Scores:
Pred. No.:              1.99e-113       Length:         1316
Score:                  940.50          Matches:        187
Percent Similarity:     88.29%          Conservative:   9
Best Local Similarity:  84.23%          Mismatches:     23
Query Match:            83.38%          Indels:         3
DB:                     4               Gaps:           1

US-09-917-265-47 (1-222) x US-09-851-520-3 (1-1316)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||  ||||||||||||      |||||||||         ||||||
Db        204 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTC---------CTGGAC 254

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db        255 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 314

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        315 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 374

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        375 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 434

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db        435 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 494

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              |||||||||   |||   ||||||||||||||||||||||||||||   |||   |||
Db        495 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 554

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||:::|||
Db        555 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 614

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        615 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 674

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||||:::||||||||||||||||||||||   ||||||
Db        675 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 734

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        735 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 794

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        795 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 854

Qy        221 SerSer 222
              :::|||
Db        855 GCTTCC 860

RESULT 8
US-08-265-087-3
; Sequence 3, Application US/08265087
; Patent No. 5571515
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/265,087
;      FILING DATE:
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
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US-08-265-087-3

Alignment Scores:
Pred. No.:              2.11e-113       Length:         1364
Score:                  940.50          Matches:        187
Percent Similarity:     88.29%          Conservative:   9
Best Local Similarity:  84.23%          Mismatches:     23
Query Match:            83.38%          Indels:         3
DB:                     1               Gaps:           1

US-09-917-265-47 (1-222) x US-08-265-087-3 (1-1364)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||         ||||||
Db        203 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 253

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db        254 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 313

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        314 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 373

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        374 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 433

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        434 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 493

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   ||||||||||||||||||||||||||   |||   |||
Db        494 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 553

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||:::|||
Db        554 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 613

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 673

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||||:::||||||||||||||||||||   ||||||
Db        674 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 733

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 793

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||
Db        794 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 853

Qy        221 SerSer 222
              ::::||
Db        854 GCTTCC 859

RESULT 9
US-08-621-493-3
; Sequence 3, Application US/08621493
; Patent No. 5723127
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/621,493
;      FILING DATE:  25-MAR-1996
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-621-493-3

Alignment Scores:
Pred. No.:              2.11e-113       Length:         1364
Score:                  940.50          Matches:        187
Percent Similarity:     88.29%          Conservative:   9
Best Local Similarity:  84.23%          Mismatches:     23
Query Match:            83.38%          Indels:         3
DB:                     1               Gaps:           1

US-09-917-265-47 (1-222) x US-08-621-493-3 (1-1364)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||         ||||||
Db        203 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 253

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db        254 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 313

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        314 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 373

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        374 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 433

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        434 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 493

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   ||||||||||||||||||||||||||   |||   |||
Db        494 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 553

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||:::|||
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Db        554 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 613

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 673

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||||:::||||||||||||||||||||||  ||||||
Db        674 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 733

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 793

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        794 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 853

Qy        221 SerSer 222
              :::|||
Db        854 GCTTCC 859

RESULT 10
US-08-965-688-3
; Sequence 3, Application US/08965688
; Patent No. 5976539
;  GENERAL INFORMATION:
;    APPLICANT:  Scott, Phillip
;    APPLICANT:  Trinchieri, Giorgio
;    TITLE OF INVENTION:  Compositions and Methods for Use of
;    TITLE OF INVENTION:  IL-12 as an Adjuvant
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-965-688-3

Alignment Scores:
Pred. No.:              2.11e-113      Length:          1364
Score:                  940.50         Matches:         187
Percent Similarity:     88.29%         Conservative:    9
Best Local Similarity:  84.23%         Mismatches:      23
Query Match:            83.38%         Indels:          3
DB:                     2              Gaps:            1

US-09-917-265-47 (1-222) x US-08-965-688-3 (1-1364)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||         ||||||
Db        203 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 253

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   |||||:::|||||||   |||:::|||   ||||||:::|||   |||
Db        254 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 313

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        314 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 373

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||
Db        374 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 433

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        434 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 493

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   |||||||||||||||||||||||||||   |||   |||
Db        494 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 553

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||:::|||
Db        554 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 613

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 673

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||||:::||||||||||||||||||||||  ||||||
Db        674 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 733

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 793

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        794 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 853

Qy        221 SerSer 222
              :::|||
Db        854 GCTTCC 859

RESULT 11
US-09-260-173-3
; Sequence 3, Application US/09260173
; Patent No. 6168923
;  GENERAL INFORMATION:
;       APPLICANT: Scott, Phillip
;                  Trinchieri, Giorgio
;       TITLE OF INVENTION: Compositions and Methods for Use of
;                           IL-12 as an Adjuvant
;       NUMBER OF SEQUENCES: 4
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Howson and Howson
;            STREET: Spring House Corporate Center, PO Box 457
;            CITY: Spring House
```

```
;              STATE: Pennsylvania
;              COUNTRY: USA
;              ZIP: 19477
;         COMPUTER READABLE FORM:
;              MEDIUM TYPE: Floppy disk
;              COMPUTER: IBM PC compatible
;              OPERATING SYSTEM: PC-DOS/MS-DOS
;              SOFTWARE: PatentIn Release #1.0, Version #1.25
;         CURRENT APPLICATION DATA:
;              APPLICATION NUMBER: US/09/260,173
;              FILING DATE: 01-Mar-1999
;              CLASSIFICATION: <Unknown>
;                              17-JUN-1994
;                              18-APR-1994
;         PRIOR APPLICATION DATA:
;              APPLICATION NUMBER: 08/965,688
;              FILING DATE: <Unknown>
;              APPLICATION NUMBER: 08/265,087
;              FILING DATE: 17-JUN-1994
;              APPLICATION NUMBER: US 08/229,282
;              FILING DATE: 18-APR-1994
;         ATTORNEY/AGENT INFORMATION:
;              NAME: Bak, Mary E.
;              REGISTRATION NUMBER: 31,215
;              REFERENCE/DOCKET NUMBER: WST51AUSA
;         TELECOMMUNICATION INFORMATION:
;              TELEPHONE: 215-540-9206
;              TELEFAX: 215-540-5818
;    INFORMATION FOR SEQ ID NO: 3:
;         SEQUENCE CHARACTERISTICS:
;              LENGTH: 1364 base pairs
;              TYPE: nucleic acid
;              STRANDEDNESS: double
;              TOPOLOGY: unknown
;         MOLECULE TYPE: cDNA
;         FEATURE:
;              NAME/KEY:  CDS
;              LOCATION:  101..859
;         SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-260-173-3

Alignment Scores:
Pred. No.:                2.11e-113      Length:          1364
Score:                    940.50         Matches:         187
Percent Similarity:       88.29%         Conservative:    9
Best Local Similarity:    84.23%         Mismatches:      23
Query Match:              83.38%         Indels:          3
DB:                       4              Gaps:            1

US-09-917-265-47 (1-222) x US-09-260-173-3 (1-1364)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||         ||||||
Db        203 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 253

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db        254 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 313

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        314 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 373

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        374 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 433

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        434 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 493

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   |||||||||||||||||||||||||||   |||   |||

Db        494 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 553

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||:::|||
Db        554 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 613

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        614 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 673

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||||:::||||||||||||||||||||   ||||||
Db        674 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 733

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        734 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 793

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||
Db        794 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 853

Qy        221 SerSer 222
              :::|||
Db        854 GCTTCC 859

RESULT 12
US-09-310-842-2
; Sequence 2, Application US/09310842A
; Patent No. 6451593
; GENERAL INFORMATION:
;  APPLICANT: Wittig, Prof. Burghardt
;  APPLICANT: Junghans, Claas
;  TITLE OF INVENTION: Design Principle for Constructing Expression Constructs for Ge
;  TITLE OF INVENTION: Therapy
;  FILE REFERENCE: XI 597/99
;  CURRENT APPLICATION NUMBER: US/09/310,842A
;  CURRENT FILING DATE: 1999-05-12
;  EARLIER APPLICATION NUMBER: DE 196 48 625.4
;  EARLIER FILING DATE: 1996-11-13
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 1645
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: gene
;   LOCATION: (1)..(1645)
;   OTHER INFORMATION: Interleukin-12 (IL-12, p35-subunit); Oligo DNA
;   OTHER INFORMATION: Dumbbell
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1)..(2)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at
;   OTHER INFORMATION: position 1 to 2  can be modified with amino or caroxy
;   OTHER INFORMATION: features
;   FEATURE:
;   NAME/KEY: misc_binding
;   LOCATION: (1644)..(1645)
;   OTHER INFORMATION: intramolecular binding site; the T-nucleotides at position 164
;   OTHER INFORMATION: to 1645  can be modified with amino or caroxy features
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Strandness: both;  nuclei
;   OTHER INFORMATION: acid (linear),  hypothetical: No. 6451593 anti-sense: No
US-09-310-842-2

Alignment Scores:
Pred. No.:                2.86e-113      Length:          1645
Score:                    940.50         Matches:         187
Percent Similarity:       88.29%         Conservative:    9
Best Local Similarity:    84.23%         Mismatches:      23
Query Match:              83.38%         Indels:          3
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DB:                    4              Gaps:          1

US-09-917-265-47 (1-222) x US-09-310-842-2 (1-1645)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||          ||||||
Db        735 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTC---------CTGGAC 785

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db        786 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 845

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        846 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 905

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        906 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 965

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        966 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 1025

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   |||||||||||||||||||||||||   |||   |||
Db       1026 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 1085

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||:::|||
Db       1086 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 1145

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1146 TTCAAGACCATGAATGCAAAACTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 1205

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||:::||||||||||||||||||   ||||||
Db       1206 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 1265

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1266 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 1325

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db       1326 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 1385

Qy        221 SerSer 222
              :::|||
Db       1386 GCTTCC 1391

RESULT 13
US-08-184-009-199
; Sequence 199, Application US/08184009
; Patent No. 5833975
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,009
;      FILING DATE:  19-JAN-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-184-009-199

Alignment Scores:
Pred. No.:              4.55e-113      Length:          721
Score:                  934.50         Matches:         186
Percent Similarity:     87.84%         Conservative:    9
Best Local Similarity:  83.78%         Mismatches:      24
Query Match:            82.85%         Indels:          3
DB:                     2              Gaps:            1

US-09-917-265-47 (1-222) x US-08-184-009-199 (1-721)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||          ||||||
Db         62 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 112

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db        113 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 172

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::|||||||||||||||||||||||||||||||   |||||||||||||||||||
Db        173 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 232

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||
Db        233 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 292

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||   |||||||||||||||||||
Db        293 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 352

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   |||||||||||||||||||||||||   |||   |||
Db        353 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 412

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||:::|||
Db        413 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 472

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 532

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||:::||||||||||||||||||   ||||||
Db        533 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 592

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 652

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
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                ||||||||||||||||||||||||||||||||||||||||||:::   ||||||||||||
Db        653 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAAT 712

Qy        221 SerSer 222
                :::|||
Db        713 GCTTCC 718

RESULT 14
US-08-458-356-199
; Sequence 199, Application US/08458356
; Patent No. 5942235
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/458,356
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-458-356-199

Alignment Scores:
Pred. No.:              4.55e-113       Length:         721
Score:                  934.50          Matches:        186
Percent Similarity:     87.84%          Conservative:   9
Best Local Similarity:  83.78%          Mismatches:     24
Query Match:            82.85%          Indels:         3
DB:                     2               Gaps:           1

US-09-917-265-47 (1-222) x US-08-458-356-199 (1-721)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||      |||||||||         ||||||
Db         62 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 112

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db        113 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 172

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::||||||||||||||||||||||||||||||||   ||||||||||||||||||

Db        173 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 232

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||
Db        233 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 292

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||
Db        293 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 352

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   |||||||||||||||||||||||||   |||   |||
Db        353 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 412

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||:::|||
Db        413 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 472

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 532

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||:::||||||||||||||||||||   ||||||
Db        533 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 592

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        593 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 652

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||:::   ||||||||||||
Db        653 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGACAGAGTGACGAGCTATCTGAAT 712

Qy        221 SerSer 222
                :::|||
Db        713 GCTTCC 718

RESULT 15
US-08-460-736-199
; Sequence 199, Application US/08460736
; Patent No. 6265189
;  GENERAL INFORMATION:
;    APPLICANT:  Paoletti, Enzo
;    APPLICANT:  Tartaglia, James
;    APPLICANT:  Cox, William I.
;    TITLE OF INVENTION:  RECOMBINANT VIRUS IMMUNOTHERAPY
;    NUMBER OF SEQUENCES:  217
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  NY
;      COUNTRY:  USA
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/460,736
;      FILING DATE:  02-JUN-1995
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/184,009
;      FILING DATE:  19-JAN-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer, William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454310-2530
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
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;      TELEFAX:  (212) 840-0712
;      TELEX:  425066CURTMS
;  INFORMATION FOR SEQ ID NO:  199:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  721 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-460-736-199

Alignment Scores:
Pred. No.:              4.55e-113      Length:          721
Score:                  934.50         Matches:         186
Percent Similarity:     87.84%         Conservative:    9
Best Local Similarity:  83.78%         Mismatches:      24
Query Match:            82.85%         Indels:          3
DB:                     4              Gaps:            1

US-09-917-265-47 (1-222) x US-08-460-736-199 (1-721)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
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Db         62 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTGGCTACCCTGGTCCTC---------CTGGAC 112

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
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Db        113 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 172

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
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Db        173 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 232

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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Db        293 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 352

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
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Db        353 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 412

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
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Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
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Db        473 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 532

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
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Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
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Db        593 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 652

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
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Qy        221 SerSer 222
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Db        713 GCTTCC 718


Search completed: July 17, 2003, 09:32:02
Job time : 34.3063 secs
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GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 16, 2003, 19:59:04 ; Search time 151.667 Seconds
(without alignments)
3019.692 Million cell updates/sec

Title: US-09-917-265-47
Perfect score: 1128
Sequence: 1 MCPPRGLLLVTILVLLSHLD.....HAFRIRAVTIDRMMSYLNSS 222

Scoring table: BLOSUM62
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
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Searched: 1439767 seqs, 1031500376 residues

Total number of hits satisfying chosen parameters: 2879534

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
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17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1128	100.0	666	10	US-09-917-265-46	Sequence 46, Appl
c 2	1128	100.0	666	10	US-09-917-265-48	Sequence 48, Appl
3	1128	100.0	1455	10	US-09-917-265-104	Sequence 104, App
c 4	1128	100.0	1455	10	US-09-917-265-106	Sequence 106, App
5	1046	92.7	689	15	US-10-079-616-26	Sequence 26, Appl
6	1046	92.7	1441	15	US-10-079-616-8	Sequence 8, Appli
7	1043	92.5	666	10	US-09-917-265-32	Sequence 32, Appl
c 8	1043	92.5	666	10	US-09-917-265-34	Sequence 34, Appl
9	994	88.1	591	10	US-09-917-265-49	Sequence 49, Appl
c 10	994	88.1	591	10	US-09-917-265-51	Sequence 51, Appl
11	970	86.0	1533	10	US-09-917-265-66	Sequence 66, Appl
c 12	970	86.0	1533	10	US-09-917-265-68	Sequence 68, Appl
13	970	86.0	1599	10	US-09-917-265-61	Sequence 61, Appl
c 14	970	86.0	1599	10	US-09-917-265-63	Sequence 63, Appl
15	940.5	83.4	762	11	US-09-826-025-21	Sequence 21, Appl
16	940.5	83.4	1395	11	US-09-924-703-5	Sequence 5, Appli
17	940.5	83.4	1645	15	US-10-228-811-2	Sequence 2, Appli
18	938.5	83.2	660	11	US-09-754-014-6	Sequence 6, Appli
19	938.5	83.2	660	11	US-09-836-866-4	Sequence 4, Appli
20	934.5	82.8	1026	15	US-10-172-399-5	Sequence 5, Appli
21	932	82.6	591	15	US-10-079-616-9	Sequence 9, Appli
22	930	82.4	1533	10	US-09-917-265-43	Sequence 43, Appl
c 23	930	82.4	1533	10	US-09-917-265-45	Sequence 45, Appl
24	930	82.4	1599	10	US-09-917-265-38	Sequence 38, Appl
c 25	930	82.4	1599	10	US-09-917-265-40	Sequence 40, Appl
26	929	82.4	591	10	US-09-917-265-35	Sequence 35, Appl
c 27	929	82.4	591	10	US-09-917-265-37	Sequence 37, Appl
28	912.5	80.9	660	11	US-09-754-014-7	Sequence 7, Appli
29	909.5	80.6	660	11	US-09-754-014-8	Sequence 8, Appli
30	889	78.8	561	10	US-09-917-265-101	Sequence 101, App
c 31	889	78.8	561	10	US-09-917-265-103	Sequence 103, App
32	876.5	77.7	8578	10	US-09-828-825-1	Sequence 1, Appli
33	876.5	77.7	8578	10	US-09-828-825-3	Sequence 3, Appli
34	875.5	77.6	8608	10	US-09-828-825-7	Sequence 7, Appli
35	875.5	77.6	8623	10	US-09-828-825-5	Sequence 5, Appli
36	875.5	77.6	8629	10	US-09-828-825-15	Sequence 15, Appl
37	875.5	77.6	8638	10	US-09-828-825-9	Sequence 9, Appli
38	875.5	77.6	8644	10	US-09-828-825-13	Sequence 13, Appl
39	875.5	77.6	8659	10	US-09-828-825-11	Sequence 11, Appl
40	591.5	52.4	1265	15	US-10-172-399-1	Sequence 1, Appli
41	134	11.9	79	15	US-10-079-616-24	Sequence 24, Appl
42	112	9.9	95	15	US-10-079-616-22	Sequence 22, Appl
43	94.5	8.4	1149	10	US-09-841-132-545	Sequence 545, App
44	92.5	8.2	1971	14	US-10-137-866-139	Sequence 139, App
45	92.5	8.2	1971	14	US-10-146-726-139	Sequence 139, App

ALIGNMENTS

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RESULT 1
US-09-917-265-46
; Sequence 46, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-46
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Alignment Scores:
Pred. No.:              1.03e-134       Length:         666
Score:                  1128.00         Matches:        222
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-46 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
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Db          1 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
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Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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Db        181 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
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Db        301 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
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Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
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Db        421 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
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Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
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Qy        221 SerSer 222
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Db        661 TCTTCC 666

RESULT 2
US-09-917-265-48/c
; Sequence 48, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-48

Alignment Scores:
Pred. No.:              1.03e-134       Length:         666
Score:                  1128.00         Matches:        222
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
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DB:                     10              Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-48 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
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Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
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Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
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Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
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Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
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Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
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Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
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Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
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Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
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Qy        221 SerSer 222
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Db          6 TCTTCC 1

RESULT 3
US-09-917-265-104
; Sequence 104, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
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;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 104
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (232)..(897)
;   OTHER INFORMATION:
US-09-917-265-104

Alignment Scores:
Pred. No.:              3.54e-134       Length:         1455
Score:                  1128.00         Matches:        222
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-104 (1-1455)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
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Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        292 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 351

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        352 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 411

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        412 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 471

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        472 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 531

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        532 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 591

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        592 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 651

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        652 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 711

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        712 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 771

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        772 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 831

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        832 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 891

Qy        221 SerSer 222
              ||||||
Db        892 TCTTCC 897
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RESULT 4
US-09-917-265-106/c
; Sequence 106, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
;   LENGTH: 1455
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-106

Alignment Scores:
Pred. No.:              3.54e-134       Length:         1455
Score:                  1128.00         Matches:        222
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     10              Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-106 (1-1455)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1224 ATGTGCCCGCCGCGCGGCCTCCTCCTTGTGACCATCCTGGTCCTGCTAAGCCACCTGGAC 1165

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1164 CACCTTACTTGGGCCAGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGC 1105

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1104 CTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAA 1045

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1044 ACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGAT 985

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        984 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 925

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        924 GCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCT 865

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        864 TTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAA 805

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        804 TTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAA 745

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        744 AACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTG 685

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        684 CCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 625

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        624 CTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAAT 565

Qy        221 SerSer 222
                ||||||
Db        564 TCTTCC 559

RESULT 5
US-10-079-616-26
; Sequence 26, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;        ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 26:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 689 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-079-616-26

Alignment Scores:
Pred. No.:              3.46e-124       Length:         689
Score:                  1046.00         Matches:        205
Percent Similarity:     95.95%          Conservative:   8
Best Local Similarity:  92.34%          Mismatches:     9
Query Match:            92.73%          Indels:         0
DB:                     15              Gaps:           0

US-09-917-265-47 (1-222) x US-10-079-616-26 (1-689)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          7 ATGTGCCCCCCCCGTGGCCTCCTCCTGGTGACCATCCTGGTCCTGCTGAACCACCTGGAC 66

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||||:::|||||||||
Db         67 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 126

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||||
Db        127 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 186

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 246

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        247 AAAACCAGCACAGTGGAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTG 306

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        307 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 366

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        367 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 426

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        427 TTCAAGGCCATGAATGCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 486

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        487 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 546

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 606

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        607 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 666

Qy        221 SerSer 222
              ||||||
Db        667 TCTTCC 672

RESULT 6
US-10-079-616-8
; Sequence 8, Application US/10079616
; Publication No. US20020107366A1
;   GENERAL INFORMATION:
;        APPLICANT: IMAMURA, Takayuki
;                   MAEDA, Hiroaki
;                   FUJIYASU, Takeshi
;                   IMAGAWA, Yoshitaka
;                   TOKIYOSHI, Sachio
;        TITLE OF INVENTION: NOVEL FELINE CYTOKINE PROTEIN
;        NUMBER OF SEQUENCES: 26
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: BROWDY AND NEIMARK
;             STREET: 419 Seventh Street, N.W., Suite 300
;             CITY: Washington
;             STATE: D.C.
;             COUNTRY: USA
;             ZIP: 20004
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/079,616
;             FILING DATE: 22-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
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;             APPLICATION NUMBER: 09/011,143
;             FILING DATE: 04-FEB-1998
;             APPLICATION NUMBER: PCT/JP97/01824
;             FILING DATE: 29-MAY-1997
;             APPLICATION NUMBER: JP 165249/1996
;             FILING DATE: 04-JUN-1996
;       ATTORNEY/AGENT INFORMATION:
;             NAME: BROWDY, Roger L.
;             REGISTRATION NUMBER: 25,618
;             REFERENCE/DOCKET NUMBER: IMAMURA=1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 202-628-5197
;             TELEFAX: 202-737-3528
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 1441 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: cDNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-079-616-8

Alignment Scores:
Pred. No.:              1.11e-123       Length:         1441
Score:                  1046.00         Matches:        205
Percent Similarity:     95.95%          Conservative:   8
Best Local Similarity:  92.34%          Mismatches:     9
Query Match:            92.73%          Indels:         0
DB:                     15              Gaps:           0

US-09-917-265-47 (1-222) x US-10-079-616-8 (1-1441)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        143 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 202

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||||   :::|||||||||||:::|||||||||
Db        203 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 262

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||
Db        263 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 322

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        323 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 382

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        383 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 442

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        443 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 502

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        503 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 562

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        563 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 622

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        623 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 682

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        683 CCACAGAACTCCTCCCTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATA 742

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        743 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAAT 802

Qy        221 SerSer 222
              ||||||
Db        803 TCTTCC 808

RESULT 7
US-09-917-265-32
; Sequence 32, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(666)
;   OTHER INFORMATION:
US-09-917-265-32

Alignment Scores:
Pred. No.:              7.95e-124       Length:         666
Score:                  1043.00         Matches:        204
Percent Similarity:     95.95%          Conservative:   9
Best Local Similarity:  91.89%          Mismatches:     9
Query Match:            92.46%          Indels:         0
DB:                     10              Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-32 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db          1 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 60

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||||   :::|||||||||||:::|||||||||
Db         61 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 120

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||||:::|||||||||||||||||||||||||||
Db        121 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 180

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              ||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 240

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 300

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        301 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 360

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||||   ||||||||||||||||||||||||||||||||||||||:::|||
Db        361 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 420

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        421 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 480

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db        481 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 540

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 600

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db        601 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 660

Qy        221 SerSer 222
              :::|||
Db        661 GCTTCC 666

RESULT 8
US-09-917-265-34/c
; Sequence 34, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
;   LENGTH: 666
;   TYPE: DNA
;   ORGANISM: Felis catus
US-09-917-265-34

Alignment Scores:
Pred. No.:              7.95e-124       Length:         666
Score:                  1043.00         Matches:        204
Percent Similarity:     95.95%          Conservative:   9
Best Local Similarity:  91.89%          Mismatches:     9
Query Match:            92.46%          Indels:         0
DB:                     10              Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-34 (1-666)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        666 ATGTGCCCGCCGCGTGGCCTCCTCCTTGTAACCATCCTGGTCCTGTTAAACCACCTGGAC 607

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::|||||||||   :::|||||||||||:::|||||||||
Db        606 CACCTCAGTTTGGCCAGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGC 547

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              ||||||||||||||   ||||||||||:::|||||||||||||||||||||||||||||
Db        546 CTCAACCACTCCCAAACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAA 487

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db        486 ACTCTAGAATTTTACTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGAT 427

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        426 AAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTG 367

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
              ||||||||||||||||||||||||||||||||||||||||||||||||   |||   |||
Db        366 GCTTCCAGAGAGATCTCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 307

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||:::|||
Db        306 TTTATGACGACCCTGTGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAG 247

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        246 TTCAAGGCCATGAATGCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAA 187

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              ||||||||||||||||||||||||||||||||||||||||||    ||||||||||||||
Db        186 AACATGCTGACAGCTATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTG 127

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        126 CCACAGAACTCCTCCCTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 67

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||:::||||||||||||||||||||||
Db         66 CTTCTTCATGCTTTCAGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAAT 7

Qy        221 SerSer 222
              :::|||
Db          6 GCTTCC 1

RESULT 9
US-09-917-265-49
; Sequence 49, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(591)
;   OTHER INFORMATION:
US-09-917-265-49

Alignment Scores:
Pred. No.:              1.25e-117       Length:         591
Score:                  994.00          Matches:        197
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.12%          Indels:         0
DB:                     10              Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-49 (1-591)

Qy         26 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60

Qy         46 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120

Qy         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180

Qy         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        106 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        206 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591

RESULT 10
US-09-917-265-51/c
; Sequence 51, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
;   LENGTH: 591
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-51

Alignment Scores:
Pred. No.:              1.25e-117       Length:         591
Score:                  994.00          Matches:        197
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            88.12%          Indels:         0
DB:                     10              Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-51 (1-591)

Qy         26 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 45
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        591 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 532

Qy         46 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 65
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        531 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 472

Qy         66 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 85
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        471 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 412

Qy         86 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 105
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        411 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 352

Qy        106 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        351 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 292

Qy        126 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 145
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        291 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 232

Qy        146 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 165
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        231 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 172

Qy        166 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 185
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        171 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 112

Qy        186 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 205
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        111 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 52

Qy        206 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         51 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 1

RESULT 11
US-09-917-265-66
; Sequence 66, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 66
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1533)
;   OTHER INFORMATION:
US-09-917-265-66

Alignment Scores:
Pred. No.:              6.68e-114       Length:         1533
Score:                  970.00          Matches:        191
Percent Similarity:     98.99%          Conservative:   5
Best Local Similarity:  96.46%          Mismatches:     2
Query Match:            85.99%          Indels:         0
DB:                     10              Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-66 (1-1533)

Qy         25 AlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSer 44
              :::|||:::|||||||||   :::|||||||||||:::|||||||||||||||||||||
Db        940 TCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCC 999

Qy         45 GlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeu 64
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1000 CAAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTA 1059

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1060 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1119

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db       1120 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1179

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrVal 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1180 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTC 1239

Qy        125 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMet 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1240 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATG 1299

Qy        145 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThr 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1300 AACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACA 1359

Qy        165 AlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSer 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1360 GCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCC 1419

Qy        185 SerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAla 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1420 TCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCT 1479

Qy        205 PheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 222
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||
Db       1480 TTCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1533

RESULT 12
US-09-917-265-68/c
; Sequence 68, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 68
;   LENGTH: 1533
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-68

Alignment Scores:
Pred. No.:              6.68e-114      Length:         1533
Score:                  970.00         Matches:        191
Percent Similarity:     98.99%         Conservative:   5
Best Local Similarity:  96.46%         Mismatches:     2
Query Match:            85.99%         Indels:         0
DB:                     10             Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-68 (1-1533)

Qy         25 AlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSer 44
              :::|||:::|||||||||   :::|||||||||||||:::||||||||||||||||||||
Db        594 TCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCC 535

Qy         45 GlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeu 64
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 CAAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTA 475

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrVal 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTC 295

Qy        125 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMet 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATG 235

Qy        145 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThr 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 AACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACA 175

Qy        165 AlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSer 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCC 115

Qy        185 SerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAla 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 TCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCT 55

Qy        205 PheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 222
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||
Db         54 TTCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 13
US-09-917-265-61
; Sequence 61, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES TH
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1599)
;   OTHER INFORMATION:
US-09-917-265-61

Alignment Scores:
Pred. No.:              7.14e-114      Length:         1599
Score:                  970.00         Matches:        191
Percent Similarity:     98.99%         Conservative:   5
Best Local Similarity:  96.46%         Mismatches:     2
Query Match:            85.99%         Indels:         0
DB:                     10             Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-61 (1-1599)

Qy         25 AlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSer 44
              :::|||:::|||||||||   :::|||||||||||||:::||||||||||||||||||||
Db       1006 TCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCC 1065

Qy         45 GlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeu 64
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1066 CAAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTA 1125

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1126 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 1185

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Db       1186 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 1245

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrVal 124
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1246 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTC 1305

Qy        125 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMet 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1306 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATG 1365

Qy        145 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThr 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1366 AACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACA 1425

Qy        165 AlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSer 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1426 GCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCC 1485

Qy        185 SerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAla 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1486 TCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCT 1545

Qy        205 PheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 222
              ||||||||||||||||||||||:::||||||||||||||||||||||||||||
Db       1546 TTCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1599

RESULT 14
US-09-917-265-63/c
; Sequence 63, Application US/09917265
; Patent No. US20020052030A1
; GENERAL INFORMATION:
;  APPLICANT: Wonderling, Ramani S.
;  APPLICANT:  Boroughs, Karen L.
;  TITLE OF INVENTION: CANINE AND FELINE PROTEINS, NUCLEIC ACID MOLECULES AND USES THERE
;  FILE REFERENCE: IM-5
;  CURRENT APPLICATION NUMBER: US/09/917,265
;  CURRENT FILING DATE:  2001-07-27
;  PRIOR APPLICATION NUMBER: 60/223,016
;  PRIOR FILING DATE: 2000-08-04
;  NUMBER OF SEQ ID NOS: 109
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
;   LENGTH: 1599
;   TYPE: DNA
;   ORGANISM: Canis familiaris
US-09-917-265-63

Alignment Scores:
Pred. No.:              7.14e-114       Length:         1599
Score:                  970.00          Matches:        191
Percent Similarity:     98.99%          Conservative:   5
Best Local Similarity:  96.46%          Mismatches:     2
Query Match:            85.99%          Indels:         0
DB:                     10              Gaps:           0

US-09-917-265-47 (1-222) x US-09-917-265-63 (1-1599)

Qy         25 AlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSer 44
              :::|||:::|||||||||   :::||||||||||||:::||||||||||||||||||||
Db        594 TCTAGAAACTTGCCAACCCCTACTCCATCCCCGGGTATGTTCCAATGTTTGAACCACTCC 535

Qy         45 GlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeu 64
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        534 CAAACCTTGTTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTA 475

Qy         65 TyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThr 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        474 TATTCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACA 415

Qy         85 ValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGlu 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        414 GTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAG 355

Qy        105 IleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrVal 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        354 ATCTCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTC 295

Qy        125 LeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMet 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        294 CTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATG 235

Qy        145 AsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThr 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        234 AACGCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACA 175

Qy        165 AlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSer 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 GCTATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCC 115

Qy        185 SerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAla 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        114 TCCCTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCT 55

Qy        205 PheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 222
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||
Db         54 TTCAGAATTCGTGCGGTGACCATCAATAGAATGATGTCCTACTTGAACTCTTCC 1

RESULT 15
US-09-826-025-21
; Sequence 21, Application US/09826025
; Patent No. US20020162123A1
;   GENERAL INFORMATION:
;        APPLICANT: Chang, Lung-Ji
;        TITLE OF INVENTION: Combination Immunogene Therapy
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Medlen & Carroll, LLP
;             STREET: 220 Montgomery Street, Suite 2200
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: United States of America
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/826,025
;             FILING DATE: 04-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/838,702
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Ingolia, Diane E.
;             REGISTRATION NUMBER: 40,027
;             REFERENCE/DOCKET NUMBER: CHANG-02687
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 705-8410
;             TELEFAX: (415) 397-8338
;   INFORMATION FOR SEQ ID NO: 21:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 762 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        MOLECULE TYPE: other nucleic acid
;             DESCRIPTION: /desc = "DNA"
;        SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-826-025-21

Alignment Scores:
Pred. No.:              1.33e-110       Length:         762
Score:                  940.50          Matches:        187
Percent Similarity:     88.29%          Conservative:   9
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Best Local Similarity:  84.23%          Mismatches:    23
Query Match:            83.38%          Indels:        3
DB:                     11              Gaps:          1

US-09-917-265-47 (1-222) x US-09-826-025-21 (1-762)

Qy          1 MetCysProProArgGlyLeuLeuLeuValThrIleLeuValLeuLeuSerHisLeuAsp 20
              |||||||||   |||   ||||||||||||       |||||||||          ||||||
Db        103 ATGTGTCCAGCGCGCAGCCTCCTCCTTGTCGCTACCCTGGTCCTC---------CTGGAC 153

Qy         21 HisLeuThrTrpAlaArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCys 40
              ||||||:::   ||||||:::||||||   |||:::|||   ||||||:::|||   |||
Db        154 CACCTCAGTTTGGCCAGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGC 213

Qy         41 LeuAsnHisSerGlnAsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGln 60
              |||:::||||||||||||||||||||||||||||||||   ||||||||||||||||||
Db        214 CTTCACCACTCCCAAAACCTGCTGAGGGCCGTCAGCAACATGCTCCAGAAGGCCAGACAA 273

Qy         61 ThrLeuGluLeuTyrSerCysThrSerGluGluIleAspHisGluAspIleThrLysAsp 80
              |||||||||   |||   ||||||||||||||||||||||||||||||||||||||||||
Db        274 ACTCTAGAATTTTACCCTTGCACTTCTGAAGAGATTGATCATGAAGATATCACAAAAGAT 333

Qy         81 LysThrSerThrValGluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeu 100
              ||||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        334 AAAACCAGCACAGTGGAGGCCTGTTTACCATTGGAATTAACCAAGAATGAGAGTTGCCTA 393

Qy        101 AlaSerArgGluIleSerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSer 120
                 |||||||||   |||   ||||||||||||||||||||||||   |||   |||
Db        394 AATTCCAGAGAGACCTCTTTCATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCT 453

Qy        121 PheMetThrValLeuCysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGlu 140
              ||||||      ||||||||||||||||||||||||||||||||||||||:::|||
Db        454 TTTATGATGGCCCTGTGCCTTAGTAGTATTTATGAAGACTTGAAGATGTACCAGGTGGAG 513

Qy        141 PheLysAlaMetAsnAlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGln 160
              ||||||   ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 TTCAAGACCATGAATGCAAAGCTTCTGATGGATCCTAAGAGGCAGATCTTTCTAGATCAA 573

Qy        161 AsnMetLeuThrAlaIleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrVal 180
              |||||||||      ||||||||||||:::||||||||||||||||||   ||||||
Db        574 AACATGCTGGCAGTTATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGAGACTGTG 633

Qy        181 ProGlnLysSerSerLeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIle 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 CCACAAAAATCCTCCCTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATA 693

Qy        201 LeuLeuHisAlaPheArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsn 220
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        694 CTTCTTCATGCTTTCAGAATTCGGGCAGTGACTATTGATAGAGTGATGAGCTATCTGAAT 753

Qy        221 SerSer 222
              :::|||
Db        754 GCTTCC 759


Search completed: July 17, 2003, 09:56:07
Job time : 155.667 secs
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 13:00:49 ; Search time 1642.12 Seconds
(without alignments)
10474.108 Million cell updates/sec

Title: US-09-917-265-49
Perfect score: 591
Sequence: 1 aggagcctccccacagcctc.....tgagttatctgaattcttcc 591

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2054640 seqs, 14551402878 residues

Word size : 0

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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13: gb_un:*
14: gb_vi:*
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16: em_fun:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	567	95.9	669	6	AR151072	AR151072 Sequence
2	567	95.9	669	6	E15018	E15018 Canine mRNA
3	488	82.6	669	6	AR151062	AR151062 Sequence
4	419	70.9	669	4	CFU49085	U49085 Canis famil
5	81	13.7	285	4	AF054605	AF054605 Felis cat
6	81	13.7	669	4	FCU83185	U83185 Felis catus
7	81	13.7	669	4	FCIL12P35	Y07761 F.catus mRN
8	75	12.7	666	6	AX154613	AX154613 Sequence
9	66	11.2	666	6	AX154612	AX154612 Sequence
10	62	10.5	660	6	AX154615	AX154615 Sequence
11	62	10.5	660	6	AX154616	AX154616 Sequence
12	59	10.0	660	6	AR008951	AR008951 Sequence
13	59	10.0	660	6	AX154614	AX154614 Sequence
14	59	10.0	660	6	AX154617	AX154617 Sequence
15	59	10.0	660	6	AX154618	AX154618 Sequence
16	59	10.0	660	6	AX154619	AX154619 Sequence
17	59	10.0	660	6	AX154621	AX154621 Sequence
18	59	10.0	660	6	AX154634	AX154634 Sequence
19	59	10.0	660	6	BD007071	BD007071 IL-12 gen
20	59	10.0	660	6	BD007079	BD007079 Gene expr
21	59	10.0	660	6	I28592	I28592 Sequence 3
22	59	10.0	721	6	AR052862	AR052862 Sequence
23	59	10.0	762	9	AF101062	AF101062 Homo sapi
24	59	10.0	780	9	MMU19842	U19842 Macaca mula
25	59	10.0	823	9	AF180562	AF180562 Homo sapi
26	59	10.0	1026	6	AR091390	AR091390 Sequence
27	59	10.0	1026	9	HUMCLMF35	M65271 Human cytot
28	59	10.0	1287	6	AX084108	AX084108 Sequence
29	59	10.0	1316	6	AR050785	AR050785 Sequence
30	59	10.0	1316	6	AR212036	AR212036 Sequence
31	59	10.0	1316	9	HUMNKSFP35	M65291 Human natur
32	59	10.0	1364	6	AR082685	AR082685 Sequence
33	59	10.0	1364	6	AR122961	AR122961 Sequence
34	59	10.0	1364	6	I28326	I28326 Sequence 3
35	59	10.0	1364	6	I89771	I89771 Sequence 3
36	59	10.0	1560	6	AR091395	AR091395 Sequence
37	59	10.0	1623	6	AR091394	AR091394 Sequence
38	59	10.0	1645	6	A92078	A92078 Sequence 2
39	59	10.0	6139	6	AR091393	AR091393 Sequence
40	59	10.0	11792	9	AF404773	AF404773 Homo sapi
41	59	10.0	157079	9	AC010370	AC010370 Homo sapi
42	59	10.0	176108	9	AC026118	AC026118 Homo sapi
c 43	59	10.0	275547	2	AC129109	AC129109 Homo sapi
44	56	9.5	669	6	AX076201	AX076201 Sequence
45	56	9.5	669	6	AX076483	AX076483 Sequence

ALIGNMENTS

RESULT 1
AR151072
LOCUS AR151072 669 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 12 from patent US 6231850.
ACCESSION AR151072
VERSION AR151072.1 GI:15117122
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 669)
AUTHORS Okano,F., Satoh,M. and Yamada,K.
TITLE Canine interleukin 12
JOURNAL Patent: US 6231850-A 12 15-MAY-2001;
FEATURES Location/Qualifiers

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                     /organism="unknown"
BASE COUNT      185 a    177 c    144 g    163 t
ORIGIN

  Query Match             95.9%;  Score 567;  DB 6;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-313;
  Matches  567;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          25 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         100 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 159

Qy          85 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 144
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         160 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 219

Qy         145 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 204
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         220 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

Qy         205 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 264
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         280 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 339

Qy         265 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 324
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         340 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 399

Qy         325 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 384
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         400 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 459

Qy         385 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 444
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         460 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 519

Qy         445 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 504
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         520 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 579

Qy         505 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGAT 564
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         580 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGAT 639

Qy         565 AGAATGATGAGTTATCTGAATTCTTCC 591
               ||||||||||||||||||||||||||
Db         640 AGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 2
E15018
LOCUS       E15018                   669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
            FT                   /product='interleukin12 35kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /db_xref="taxon:9616"
BASE COUNT      185 a    177 c    144 g    163 t
ORIGIN

  Query Match             95.9%;  Score 567;  DB 6;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-313;
  Matches  567;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          25 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         100 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 159

Qy          85 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 144
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         160 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 219

Qy         145 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 204
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         220 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

Qy         205 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 264
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         280 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 339

Qy         265 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 324
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         340 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 399

Qy         325 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 384
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         400 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 459

Qy         385 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 444
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         460 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 519

Qy         445 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 504
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         520 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 579

Qy         505 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGAT 564
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         580 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGAT 639

Qy         565 AGAATGATGAGTTATCTGAATTCTTCC 591
               ||||||||||||||||||||||||||
Db         640 AGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 3
AR151062
LOCUS       AR151062                 669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6231850.
ACCESSION   AR151062
VERSION     AR151062.1  GI:15117112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

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REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
BASE COUNT      183 a    178 c    146 g    162 t
ORIGIN

  Query Match             82.6%;  Score 488;  DB 6;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 6.8e-268;
  Matches  538;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          25 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         100 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 159

Qy          85 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 144
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         160 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 219

Qy         145 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 204
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         220 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

Qy         205 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 264
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         280 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 339

Qy         265 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 324
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         340 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 399

Qy         325 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 384
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         400 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 459

Qy         385 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 444
               |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db         460 AGGCAGATCTTTCTGGATCAAAACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTG 519

Qy         445 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 504
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         520 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 579

Qy         505 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGA 563
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         580 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGA 638


RESULT 4
CFU49085
LOCUS       CFU49085                669 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U49085
VERSION     U49085.1  GI:1223905
KEYWORDS    .
SOURCE      Canis familiaris.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis familiaris"
                     /db_xref="taxon:9615"
     CDS             1. .669
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAA92058.1"
                     /db_xref="GI:1223906"
                     /translation="MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHS
                     QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                     LNSS"
BASE COUNT      183 a    177 c    145 g    164 t
ORIGIN

  Query Match             70.9%;  Score 419;  DB 4;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 2.4e-228;
  Matches  469;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         122 CCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGG 181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         197 CCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTGG 256

Qy         182 AGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCT 241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         257 AGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCT 316

Qy         242 CTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGT 301
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         317 CTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGT 376

Qy         302 GCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACG 361
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         377 GCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACG 436

Qy         362 CAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTA 421
               ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db         437 CAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGTTGACAGCTA 496

Qy         422 TCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCC 481
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         497 TCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCC 556

Qy         482 TTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCA 541
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         557 TTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCA 616

Qy         542 GAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
               ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         617 GAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 5
AF054605
LOCUS       AF054605                285 bp    mRNA    linear   MAM 26-JUL-2000
DEFINITION  Felis catus interleukin 12 p35 subunit mRNA, partial cds.
ACCESSION   AF054605
VERSION     AF054605.1  GI:3126818
KEYWORDS    .
SOURCE      Felis catus.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 285)
  AUTHORS   Harley,R., Helps,C.R., Harbour,D.A., Gruffydd-Jones,T.J. and
            Day,M.J.
  TITLE     Cytokine mRNA expression in lesions in cats with chronic
            gingivostomatitis
  JOURNAL   Clin. Diagn. Lab. Immunol. 6 (4), 471-478 (1999)
  MEDLINE   99322318
   PUBMED   10391845
REFERENCE   2  (bases 1 to 285)
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  AUTHORS   Harley,R., Helps,C.R., Gruffydd-Jones,T.J., Day,M.J. and
            Harbour,D.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (19-MAR-1998) Clinical Veterinary Science, University of
            Bristol, Langford House, Langford, Bristol BS40 7DU, U.K.
FEATURES             Location/Qualifiers
     source          1. .285
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
                     /cell_line="FL4"
                     /cell_type="T cell"
                     /note="persistant FIV infection"
     CDS             <1. .>285
                     /codon_start=3
                     /product="interleukin 12 p35 subunit"
                     /protein_id="AAC15978.1"
                     /db_xref="GI:3126819"
                     /translation="LLRAISNTLHKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLP
                     LELTMNESCLASREISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVE"
BASE COUNT       84 a     70 c     64 g     67 t
ORIGIN

  Query Match             13.7%;  Score 81;  DB 4;  Length 285;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        102 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 161

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        162 CTGGCTTCCAGAGAGATCTCT 182


RESULT 6
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
  MEDLINE   98182592
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
     CDS             1. .669
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAB93836.1"
                     /db_xref="GI:2735053"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNSS"
BASE COUNT      191 a    179 c    137 g    162 t
ORIGIN

  Query Match             13.7%;  Score 81;  DB 4;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 7
FCIL12P35
LOCUS       FCIL12P35               669 bp    mRNA    linear   MAM 13-MAY-1997
DEFINITION  F.catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      cat.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
  MEDLINE   97246745
   PUBMED   9089110
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .669
                     /gene="IL-12.p35"
     CDS             1. .669
                     /gene="IL-12.p35"
                     /function="heterodimer with IL-12 p40 chain"
                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
                     /db_xref="SWISS-PROT:O02743"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNAS"
BASE COUNT      190 a    178 c    139 g    162 t
ORIGIN

  Query Match             13.7%;  Score 81;  DB 4;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-34;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297
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Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 8
AX154613
LOCUS       AX154613                 666 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 17 from Patent WO0140257.
ACCESSION   AX154613
VERSION     AX154613.1  GI:14536188
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 17 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      186 a    179 c    141 g    160 t
ORIGIN

  Query Match            12.7%;  Score 75;  DB 6;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 3.6e-31;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        297 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCAT 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCAT 428

Qy        357 GAACGCAAAGCTTTT 371
              |||||||||||||||
Db        429 GAACGCAAAGCTTTT 443


RESULT 9
AX154612
LOCUS       AX154612                 666 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 16 from Patent WO0140257.
ACCESSION   AX154612
VERSION     AX154612.1  GI:14536187
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 666)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 16 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .666
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      186 a    181 c    141 g    158 t
ORIGIN

  Query Match            11.2%;  Score 66;  DB 6;  Length 666;
  Best Local Similarity  100.0%;  Pred. No. 5.2e-26;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        306 TAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAA 365
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 TAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAA 437

Qy        366 GCTTTT 371
              ||||||
Db        438 GCTTTT 443


RESULT 10
AX154615
LOCUS       AX154615                 660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 19 from Patent WO0140257.
ACCESSION   AX154615
VERSION     AX154615.1  GI:14536190
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 19 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      182 a    178 c    142 g    158 t
ORIGIN

  Query Match            10.5%;  Score 62;  DB 6;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 1e-23;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGT 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGT 615

Qy        550 GC 551
              ||
Db        616 GC 617


RESULT 11
AX154616
LOCUS       AX154616                 660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 20 from Patent WO0140257.
ACCESSION   AX154616
VERSION     AX154616.1  GI:14536191
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 20 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      190 a    171 c    137 g    162 t
ORIGIN

  Query Match            10.5%;  Score 62;  DB 6;  Length 660;
  Best Local Similarity  100.0%;  Pred. No. 1e-23;
  Matches   62;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGT 549
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGT 615

Qy        550 GC 551
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```
              ||
Db        616 GC 617


RESULT 12
AR008951
LOCUS       AR008951                660 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 3 from patent US 5756085.
ACCESSION   AR008951
VERSION     AR008951.1  GI:3967756
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Sykes,M. and Wolf,S.F.
  TITLE     Use of interleukin-12 to prevent graft versus host disease
  JOURNAL   Patent: US 5756085-A 3 26-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="unknown"
BASE COUNT      188 a    164 c    139 g    169 t
ORIGIN

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Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 614


RESULT 13
AX154614
LOCUS       AX154614                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 18 from Patent WO0140257.
ACCESSION   AX154614
VERSION     AX154614.1  GI:14536189
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 18 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
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Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
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Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 614


RESULT 14
AX154617
LOCUS       AX154617                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 21 from Patent WO0140257.
ACCESSION   AX154617
VERSION     AX154617.1  GI:14536192
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 21 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
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                     /note="Synthetic Sequence"
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ORIGIN

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  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 614


RESULT 15
AX154618
LOCUS       AX154618                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 22 from Patent WO0140257.
ACCESSION   AX154618
VERSION     AX154618.1  GI:14536193
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
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                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    173 c    136 g    162 t
ORIGIN

  Query Match             10.0%;  Score 59;  DB 6;  Length 660;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-22;
  Matches   59;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        490 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 548
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCG 614


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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 06:46:54 ; Search time 152.092 Seconds
(without alignments)
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Perfect score: 591
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 2185239 seqs, 1125999159 residues

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	591	100.0	591	20	AAX18179	Canine mature CLAF
2	591	100.0	669	20	AAX35626	Nucleic acid encod
3	591	100.0	669	20	AAX03163	Nucleic acid encod
4	591	100.0	669	22	AAI64389	Canine coding sequ
5	591	100.0	1282	20	AAX18178	Canine full length
6	567	95.9	669	19	AAV13819	Canine IL-12 P35 s
7	488	82.6	669	19	AAV13818	Canine IL-12 P35 s
8	488	82.6	669	20	AAX35616	Nucleic acid encod
9	488	82.6	669	20	AAX03153	Nucleic acid encod
10	488	82.6	669	22	AAI64379	Canine coding sequ
11	81	13.7	591	19	AAV56629	Feline FLAFp35 cDN
12	81	13.7	679	22	AAF26097	Feline fil12p35a D
13	81	13.7	1441	19	AAV56628	Feline FLAFp35 cDN
14	75	12.7	666	22	AAD15212	Modified human cyt
15	66	11.2	666	22	AAD15211	Modified human cyt
16	62	10.5	660	22	AAD15214	Modified human cyt
17	62	10.5	660	22	AAD15215	Modified human cyt
18	59	10.0	660	16	AAQ97485	Human interleukin-
19	59	10.0	660	19	AAV07274	Human Interleukin-
20	59	10.0	660	19	AAV07218	DNA encoding human
21	59	10.0	660	20	AAZ40407	Human interleukin
22	59	10.0	660	22	AAD15213	Modified human cyt
23	59	10.0	660	22	AAD15216	Modified human cyt
24	59	10.0	660	22	AAD15217	Modified human cyt
25	59	10.0	660	22	AAD15218	Modified human cyt
26	59	10.0	660	22	AAD15220	Modified human cyt
27	59	10.0	660	22	AAD15221	Human cytokine p35
28	59	10.0	689	19	AAV56641	Feline FLAFp35 DNA
29	59	10.0	721	15	AAQ67880	EPV 42 kD promoter
30	59	10.0	721	20	AAZ08515	Vaccinia E3L/human
31	59	10.0	762	20	AAV83207	Interleukin (IL)-1
32	59	10.0	762	21	AAF21323	Human low adenosin
33	59	10.0	762	21	AAA35201	Human adenosine re
34	59	10.0	856	12	AAQ12150	Cytotoxic lymphocy
35	59	10.0	856	18	AAT77850	35 kDa subunit of
36	59	10.0	856	18	AAV00402	35 kDa subunit of
37	59	10.0	856	18	AAT97970	35 kDa subunit of
38	59	10.0	856	19	AAV37772	Cytotoxic lymphocy
39	59	10.0	1026	21	AAZ40020	Human p35 coding s
40	59	10.0	1287	22	AAF76882	DNA encoding fusio
41	59	10.0	1316	18	AAT63621	Interleukin-12 p35
42	59	10.0	1364	17	AAT48099	Human interleukin-
43	59	10.0	1364	19	AAV42536	Human interleukin-
44	59	10.0	1364	19	AAV15228	Heterodimeric huma
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ALIGNMENTS

RESULT 1
AAX18179
ID AAX18179 standard; cDNA; 591 BP.
XX
AC AAX18179;
XX
DT 07-MAY-1999 (first entry)
XX
DE Canine mature CLAF p35 subunit coding sequence.
XX
KW CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis; ds.
XX
OS Canis sp.
XX
PN WO9855511-A1.
XX
PD 10-DEC-1998.
XX
PF 26-MAY-1998; 98WO-JP02295.
XX
PR 03-JUN-1997; 97JP-0161936.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Eda Y, Imamura T, Maeda H, Tokiyoshi S;
XX
DR WPI; 1999-070260/06.
DR P-PSDB; AAW74325.
XX
PT Canine cytokine protein which activates canine cytotoxic T

PT lymphocytes - is useful for treatment of viral and autoimmune
PT diseases in dogs
XX
PS Claim 8; Page 34-35; 51pp; Japanese.
XX
CC This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC recognising it may be used in the treatment of viral diseases in dogs
CC (such as canine distemper, canine parvovirus and canine infectious
CC hepatitis). The antibodies may also be used in isolation of CLAF from
CC culture of the transformant host cells by affinity chromatography. The
CC p40 homodimer can be used for the treatment of autoimmune diseases in
CC dogs.
XX
SQ Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 other;

Query Match 100.0%; Score 591; DB 20; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.6e-280;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Db         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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RESULT 2
AAX35626
ID AAX35626 standard; cDNA to mRNA; 669 BP.
XX
AC AAX35626;
XX
DT 09-JUL-1999 (first entry)
XX
DE Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1..669
FT /*tag= a
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-308068/26.
DR P-PSDB; AAY02343.
XX
PT A prevention and treating agent containing interleukin 12 (CaIL12) -
PT for prevention and treatment of dog and cat immune diseases
XX
PS Claim 1; Page 15-16; 16pp; Japanese.
XX
CC The present sequence encodes canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment
CC of dog and cat immune diseases. The treatment used an agent comprising
CC dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC useful for preventing and treating dog and cat immune diseases,
CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.
XX
SQ Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

Query Match 100.0%; Score 591; DB 20; Length 669;
Best Local Similarity 100.0%; Pred. No. 2.6e-280;
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555
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Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 3
AAX03163
ID   AAX03163 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03163;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84374.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

  Query Match             100.0%;  Score 591;  DB 20;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 2.6e-280;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 4
AAI64389
ID   AAI64389 standard; DNA; 669 BP.
XX
AC   AAI64389;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #4.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= "Canine protein #4"
FT   sig_peptide     1..75
FT                   /*tag=  b
FT   mat_peptide     76..666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
```

```
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66483.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian -
XX
PS   Claim 6; Page 18; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

  Query Match            100.0%;  Score 591;  DB 22;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 2.6e-280;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 5
AAX18178
ID   AAX18178 standard; cDNA; 1282 BP.
XX
AC   AAX18178;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74324.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 33-34; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 other;

  Query Match            100.0%;  Score 591;  DB 20;  Length 1282;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-280;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 200

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 260

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 320

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 380

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 440

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 500

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 560
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Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 620

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 680

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 731


RESULT 6
AAV13819
ID   AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13819;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41793.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 11; Pages 11-12; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 other;

  Query Match             95.9%;  Score 567;  DB 19;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-268;
  Matches  567;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         25 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 159

Qy         85 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 219

Qy        145 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

Qy        205 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 339

Qy        265 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 399

Qy        325 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 459

Qy        385 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 444
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        460 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 519

Qy        445 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 504
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 579

Qy        505 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGAT 564
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGAT 639

Qy        565 AGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||||||||||
Db        640 AGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 7
AAV13818
ID   AAV13818 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13818;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41792.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
```

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PT   activities are expected
XX
PS   Claim 9; Page 9; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             82.6%;  Score 488;  DB 19;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 1e-229;
  Matches  538;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         25 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 159

Qy         85 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 144
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 219

Qy        145 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 204
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

Qy        205 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 264
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 339

Qy        265 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 324
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 399

Qy        325 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 384
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 459

Qy        385 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 444
               |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        460 AGGCAGATCTTTCTGGATCAAAACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTG 519

Qy        445 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 504
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 579

Qy        505 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGA 563
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGA 638


RESULT 8
AAX35616
ID   AAX35616 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35616;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02340.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 13; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             82.6%;  Score 488;  DB 20;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 1e-229;
  Matches  538;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         25 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 84
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 159

Qy         85 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 144
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 219

Qy        145 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 204
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

Qy        205 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 264
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 339

Qy        265 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 324
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 399

Qy        325 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 384
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 459

Qy        385 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 444
               |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        460 AGGCAGATCTTTCTGGATCAAAACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTG 519

Qy        445 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 504
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 579

Qy        505 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGA 563
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGA 638


RESULT 9
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```
AAX03153
ID   AAX03153 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03153;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84372.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 26-27; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             82.6%;  Score 488;  DB 20;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 1e-229;
  Matches  538;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         25 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 159

Qy         85 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 219

Qy        145 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

Qy        205 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 339

Qy        265 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 399

Qy        325 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 459

Qy        385 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 444
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        460 AGGCAGATCTTTCTGGATCAAAACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTG 519

Qy        445 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 504
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 579

Qy        505 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGA 563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGA 638


RESULT 10
AAI64379
ID   AAI64379 standard; DNA; 669 BP.
XX
AC   AAI64379;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= "Canine protein #2"
FT   sig_peptide     1..75
FT                   /*tag= b
FT   mat_peptide     76..666
FT                   /*tag= c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66481.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Claim 6; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
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CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             82.6%;  Score 488;  DB 22;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 1e-229;
  Matches  538;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         25 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        100 AGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAAAACCTGCTGAGAGCCGTCAGCAAC 159

Qy         85 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        160 ACGCTTCAGAAGGCCAGACAAACTCTAGAATTATATTCCTGCACTTCCGAAGAGATTGAT 219

Qy        145 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        220 CATGAAGATATCACAAAGGATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTA 279

Qy        205 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 264
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        280 ACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATCTCTTTGATAACTAACGGGAGTTGC 339

Qy        265 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 324
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        340 CTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTGTGCCTTAGCAGCATCTATGAGGAC 399

Qy        325 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 384
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        400 TTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAAGCTTTTAATGGATCCCAAG 459

Qy        385 AGGCAGATCTTTCTGGATCAAAACATGCTGACAGCTATCGATGAGCTGTTACAGGCCCTG 444
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        460 AGGCAGATCTTTCTGGATCAAAACATGCTGACGGCTATCGATGAGCTGTTACAGGCCCTG 519

Qy        445 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 504
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        520 AATTTCAACAGTGTGACTGTGCCACAGAAATCCTCCCTTGAAGAGCCGGATTTTTATAAA 579

Qy        505 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGA 563
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        580 ACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTCAGAATTCGTGCGGTGACCATCGA 638


RESULT 11
AAV56629
ID   AAV56629 standard; cDNA; 591 BP.
XX
AC   AAV56629;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA mature transcript.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76176.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 23; Page 59; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp35.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus.
XX
SQ   Sequence 591 BP; 179 A; 151 C; 120 G; 141 T; 0 other;

  Query Match             13.7%;  Score 81;  DB 19;  Length 591;
  Best Local Similarity   100.0%;  Pred. No. 9.9e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        223 CTGGCTTCCAGAGAGATCTCT 243


RESULT 12
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02263.
XX
PR   08-JUL-1999;   99CH-0001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs -
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
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CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 other;

  Query Match             13.7%;  Score 81;  DB 22;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 9.8e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        238 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 297

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        298 CTGGCTTCCAGAGAGATCTCT 318


RESULT 13
AAV56628
ID   AAV56628 standard; cDNA; 1441 BP.
XX
AC   AAV56628;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             133..811
FT                   /*tag=  a
FT   sig_peptide     133..217
FT                   /*tag=  b
FT   mat_peptide     218..808
FT                   /*tag=  c
FT                   /product= "FLAFp35"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 other;

  Query Match             13.7%;  Score 81;  DB 19;  Length 1441;
  Best Local Similarity   100.0%;  Pred. No. 9.5e-30;
  Matches   81;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        163 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 222
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        380 GATAAAACCAGCACAGTGGAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGC 439

Qy        223 CTGGCTTCCAGAGAGATCTCT 243
              |||||||||||||||||||||
Db        440 CTGGCTTCCAGAGAGATCTCT 460


RESULT 14
AAD15212
ID   AAD15212 standard; DNA; 666 BP.
XX
AC   AAD15212;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-146.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..666
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1..75
FT                   /*tag=  b
FT   mat_peptide     76..663
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08605.
XX
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```
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 87; Page 139; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA.
XX
SQ   Sequence 666 BP; 186 A; 179 C; 141 G; 160 T; 0 other;

  Query Match             12.7%;  Score 75;  DB 22;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 8.7e-27;
  Matches   75;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        297 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCAT 356
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 CCTGTGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCAT 428

Qy        357 GAACGCAAAGCTTTT 371
              |||||||||||||||
Db        429 GAACGCAAAGCTTTT 443


RESULT 15
AAD15211
ID   AAD15211 standard; DNA; 666 BP.
XX
AC   AAD15211;
XX
DT   01-NOV-2001  (first entry)
XX
DE   Modified human cytokine p35 encoding DNA from clone R2-42.
XX
KW   Cytokine; T-cell; interferon-gamma; IFN-gamma; bacterial infection;
KW   AIDS; diabetic retinopathy; cancer; vaccine; cell-mediated immunity;
KW   human; p35; mutant; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..666
FT                   /*tag=  a
FT                   /product= "Modified p35 protein precursor"
FT   sig_peptide     1..75
FT                   /*tag=  b
FT   mat_peptide     76..663
FT                   /*tag=  c
FT                   /product= "Mature modified p35 protein"
XX
PN   WO200140257-A2.
XX
PD   07-JUN-2001.
XX
PF   30-NOV-2000; 2000WO-US32664.
XX
PR   02-DEC-1999;   99US-0169035.
PR   28-NOV-2000; 2000US-0169035.
XX
PA   (MAXY-) MAXYGEN INC.
XX
PI   Leong SR,  Punnonen J;
XX
DR   WPI; 2001-502381/55.
DR   P-PSDB; AAE08604.
XX
PT   Nucleic acids encoding modified cytokine polypeptides (i.e. modified
PT   p40 and p35 polypeptides), useful for treating various diseases e.g.
PT   diabetic retinopathy and cancer -
XX
PS   Claim 87; Page 139; 223pp; English.
XX
CC   The invention relates to nucleic acids encoding modified cytokine
CC   polypeptides (i.e. modified p40 and p35 polypeptides). The modified
CC   cytokine polypeptides have T-cell proliferative and interferon (IFN)-
CC   gamma induction activities. The polypeptides and polynucleotides of the
CC   invention are useful for treating various diseases e.g. bacterial
CC   infections, AIDS, diabetic retinopathy and cancer. The polypeptide and
CC   polynucleotide may also be useful as a vaccine adjuvant, to enhance a
CC   vaccinated host's cell-mediated immunity for protective response to a
CC   pathogen. The present sequence is a modified human p35 protein encoding
CC   DNA.
XX
SQ   Sequence 666 BP; 186 A; 181 C; 141 G; 158 T; 0 other;

  Query Match             11.2%;  Score 66;  DB 22;  Length 666;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-22;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        306 TAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAA 365
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Db        378 TAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAACGCAAA 437

Qy        366 GCTTTT 371
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Db        438 GCTTTT 443


Search completed: July 16, 2003, 13:41:40
Job time : 152.092 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 16, 2003, 05:27:32 ; Search time 1674.13 Seconds
(without alignments)
10273.834 Million cell updates/sec

Title: US-09-917-265-49
Perfect score: 591
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
3: gb_in:*
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37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	589.4	99.7	669	6	AR151072	AR151072 Sequence
2	589.4	99.7	669	6	E15018	E15018 Canine mRNA
3	583	98.6	669	6	AR151062	AR151062 Sequence
4	579.8	98.1	669	4	CFU49085	U49085 Canis famil
5	535	90.5	669	4	FCU83185	U83185 Felis catus
6	535	90.5	669	4	FCIL12P35	Y07761 F.catus mRN
7	528.6	89.4	669	6	AX076201	AX076201 Sequence
8	528.6	89.4	669	6	AX076483	AX076483 Sequence
9	528.6	89.4	4201	6	AX076477	AX076477 Sequence
10	509.4	86.2	660	6	AX154617	AX154617 Sequence
11	504.6	85.4	660	6	AX154614	AX154614 Sequence
12	504.6	85.4	660	6	AX154621	AX154621 Sequence
13	503	85.1	660	6	AX154618	AX154618 Sequence
14	499.8	84.6	660	6	AX154619	AX154619 Sequence
15	499.8	84.6	660	6	AX154620	AX154620 Sequence
16	498.2	84.3	660	6	AX154615	AX154615 Sequence
17	498.2	84.3	660	6	AX154616	AX154616 Sequence
18	487	82.4	660	6	AR008951	AR008951 Sequence
19	487	82.4	660	6	I28592	I28592 Sequence 3
20	487	82.4	762	9	AF101062	AF101062 Homo sapi
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22	487	82.4	1316	6	AR050785	AR050785 Sequence
23	487	82.4	1316	6	AR212036	AR212036 Sequence
24	487	82.4	1316	9	HUMNKSFP35	M65291 Human natur
25	487	82.4	1364	6	AR082685	AR082685 Sequence
26	487	82.4	1364	6	AR122961	AR122961 Sequence
27	487	82.4	1364	6	I28326	I28326 Sequence 3
28	487	82.4	1364	6	I89771	I89771 Sequence 3
29	487	82.4	1426	4	PIGIL12PSU	L35765 Sus scrofa
30	485.4	82.1	666	6	AX154612	AX154612 Sequence
31	485.4	82.1	1645	6	A92078	A92078 Sequence 2
32	483.8	81.9	660	6	AX154634	AX154634 Sequence
33	483.8	81.9	660	6	BD007071	BD007071 IL-12 gen
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35	483.8	81.9	721	6	AR052862	AR052862 Sequence
36	483.8	81.9	1026	6	AR091390	AR091390 Sequence
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38	483.8	81.9	1287	6	AX084108	AX084108 Sequence
39	483.8	81.9	1560	6	AR091395	AR091395 Sequence
40	483.8	81.9	1623	6	AR091394	AR091394 Sequence
41	483.8	81.9	6139	6	AR091393	AR091393 Sequence
42	480.6	81.3	666	6	AX154613	AX154613 Sequence
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44	469.4	79.4	669	4	ECIL12P35	Y11130 Equus cabal
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ALIGNMENTS

RESULT 1
AR151072
LOCUS AR151072 669 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 12 from patent US 6231850.
ACCESSION AR151072
VERSION AR151072.1 GI:15117122
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 669)
AUTHORS Okano,F., Satoh,M. and Yamada,K.
TITLE Canine interleukin 12
JOURNAL Patent: US 6231850-A 12 15-MAY-2001;
FEATURES Location/Qualifiers

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     source          1. .669
                     /organism="unknown"
BASE COUNT      185 a    177 c    144 g    163 t
ORIGIN

  Query Match             99.7%;  Score 589.4;  DB 6;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 2e-164;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
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Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 2
E15018
LOCUS       E15018                   669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
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FEATURES             Location/Qualifiers
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BASE COUNT      185 a    177 c    144 g    163 t
ORIGIN

  Query Match             99.7%;  Score 589.4;  DB 6;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 2e-164;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
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Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 3
AR151062
LOCUS       AR151062                 669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6231850.
ACCESSION   AR151062
VERSION     AR151062.1  GI:15117112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
```

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REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
BASE COUNT      183 a    178 c    146 g    162 t
ORIGIN

  Query Match             98.6%;  Score 583;  DB 6;  Length 669;
  Best Local Similarity   99.2%;  Pred. No. 1.6e-162;
  Matches  586;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
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Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db        616 AGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 666


RESULT 4
CFU49085
LOCUS       CFU49085                669 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U49085
VERSION     U49085.1  GI:1223905
KEYWORDS    .
SOURCE      Canis familiaris.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis familiaris"
                     /db_xref="taxon:9615"
     CDS             1. .669
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAA92058.1"
                     /db_xref="GI:1223906"
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                     QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
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                     LNSS"
BASE COUNT      183 a    177 c    145 g    164 t
ORIGIN

  Query Match             98.1%;  Score 579.8;  DB 4;  Length 669;
  Best Local Similarity   98.8%;  Pred. No. 1.4e-161;
  Matches  584;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGATTATATT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
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Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 5
FCU83185
LOCUS       FCU83185                669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus.
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  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
  MEDLINE   98182592
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
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                     /organism="Felis catus"
                     /db_xref="taxon:9685"
     CDS             1. .669
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAB93836.1"
                     /db_xref="GI:2735053"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
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                     LNSS"
BASE COUNT      191 a    179 c    137 g    162 t
ORIGIN

  Query Match             90.5%;  Score 535;  DB 4;  Length 669;
  Best Local Similarity   94.1%;  Pred. No. 3.2e-148;
  Matches  556;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
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Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        556 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 666


RESULT 6
FCIL12P35
LOCUS       FCIL12P35               669 bp    mRNA    linear   MAM 13-MAY-1997
DEFINITION  F.catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      cat.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
  MEDLINE   97246745
   PUBMED   9089110
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
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                     /gene="IL-12.p35"
     CDS             1. .669
                     /gene="IL-12.p35"
                     /function="heterodimer with IL-12 p40 chain"
                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
                     /db_xref="SWISS-PROT:O02743"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
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                     LNAS"
BASE COUNT      190 a    178 c    139 g    162 t
ORIGIN

  Query Match             90.5%;  Score 535;  DB 4;  Length 669;
  Best Local Similarity   94.1%;  Pred. No. 3.2e-148;
  Matches  556;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

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Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
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Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 7
AX076201
LOCUS       AX076201                669 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104155.
ACCESSION   AX076201
VERSION     AX076201.1  GI:12710826
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p35"
BASE COUNT      189 a    179 c    140 g    161 t
ORIGIN

  Query Match             89.4%;  Score 528.6;  DB 6;  Length 669;
  Best Local Similarity   93.4%;  Pred. No. 2.6e-146;
  Matches  552;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
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Db        496 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 8
AX076483
LOCUS       AX076483                669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
BASE COUNT      189 a    179 c    140 g    161 t
ORIGIN

  Query Match             89.4%;  Score 528.6;  DB 6;  Length 669;
  Best Local Similarity   93.4%;  Pred. No. 2.6e-146;
  Matches  552;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375
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Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| |||||||||| || ||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || ||||||||| | ||||||||||||||||||||||||||||||||||||| ||||||
Db        496 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||| ||||| ||||||||| |||||||||||| ||||||||| |||||
Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666


RESULT 9
AX076477
LOCUS       AX076477               4201 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104280.
ACCESSION   AX076477
VERSION     AX076477.1  GI:12711029
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 4201)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4201
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="IL-12p35 (pMOLfIL-12p35 (e-,_e31-)clone61)"
BASE COUNT     1086 a   1055 c    999 g   1061 t
ORIGIN

  Query Match            89.4%;  Score 528.6;  DB 6;  Length 4201;
  Best Local Similarity  93.4%;  Pred. No. 3.1e-146;
  Matches  552;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Db       3122 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 3181

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
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Db       3182 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 3241

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
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Db       3242 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 3301

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
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Db       3302 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 3361

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
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Db       3362 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 3421

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db       3422 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 3481

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
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Db       3482 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 3541

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
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Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db       3662 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 3712


RESULT 10
AX154617
LOCUS       AX154617               660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 21 from Patent WO0140257.
ACCESSION   AX154617
VERSION     AX154617.1  GI:14536192
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 21 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      184 a    172 c    141 g    163 t
ORIGIN

  Query Match            86.2%;  Score 509.4;  DB 6;  Length 660;
  Best Local Similarity  91.4%;  Pred. No. 1.4e-140;
  Matches  540;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   ||||||||| ||||  |||||  ||||||||||
Db         67 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||||| |||||||||||| ||| ||||||||||||||||||||||||| ||
Db        127 AACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAAACTCTAGAATTTTAC 186

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        187 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||||||||||| ||| ||||||||||||||||||||||||| ||||
Db        247 GAGGCCTGTTTACCACTGGAATTAGCCACGAATGAGAGTTGCCTGGCTTCCAGAGGGATC 306

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||| |||||||||| |||||||||| |||||  ||||| |||||||||||||  ||||
Db        307 TCTCTGATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 366

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||| |||| ||||||||||||||||||||||||||||| |||| ||||||| |||||||
Db        367 TGCCTTGGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 426

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | ||| |||| ||||||||||||||||||||||||||||||||||||||
Db        427 GCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 486
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Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || ||||||||||||||||||||||||||||||||||| |||||||||||| |||||||||
Db        487 ATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 546

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||||||| |||||||||||||| ||||||||||||||
Db        607 AGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 657


RESULT 11
AX154614
LOCUS       AX154614                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 18 from Patent WO0140257.
ACCESSION   AX154614
VERSION     AX154614.1  GI:14536189
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 18 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    172 c    136 g    163 t
ORIGIN

  Query Match             85.4%;  Score 504.6;  DB 6;  Length 660;
  Best Local Similarity   90.9%;  Pred. No. 3.7e-139;
  Matches  537;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | ||||||    ||| | ||  ||||||||||| ||||  |||||  ||||||||||||
Db         67 AGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||||| |||||||||||||| ||| |||||||||||||||||||||||||| ||
Db        127 AACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAAACTCTAGAATTTTAC 186

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        187 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||||||||||||||||||| || ||||||||||||||   ||||||||||
Db        247 GAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACT 306

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| |||||||||| ||||| ||||| ||||||||||||   ||||
Db        307 TCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTG 366

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        367 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 426

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | ||| |||| ||||||||||||||||||||||||||||||||||||||
Db        427 GCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 486

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || ||||||||||||||||||||||||||||||||||| |||||||||||| |||||||||
Db        487 ATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 546

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||||||| |||||||||||||| ||||||||||||||
Db        607 AGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 657


RESULT 12
AX154621
LOCUS       AX154621                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 25 from Patent WO0140257.
ACCESSION   AX154621
VERSION     AX154621.1  GI:14536196
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 25 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    172 c    136 g    163 t
ORIGIN

  Query Match             85.4%;  Score 504.6;  DB 6;  Length 660;
  Best Local Similarity   90.9%;  Pred. No. 3.7e-139;
  Matches  537;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | ||||||    ||| | ||  ||||||||||| ||||  |||||  ||||||||||||
Db         67 AGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||||| |||||||||||||| ||| |||||||||||||||||||||||||| ||
Db        127 AACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAAACTCTAGAATTTTAC 186

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        187 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||||||||||||||||||| || ||||||||||||||   ||||||||||
Db        247 GAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACT 306

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| |||||||||| ||||| ||||| ||||||||||||   ||||
Db        307 TCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTG 366

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||||| |||||||||||||||||||||||||| |||| |||||| |||||||
Db        367 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 426

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||| | ||| |||| ||||||||||||||||||||||||||||||||||||||
Db        427 GCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 486

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || ||||||||||||||||||||||||||||||||||| |||||||||||| |||||||||
Db        487 ATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 546

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||||||| |||||||||||||| ||||||||||||||
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Db        607 AGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 657


RESULT 13
AX154618
LOCUS       AX154618                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 22 from Patent WO0140257.
ACCESSION   AX154618
VERSION     AX154618.1  GI:14536193
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    173 c    136 g    162 t
ORIGIN

  Query Match             85.1%;  Score 503;  DB 6;  Length 660;
  Best Local Similarity   90.7%;  Pred. No. 1.1e-138;
  Matches  536;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | ||||||    ||| | ||  |||||||||| ||||  |||||  ||||||||||
Db         67 AGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||| |||||||||||| ||| |||||||||||||||||||||||||| ||
Db        127 AACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAAACTCTAGAATTTTAC 186

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||| |||||||||||||||||| ||||||||||||||||||
Db        187 TCCTGCACTTCCGAAGAGACTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||||||||||||||||||| || ||||||||||||||   ||||||||||
Db        247 GAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACT 306

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||| |||||||| |||||||||||| |||||  ||||| ||||||||||||   ||||
Db        307 TCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTG 366

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||||||  |||||||||||||||||||||||||||||| |||| |||||| |||||||
Db        367 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 426

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| | ||| |||| ||||||||||||||||||||||||||||||||||||||||
Db        427 GCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 486

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||||||||||||||||||||||||||| |||||||||||| |||||||||
Db        487 ATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 546

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db        607 AGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 657


RESULT 14
AX154619
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LOCUS       AX154619                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 23 from Patent WO0140257.
ACCESSION   AX154619
VERSION     AX154619.1  GI:14536194
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 23 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      182 a    180 c    144 g    154 t
ORIGIN

  Query Match             84.6%;  Score 499.8;  DB 6;  Length 660;
  Best Local Similarity   90.4%;  Pred. No. 9.9e-138;
  Matches  534;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
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Db         67 AGAAACCTCCCCGTGGCCACCCCAGGCCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||| |||||||||||| |||||||||| |||||| |||||||| ||
Db        127 AACCTGCTGAGGGCTGTCAGCAACACGCTCCAGAAGGCCAAACAAACCCTAGAATTTTAC 186

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        187 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||||||||||||| ||| |||||||||||||||||||||||||| ||||
Db        247 GAGGCCTGTTTACCACTGGAATTAGCCACGAATGAGAGTTGCCTGGCTTCCAGAGGGATC 306

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||| |||||||||| ||||||||||||||||  ||||| ||||||||||||   ||||
Db        307 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACAACCCTG 366

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
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Db        367 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 426

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| |||||||||||| || |||||||||||||||||||||||||||||| |||||
Db        427 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGGCAGCT 486

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || | ||||||   | |||||||||||| |||||||| ||||| ||||||  |||||||||
Db        487 ATTGCTGAGCTAATGCAGGCCCTGAATGTCAACAGTGAGACTGCGCCACAAAAATCCTCC 546

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              || ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||| || ||||||||| |||||||||||| ||||||||||||||
Db        607 AGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 657


RESULT 15
AX154620
LOCUS       AX154620                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 24 from Patent WO0140257.
ACCESSION   AX154620
VERSION     AX154620.1  GI:14536195
KEYWORDS    .
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SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 24 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      181 a    178 c    144 g    157 t
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Query Match 84.6%; Score 499.8; DB 6; Length 660;
Best Local Similarity 90.4%; Pred. No. 9.9e-138;
Matches 534; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

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Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              || | |||||||   ||| | ||   |||||||||| ||||  |||||  ||||||||||| 
Db         67 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              |||||||||| || ||||||||||||| |||||||||| ||||||  |||||||| || 
Db        127 AACCTGCTGAGGGCTGTCAGCAACACGCTCCAGAAGGCCAAACAAACCCTAGAATTTTAC 186

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
               |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||| 
Db        187 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||| |||||||||||||| ||| |||||||||||||||||||||||| |||| 
Db        247 GAGGCCTGTTTACCACTGGAATTAGCCACGAATGAGAGTTGCCTGGCTTCCAGAGGGATC 306

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||| |||||||||| |||||||||||||||||  ||||| ||||||||||||||  |||| 
Db        307 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 366

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||||||||||||||||||||||||||||||||||| |||| |||||||||||||| 
Db        367 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 426

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| || |||||||| || |||||||||||||||||||||||||||||| ||||| 
Db        427 GCAAAGCTGTTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGGCAGCT 486

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || | ||||||  | ||||||||||| |||||||||| ||||| ||||||  |||||||||| 
Db        487 ATTGCTGAGCTAATGCAGGCCCTGAATGTCAACAGTGAGACTGCGCCACAAAAATCCTCC 546

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| |||||||||||||| |||||||||||||||||||||||||||||||| ||| 
Db        547 CTTGAAGAACCGGATTTTTATAAGACTAAAATCAAGCTCTGCATACTTCTTCATGCCTTC 606

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
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Db        607 AGAATTCGTGCAGTGACCATCGATAGAATGATGAGCTATCTGAATTCTTCC 657
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OM nucleic - nucleic search, using sw model

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9: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
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15: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1994.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
24: /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	591	100.0	591	20	AAX18179	Canine mature CLAF
2	591	100.0	669	20	AAX35626	Nucleic acid encod
3	591	100.0	669	20	AAX03163	Nucleic acid encod
4	591	100.0	669	22	AAI64389	Canine coding sequ
5	591	100.0	1282	20	AAX18178	Canine full length
6	589.4	99.7	669	19	AAV13819	Canine IL-12 P35 s
7	583	98.6	669	19	AAV13818	Canine IL-12 P35 s
8	583	98.6	669	20	AAX35615	Nucleic acid encod
9	583	98.6	669	20	AAX03153	Nucleic acid encod
10	583	98.6	669	22	AAI64379	Canine coding sequ
11	535	90.5	591	19	AAV56629	Feline FLAFp35 cDN
12	535	90.5	1441	19	AAV56628	Feline FLAFp35 cDN
13	530.2	89.7	679	22	AAF26097	Feline fil12p35a D
14	528.6	89.4	669	22	AAF26083	Feline IL-12p35 en
15	528.6	89.4	669	22	AAF26086	Feline IL-12p35 en
16	528.6	89.4	4201	22	AAF26077	Feline IL-12p35 en
17	527	89.2	639	22	AAF26098	Plasmid pMOL-fIL12
18	525.4	88.9	689	19	AAV56641	Feline FLAFp35 DNA
19	509.4	86.2	660	22	AAD15216	Modified human cyt
20	504.6	85.4	660	22	AAD15213	Modified human cyt
21	504.6	85.4	660	22	AAD15220	Modified human cyt
22	503	85.1	660	22	AAD15217	Modified human cyt
23	499.8	84.6	660	22	AAD15218	Modified human cyt
24	499.8	84.6	660	22	AAD15219	Modified human cyt
25	498.2	84.3	660	22	AAD15214	Modified human cyt
26	498.2	84.3	660	22	AAD15215	Modified human cyt
27	487	82.4	660	16	AAQ97485	Human interleukin-
28	487	82.4	660	19	AAV07218	DNA encoding human
29	487	82.4	762	20	AAV83207	Interleukin (IL)-1
30	487	82.4	762	21	AAF21323	Human low adenosin
31	487	82.4	762	21	AAA35201	Human adenosine re
32	487	82.4	1316	18	AAT63621	Interleukin-12 p35
33	487	82.4	1364	17	AAT48099	Human interleukin-
34	487	82.4	1364	19	AAV42536	Human interleukin-
35	487	82.4	1364	19	AAV15228	Heterodimeric huma
36	487	82.4	1364	21	AAZ28863	Human interleukin-
37	487	82.4	1364	22	AAF56281	IL-12 vaccine adju
38	487	82.4	4521	21	AAF21326	Human low adenosin
39	487	82.4	4521	21	AAA35204	Human adenosine re
40	487	82.4	5686	20	AAZ40415	Plasmid pIN1143 co
41	487	82.4	8578	24	AAD31545	pIRES-hB7-1-IL12.1
42	487	82.4	8578	24	AAD31546	pIRES-hB7-1-IL12.0
43	487	82.4	8608	24	AAD31548	pIRES-hB7-1-IL12.2
44	487	82.4	8623	24	AAD31547	pIRES-hB7-1-IL12.3
45	487	82.4	8629	24	AAD31552	pIRES-IL12.2-hb7-1

ALIGNMENTS

RESULT 1
AAX18179
ID AAX18179 standard; cDNA; 591 BP.
XX
AC AAX18179;
XX
DT 07-MAY-1999 (first entry)
XX
DE Canine mature CLAF p35 subunit coding sequence.
XX
KW CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis; ds.
XX
OS Canis sp.
XX
PN WO9855511-A1.
XX
PD 10-DEC-1998.
XX
PF 26-MAY-1998; 98WO-JP02295.
XX
PR 03-JUN-1997; 97JP-0161936.
XX
PA (KAGA) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI Eda Y, Imamura T, Maeda H, Tokiyoshi S;
XX
DR WPI; 1999-070260/06.
DR P-PSDB; AAW74325.
XX
PT Canine cytokine protein which activates canine cytotoxic T

```
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 34-35; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 other;

  Query Match           100.0%;  Score 591;  DB 20;  Length 591;
  Best Local Similarity  100.0%;  Pred. No. 1e-175;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591


RESULT 2
AAX35626
ID   AAX35626 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35626;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02343.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 15-16; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

  Query Match           100.0%;  Score 591;  DB 20;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-175;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555
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Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 3
AAX03163
ID   AAX03163 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03163;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84374.
XX
PT   New therapeutic and prophylactic agents - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

  Query Match             100.0%;  Score 591;  DB 20;  Length 669;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-175;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 4
AAI64389
ID   AAI64389 standard; DNA; 669 BP.
XX
AC   AAI64389;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #4.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= "Canine protein #4"
FT   sig_peptide     1..75
FT                   /*tag= b
FT   mat_peptide     76..666
FT                   /*tag= c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
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XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66483.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian -
XX
PS   Claim 6; Page 18; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

  Query Match            100.0%;  Score 591;  DB 22;  Length 669;
  Best Local Similarity  100.0%;  Pred. No. 1.1e-175;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 5
AAX18178
ID   AAX18178 standard; cDNA; 1282 BP.
XX
AC   AAX18178;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74324.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 33-34; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 other;

  Query Match            100.0%;  Score 591;  DB 20;  Length 1282;
  Best Local Similarity  100.0%;  Pred. No. 1.5e-175;
  Matches  591;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 200

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 260

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 320

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 380

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 440

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 500

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 560
```

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Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 620

Qy        481 CTTGAAGAGCCGGATTTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 CTTGAAGAGCCGGATTTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 680

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 731


RESULT 6
AAV13819
ID   AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13819;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41793.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 11; Pages 11-12; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 other;

  Query Match             99.7%;  Score 589.4;  DB 19;  Length 669;
  Best Local Similarity   99.8%;  Pred. No. 3.4e-175;
  Matches  590;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666


RESULT 7
AAV13818
ID   AAV13818 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13818;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41792.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
```

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PT   activities are expected
XX
PS   Claim 9; Page 9; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             98.6%;  Score 583;  DB 19;  Length 669;
  Best Local Similarity   99.2%;  Pred. No. 3.5e-173;
  Matches  586;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||||| |||||||||| ||||||| |||||||
Db        616 AGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 666


RESULT 8
AAX35616
ID   AAX35616 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35616;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02340.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 13; 16pp; Japanese.
XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             98.6%;  Score 583;  DB 20;  Length 669;
  Best Local Similarity   99.2%;  Pred. No. 3.5e-173;
  Matches  586;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||||||| |||||||||| ||||||| |||||||
Db        616 AGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 666


RESULT 9
AAX03153
ID   AAX03153 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03153;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84372.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 26-27; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match            98.6%;  Score 583;  DB 20;  Length 669;
  Best Local Similarity  99.2%;  Pred. No. 3.5e-173;
  Matches  586;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||||| |||||||||| ||||||| |||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||||||| |||||||||| ||||||| |||||||
Db        616 AGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 666


RESULT 10
AAI64379
ID   AAI64379 standard; DNA; 669 BP.
XX
AC   AAI64379;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= "Canine protein #2"
FT   sig_peptide     1..75
FT                   /*tag=  b
FT   mat_peptide     76..666
FT                   /*tag=  c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
```

```
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66481.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian -
XX
PS   Claim 6; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

  Query Match             98.6%;  Score 583;  DB 22;  Length 669;
  Best Local Similarity   99.2%;  Pred. No. 3.5e-173;
  Matches  586;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              ||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||||||||||||||||||| |||||||||| ||||||| |||||||
Db        616 AGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 666


RESULT 11
AAV56629
ID   AAV56629 standard; cDNA; 591 BP.
XX
AC   AAV56629;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA mature transcript.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76176.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 23; Page 59; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp35.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus.
XX
SQ   Sequence 591 BP; 179 A; 151 C; 120 G; 141 T; 0 other;

  Query Match             90.5%;  Score 535;  DB 19;  Length 591;
  Best Local Similarity   94.1%;  Pred. No. 4.4e-158;
  Matches  556;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              |||| |||||||||| || |||| |||||||||| |||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | ||||||| ||||| ||||||||||||||||||||||||||||||||||||| ||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||| |||||||||| ||||||||||||||||  ||||| ||||||||||||||  ||||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||||| |||||||||||||||||||||||||||| |||| ||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| |||||||||| || ||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||||||||||||||||| |||||||||||||||||||||| ||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
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              || ||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||| |||||||| |||||||||||| || ||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591


RESULT 12
AAV56628
ID   AAV56628 standard; cDNA; 1441 BP.
XX
AC   AAV56628;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             133..811
FT                   /*tag=  a
FT   sig_peptide     133..217
FT                   /*tag=  b
FT   mat_peptide     218..808
FT                   /*tag=  c
FT                   /product= "FLAFp35"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 other;

  Query Match           90.5%;  Score 535;  DB 19;  Length 1441;
  Best Local Similarity  94.1%;  Pred. No. 6.9e-158;
  Matches  556;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              |||| |||||||||| || |||| |||||||||| |||||||||||||||||||||||||
Db        218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | ||||||| ||||| |||||||||||||||||||||||||||||||||||||||||| ||
Db        278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||| |||||||||| ||||||||||||||||  ||||| ||||||||||||||  ||||
Db        458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||||||| ||||||||||||||||||||||||||| |||| ||||||||||||||
Db        518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| |||||||||||| || ||||||||||||||||||||||||||||||||||||
Db        578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||||||||||||||||| |||||||||||||||||||||||| ||||||
Db        638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              || ||||| || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||||| |||||||| |||||||||||| || ||||||||||||
Db        758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 808


RESULT 13
AAF26097
ID   AAF26097 standard; DNA; 679 BP.
XX
AC   AAF26097;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline fil12p35a DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02263.
XX
PR   08-JUL-1999;   99CH-0001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs  -
XX
PS   Disclosure; Fig 2; 35pp; German.
XX
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CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
CC   following: (i) as immunostimulant, for preventative or therapeutic use;
CC   and (ii) treating tumors and autoimmune diseases, or diseases associated
CC   with a Th1 defect, especially pre-existing infections by feline immune
CC   deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ   Sequence 679 BP; 196 A; 180 C; 140 G; 163 T; 0 other;

  Query Match             89.7%;  Score 530.2;  DB 22;  Length 679;
  Best Local Similarity   93.6%;  Pred. No. 1.5e-156;
  Matches  553;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              |||| |||||||||| || |||| |||||||||| |||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | ||||||| ||||| |||||||||||||||||||||||||||||||||||||||| ||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||| |||||||||| |||||||| |||||||  ||||| ||||||||||||||  ||||
Db        316 TCTCTGATAACTAATGGGAGTTGGCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||||| |||||||||||||||||||||||| |||| ||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| |||||||||| || ||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||||||||||||||||| |||||||||||||||||||||||||||| |||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAAACCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              | ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              |||||||||| ||||||||| ||| | ||||||| ||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAAAGTGATGAGCTATCTGAATTCTTCC 666


RESULT 14
AAF26083
ID   AAF26083 standard; DNA; 669 BP.
XX
AC   AAF26083;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 4.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02262.
XX
PR   08-JUL-1999;   99CH-0001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats,
PT   contains nucleic acid sequence encoding viral protein under control of
PT   eukaryotic promoter  -
XX
PS   Claim 14; Page 37; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response.
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 other;

  Query Match             89.4%;  Score 528.6;  DB 22;  Length 669;
  Best Local Similarity   93.4%;  Pred. No. 4.8e-156;
  Matches  552;  Conservative    0;  Mismatches   39;  Indels    0;  Gaps    0;

Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              |||| |||||||||| || |||| |||||||||| |||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | ||||||| ||||| |||||||||||||||||||||||||||||||||||||||| ||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315
```

```
Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||| |||||||||| |||||||||||||  ||  ||||| ||||||||||||||  ||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||||| |||||||||||||||||||||||||| |||| ||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| |||||||||| || ||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||| | |||||||||||||||||||||||||||||||||||||| ||||||
Db        496 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||| ||||| ||||||||| |||||||||||| ||||||||| |||||
Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
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RESULT 15
AAF26086
ID AAF26086 standard; DNA; 669 BP.
XX
AC AAF26086;
XX
DT 24-APR-2001 (first entry)
XX
DE Feline IL-12p35 encoding DNA.
XX
KW Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS Felis sp.
XX
PN WO200104155-A2.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-DE02263.
XX
PR 08-JUL-1999; 99CH-0001259.
XX
PA (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA (UYZU-) UNIV ZUERICH.
PA (REGC) UNIV CALIFORNIA.
XX
PI Lutz H, Leutenegger C, Pedersen N, Schroff M, Wittig B;
XX
DR WPI; 2001-147178/15.
XX
PT Recombinant feline interleukin-12, useful as immunostimulant and for
PT treating e.g. viral infections in cats, and related nucleic acid
PT constructs -
XX
PS Claim 3; Page 31; 35pp; German.
XX
CC This invention describes a novel feline interleukin-12 (fIL-12)
CC polypeptide (I) that is expressed, by recombinant gene expression in
CC eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC of subunits p35 and p40. These proteins are formed so that, in equimolar
CC concentrations and in presence of an immunizing antigen, they can be
CC administered to carnivores, particularly domestic cats. The invention
CC also describes a nucleic acid construct (II) encoding fIL-12 containing
CC sequences at least 95% identical with the p40- and p35-encoding sequences
CC (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC as immunostimulants for immunization against infectious diseases and/or
CC for treating infections or tumors in felines, especially domestic cats.
CC The products of the invention have immunostimulatory, antiviral and
CC antitumor activity. Nucleic acid constructs that encode (II) are useful
CC as adjuvants for prophylactic immunization against viral diseases and for
CC treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC is useful for carnivores, and particularly domestic cats in the
CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 other;

Query Match 89.4%; Score 528.6; DB 22; Length 669;
Best Local Similarity 93.4%; Pred. No. 4.8e-156;
Matches 552; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

```
Qy          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60
              |||| |||||||||| || |||| |||||||||| |||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120
              | ||||||| ||||| |||||||||||||||||||||||||||||||||||||||| ||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180
               |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300
              ||| |||||||||| |||||||||||||  ||  ||||| ||||||||||||||  ||||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360
              |||||||||| |||||||||||||||||||||||||| |||| ||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420
              |||||||| |||||||||| || ||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480
              || |||||||| | |||||||||||||||||||||||||||||||||||||| ||||||
Db        496 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591
              ||||| ||||| ||||||||| |||||||||||| ||||||||| |||||
Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
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Search completed: July 16, 2003, 06:46:40
Job time : 158.899 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 16, 2003, 15:58:34 ; Search time 1761.08 Seconds
(without alignments)
3255.531 Million cell updates/sec

Title: US-09-917-265-50
Perfect score: 994
Sequence: 1 RSLPTASPSPGIFQCLNHSQ.....HAFRIRAVTIDRMMSYLNSS 197

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-Q=/cgn2_1/USPTO_spool/US09917265/runat_15072003_092106_1601/app_query.fasta_1.3114
-DB=GenEmbl -QFMT=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09917265_@CGN_1_1_11328_@runat_15072003_092106_1601 -NCPU=6 -ICPU=3
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Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
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5: gb_ov:*
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7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
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12: gb_sy:*
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14: gb_vi:*
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16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vi:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
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35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	994	100.0	669	6	AR151072	AR151072 Sequence
2	994	100.0	669	6	E15018	E15018 Canine mRNA
3	989	99.5	669	6	AR151062	AR151062 Sequence
4	973	97.9	669	4	CFU49085	U49085 Canis famil
5	929	93.5	669	4	FCIL12P35	Y07761 F.catus mRN
6	927	93.3	669	4	FCU83185	U83185 Felis catus
7	920	92.6	669	6	AX076201	AX076201 Sequence
8	920	92.6	669	6	AX076483	AX076483 Sequence
9	920	92.6	4201	6	AX076477	AX076477 Sequence
10	893	89.8	660	6	AX154617	AX154617 Sequence
11	888	89.3	660	6	AX154614	AX154614 Sequence
12	888	89.3	660	6	AX154621	AX154621 Sequence
13	883	88.8	660	6	AX154618	AX154618 Sequence
14	883	88.8	660	6	AX154620	AX154620 Sequence
15	878	88.3	660	6	AX154619	AX154619 Sequence
16	876	88.1	1426	4	PIGIL12PSU	L35765 Sus scrofa
17	875	88.0	660	6	AR008951	AR008951 Sequence
18	875	88.0	660	6	I28592	I28592 Sequence 3
19	875	88.0	762	9	AF101062	AF101062 Homo sapi
20	875	88.0	823	9	AF180562	AF180562 Homo sapi
21	875	88.0	1316	6	AR050785	AR050785 Sequence
22	875	88.0	1316	6	AR212036	AR212036 Sequence
23	875	88.0	1316	9	HUMNKSFP35	M65291 Human natur
24	875	88.0	1364	6	AR082685	AR082685 Sequence
25	875	88.0	1364	6	AR122961	AR122961 Sequence
26	875	88.0	1364	6	I28326	I28326 Sequence 3
27	875	88.0	1364	6	I89771	I89771 Sequence 3
28	875	88.0	1645	6	A92078	A92078 Sequence 2
29	871	87.6	660	6	AX154616	AX154616 Sequence
30	869	87.4	660	6	AX154634	AX154634 Sequence
31	869	87.4	660	6	BD007071	BD007071 IL-12 gen
32	869	87.4	660	6	BD007079	BD007079 Gene expr
33	869	87.4	721	6	AR052862	AR052862 Sequence
34	869	87.4	1026	6	AR091390	AR091390 Sequence
35	869	87.4	1026	9	HUMCLMF35	M65271 Human cytot
36	869	87.4	1287	6	AX084108	AX084108 Sequence
37	868	87.3	660	6	AX154615	AX154615 Sequence
38	868	87.3	1560	6	AR091395	AR091395 Sequence
39	868	87.3	1623	6	AR091394	AR091394 Sequence
40	868	87.3	6139	6	AR091393	AR091393 Sequence
41	858	86.3	669	4	ECIL12P35	Y11130 Equus cabal
42	858	86.3	1626	12	AF401989	AF401989 Synthetic
43	851.5	85.7	666	6	AX154612	AX154612 Sequence
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ALIGNMENTS

RESULT 1

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AR151072
LOCUS       AR151072                669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 12 from patent US 6231850.
ACCESSION   AR151072
VERSION     AR151072.1  GI:15117122
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 12 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
BASE COUNT      185 a    177 c    144 g    163 t
ORIGIN

Alignment Scores:
Pred. No.:                1.97e-99       Length:          669
Score:                    994.00         Matches:         197
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-917-265-50 (1-197) x AR151072 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666

RESULT 2
E15018
LOCUS       E15018                  669 bp    DNA     linear   PAT 28-JUL-1999
DEFINITION  Canine mRNA for interleukin 12 35kDa subunit,complete cds.
ACCESSION   E15018
VERSION     E15018.1  GI:5709701
KEYWORDS    JP 1998036397-A/2.
SOURCE      Canis sp.
  ORGANISM  Canis sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F.
  TITLE     CANINE INTERLEUKIN 12 AND ITS PRODUCTION
  JOURNAL   Patent: JP 1998036397-A 2 10-FEB-1998;
            TORAY IND INC
COMMENT     OS   Canis sp. (dog)
            PN   JP 1998036397-A/2
            PD   10-FEB-1998
            PF   08-NOV-1996 JP 1996296789
            PR   08-NOV-1995 JP 95P   289729, 23-MAY-1996 JP 96P   128104 PI
            OKANO FUMIYOSHI
            PC   C07K14/54,C07H21/04,C12N5/10,C12N15/09,C12P21/02,(C12N5/10, PC
              C12R1:91),
            PC   (C12P21/02,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .669
            FT                   /organism='Canis sp.'
            FT                   /tissue_type='liver'
            FT   CDS             1. .669
            FT                   /product='interleukin12 35kDa subunit'.
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis sp."
                     /db_xref="taxon:9616"
BASE COUNT      185 a    177 c    144 g    163 t
ORIGIN

Alignment Scores:
Pred. No.:                1.97e-99       Length:          669
Score:                    994.00         Matches:         197
Percent Similarity:       100.00%        Conservative:    0
Best Local Similarity:    100.00%        Mismatches:      0
Query Match:              100.00%        Indels:          0
DB:                       6              Gaps:            0

US-09-917-265-50 (1-197) x E15018 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666

RESULT 3
AR151062
LOCUS       AR151062                669 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 2 from patent US 6231850.
ACCESSION   AR151062
VERSION     AR151062.1  GI:15117112
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Okano,F., Satoh,M. and Yamada,K.
  TITLE     Canine interleukin 12
  JOURNAL   Patent: US 6231850-A 2 15-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="unknown"
BASE COUNT      183 a    178 c    146 g    162 t
ORIGIN

Alignment Scores:
Pred. No.:              6.91e-99        Length:         669
Score:                  989.00          Matches:        196
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  99.49%          Mismatches:     0
Query Match:            99.50%          Indels:         0
DB:                     6               Gaps:           0

US-09-917-265-50 (1-197) x AR151062 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        616 AGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 666

RESULT 4
CFU49085
LOCUS       CFU49085                669 bp    mRNA    linear   MAM 13-MAR-1996
DEFINITION  Canis familiaris interleukin-12 p35 subunit mRNA, complete cds.
ACCESSION   U49085
VERSION     U49085.1  GI:1223905
KEYWORDS    .
SOURCE      Canis familiaris.
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F. and Buettner,M.
  TITLE     Cloning and sequence analysis of the p35 and p40 subunits of canine
            interleukin-12
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Belke-Louis,G.F.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-FEB-1996) Georg F. Belke-Louis, Institute of Med.
            Microbiology, Veterinaerstr. 13, Muenchen, D-80539, Germany
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Canis familiaris"
                     /db_xref="taxon:9615"
     CDS             1. .669
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAA92058.1"
                     /db_xref="GI:1223906"
                     /translation="MCPPRGLLLVTILVLLSHLDHLTWARSLPTASPSPGIFQCLNHS
                     QNLLRAVSNTLQKARQTLDYIPCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASGKASFMTVLCLSSIYEDLKMYQMEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNFNSVTVPQKSSLEEPDFYKTKIKLCILLHAFRIRAVTIDRMMSY
                     LNSS"
BASE COUNT      183 a    177 c    145 g    164 t
ORIGIN

Alignment Scores:
Pred. No.:              3.87e-97        Length:         669
Score:                  973.00          Matches:        193
Percent Similarity:     98.48%          Conservative:   1
Best Local Similarity:  97.97%          Mismatches:     3
Query Match:            97.89%          Indels:         0
DB:                     4               Gaps:           0

US-09-917-265-50 (1-197) x CFU49085 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGATTATATT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGTTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666

RESULT 5
FCIL12P35
LOCUS       FCIL12P35                669 bp    mRNA    linear   MAM 13-MAY-1997
DEFINITION  F.catus mRNA for interleukin-12 p35 chain.
ACCESSION   Y07761
VERSION     Y07761.1  GI:2102662
KEYWORDS    interleukin-12 subunit p35.
SOURCE      cat.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Schijns,V.E.C.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-SEP-1996) V.E.C.J. Schijns, Virology Division,
            Veterinary Faculty Utrecht University, Yalelaan 1, NL-3584 CL
            Utrecht, NETHERLANDS
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Schijns,V.E., Wierda,C.M., Vahlenkamp,T.W. and Horzinek,M.C.
  TITLE     Molecular cloning of cat interleukin-12
  JOURNAL   Immunogenetics 45 (6), 462-463 (1997)
  MEDLINE   97246745
   PUBMED   9089110
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
                     /cell_type="lymphocyte"
                     /tissue_type="peripheral blood"
     gene            1. .669
                     /gene="IL-12.p35"
     CDS             1. .669
                     /gene="IL-12.p35"
                     /function="heterodimer with IL-12 p40 chain"
                     /codon_start=1
                     /product="interleukin-12 p35 chain"
                     /protein_id="CAA69067.1"
                     /db_xref="GI:2102663"
                     /db_xref="SWISS-PROT:O02743"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
                     QTLLRAISNTLQKARQTLEFYSCTSEEIDHEDITKDKTSTVEACLPLELTMNESCLAS
                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNAS"
BASE COUNT      190 a    178 c    139 g    162 t
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Alignment Scores:
Pred. No.:                2.47e-92        Length:          669
Score:                    929.00          Matches:         182
Percent Similarity:       95.94%          Conservative:    7
Best Local Similarity:    92.39%          Mismatches:      8
Query Match:              93.46%          Indels:          0
DB:                       4               Gaps:            0

US-09-917-265-50 (1-197) x FCIL12P35 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::|||||||||   :::|||||||||||||:::|||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
                  ||||||||||||:::|||||||||||||||||||||||||||||||||||   |||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||   |||   ||||||||||||   |||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||   ||||||||||||||||||   ||||||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||:::|||||||||||||||||||||:::|||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

RESULT 6
FCU83185
LOCUS       FCU83185                 669 bp    mRNA    linear   MAM 16-JUL-1999
DEFINITION  Felis catus interleukin-12 p35 subunit (IL-12) mRNA, complete cds.
ACCESSION   U83185
VERSION     U83185.1  GI:2735052
KEYWORDS    .
SOURCE      Felis catus.
  ORGANISM  Felis catus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Nucleotide and predicted peptide sequence of feline interleukin-12
            (IL-12)
  JOURNAL   DNA Seq. 8 (1-2), 77-82 (1997)
  MEDLINE   98182592
   PUBMED   9522125
REFERENCE   2  (bases 1 to 669)
  AUTHORS   Fehr,D., Dean,G.A., Huder,J., Fan,Z., Huettner,S., Higgins,J.W.,
            Pedersen,N.C. and Lutz,H.
  TITLE     Direct Submission
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  JOURNAL   Submitted (24-DEC-1996) Clinical Laboratory, Department of Internal
            Veterinary Medicine, University of Zurich, Winterthurerstrasse 260,
            Zurich, ZH 8057, Switzerland
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="Felis catus"
                     /db_xref="taxon:9685"
     CDS             1. .669
                     /note="cytokine"
                     /codon_start=1
                     /product="interleukin-12 p35 subunit"
                     /protein_id="AAB93836.1"
                     /db_xref="GI:2735053"
                     /translation="MCPPRGLLLVTILVLLNHLDHLSLARNLPTPTPSPGMFQCLNHS
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                     REISLITNGSCLASRKTSFMTTLCLSSIYEDLKMYQVEFKAMNAKLLMDPKRQIFLDQ
                     NMLTAIDELLQALNVNSVTVPQNSSLEEPDFYKTKIKLCILLHAFRIRAVTINRMMSY
                     LNSS"
BASE COUNT      191 a    179 c    137 g    162 t
ORIGIN

Alignment Scores:
Pred. No.:                4.09e-92       Length:          669
Score:                    927.00         Matches:         182
Percent Similarity:       95.43%         Conservative:    6
Best Local Similarity:    92.39%         Mismatches:      9
Query Match:              93.26%         Indels:          0
DB:                       4              Gaps:            0

US-09-917-265-50 (1-197) x FCU83185 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::|||||||||    :::||||||||||||:::||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||:::|||||||||||||||||||||||||||||||||||    |||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              |||||||||||||||||||||||||||||||    |||   ||||||||||||   |||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              |||||||||||||||||||||||    ||||||||||||||||||    ||||||
Db        496 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 TTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||:::||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 666

RESULT 7
AX076201
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LOCUS       AX076201                669 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 2 from Patent WO0104155.
ACCESSION   AX076201
VERSION     AX076201.1  GI:12710826
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Lutz,H., Leutenegger,C., Pedersen,N., Schroff,M. and Wittig,B.
  TITLE     Feline interleukin-12 as an immune stimulant
  JOURNAL   Patent: WO 0104155-A 2 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH) ; THE REGENTS OF THE UNIVERSITY OF
            CALIFORNIA (US)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="feline IL-12 p35"
BASE COUNT      189 a    179 c    140 g    161 t
ORIGIN

Alignment Scores:
Pred. No.:                2.38e-91       Length:          669
Score:                    920.00         Matches:         179
Percent Similarity:       94.92%         Conservative:    8
Best Local Similarity:    90.86%         Mismatches:      10
Query Match:              92.56%         Indels:          0
DB:                       6              Gaps:            0

US-09-917-265-50 (1-197) x AX076201 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::|||||||||    :::||||||||||||:::||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||:::||||||||||||||||||||||||||||||||||    |||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||    ||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||    |||   |||   ||||||||||||   |||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||:::||||||||||||||||||||||||||||||||    ||||||
Db        496 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||:::||||||||||||||||||:::|||
Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
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RESULT 8
AX076483
LOCUS       AX076483                669 bp    DNA     linear   PAT 07-FEB-2001
DEFINITION  Sequence 9 from Patent WO0104280.
ACCESSION   AX076483
VERSION     AX076483.1  GI:12711035
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 669)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 9 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .669
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Sequence coding for SEQ ID NO 3, IL-12 p35"
BASE COUNT      189 a    179 c    140 g    161 t
ORIGIN

Alignment Scores:
Pred. No.:              2.38e-91        Length:         669
Score:                  920.00          Matches:        179
Percent Similarity:     94.92%          Conservative:   8
Best Local Similarity:  90.86%          Mismatches:     10
Query Match:            92.56%          Indels:         0
DB:                     6               Gaps:           0

US-09-917-265-50 (1-197) x AX076483 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::|||||||||   :::||||||||||||:::|||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||   |||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||   |||   |||   ||||||||||||   |||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||:::|||||||||||||||||||||||||||||||   ||||||
Db        496 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||:::|||||||||||||||||||||:::|||
Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

RESULT 9
AX076477
LOCUS       AX076477                4201 bp    DNA     linear   PAT 06-FEB-2001
DEFINITION  Sequence 3 from Patent WO0104280.
ACCESSION   AX076477
VERSION     AX076477.1  GI:12711029
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 4201)
  AUTHORS   Leutenegger,C., Schroff,M., Wittig,B. and Lutz,H.
  TITLE     Vaccine against lentiviral infections, such as the feline immune
            deficiency virus of the cat
  JOURNAL   Patent: WO 0104280-A 3 18-JAN-2001;
            Mologen Forschungs-, Entwicklungs- und Vertriebs GmbH (DE) ;
            Universitaet Zuerich (CH)
FEATURES             Location/Qualifiers
     source          1. .4201
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="IL-12p35 (pMOLfIL-12p35 (e-,_e31-)clone61)"
BASE COUNT     1086 a   1055 c    999 g   1061 t
ORIGIN

Alignment Scores:
Pred. No.:              2.21e-90        Length:         4201
Score:                  920.00          Matches:        179
Percent Similarity:     94.92%          Conservative:   8
Best Local Similarity:  90.86%          Mismatches:     10
Query Match:            92.56%          Indels:         0
DB:                     6               Gaps:           0

US-09-917-265-50 (1-197) x AX076477 (1-4201)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::|||||||||   :::||||||||||||:::|||||||||||||||||||||||
Db       3122 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 3181

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||   |||
Db       3182 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 3241

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3242 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 3301

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db       3302 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 3361

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||   |||   |||   ||||||||||||   |||
Db       3362 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 3421

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db       3422 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 3481

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3482 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 3541

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||:::|||||||||||||||||||||||||||||||   ||||||
Db       3542 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 3601

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       3602 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 3661
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Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||||||:::|||||||||||||||||||||:::|||
Db       3662 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 3712

RESULT 10
AX154617
LOCUS       AX154617                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 21 from Patent WO0140257.
ACCESSION   AX154617
VERSION     AX154617.1  GI:14536192
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 21 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      184 a    172 c    141 g    163 t
ORIGIN

Alignment Scores:
Pred. No.:              2.08e-88        Length:         660
Score:                  893.00          Matches:        176
Percent Similarity:     92.89%          Conservative:   7
Best Local Similarity:  89.34%          Mismatches:     14
Query Match:            89.84%          Indels:         0
DB:                     6               Gaps:           0

US-09-917-265-50 (1-197) x AX154617 (1-660)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::||||||   |||:::|||   ||||||:::|||   ||||||:::||||||||
Db         67 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||   ||||||||||||||||||||||||   |||
Db        127 AACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAAACTCTAGAATTTTAC 186

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||      ||||||||||||||||||||||   |||
Db        247 GAGGCCTGTTTACCACTGGAATTAGCCACGAATGAGAGTTGCCTGGCTTCCAGAGGGATC 306

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||   |||   ||||||||||||   |||
Db        307 TCTCTGATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 366

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||   ||||||||||||||||||||||||||||||:::|||||||||   ||||||
Db        367 TGCCTTGGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 426

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db        427 GCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 486

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        487 ATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 546

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606
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Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db        607 AGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 657

RESULT 11
AX154614
LOCUS       AX154614                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 18 from Patent WO0140257.
ACCESSION   AX154614
VERSION     AX154614.1  GI:14536189
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 18 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    172 c    136 g    163 t
ORIGIN

Alignment Scores:
Pred. No.:              7.31e-88        Length:         660
Score:                  888.00          Matches:        175
Percent Similarity:     92.39%          Conservative:   7
Best Local Similarity:  88.83%          Mismatches:     15
Query Match:            89.34%          Indels:         0
DB:                     6               Gaps:           0

US-09-917-265-50 (1-197) x AX154614 (1-660)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::||||||   |||:::|||   ||||||:::|||   ||||||:::||||||||
Db         67 AGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||   ||||||||||||||||||||||||   |||
Db        127 AACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAAACTCTAGAATTTTAC 186

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||      ||||||||||||||   |||||||||
Db        247 GAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACT 306

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              |||   ||||||||||||||||||||||||   |||   ||||||||||||   |||
Db        307 TCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTG 366

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||:::|||||||||   ||||||
Db        367 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 426

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db        427 GCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 486

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db        487 ATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 546

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606
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Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||||:::||||||||||||||||||||||||||||
Db        607 AGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 657

RESULT 12
AX154621
LOCUS       AX154621                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 25 from Patent WO0140257.
ACCESSION   AX154621
VERSION     AX154621.1  GI:14536196
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 25 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    172 c    136 g    163 t
ORIGIN

Alignment Scores:
Pred. No.:              7.31e-88        Length:         660
Score:                  888.00          Matches:        175
Percent Similarity:     92.39%          Conservative:   7
Best Local Similarity:  88.83%          Mismatches:     15
Query Match:            89.34%          Indels:         0
DB:                     6               Gaps:           0

US-09-917-265-50 (1-197) x AX154621 (1-660)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::|||||   |||:::|||   ||||||:::|||   ||||||:::|||||||||
Db         67 AGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||   |||
Db        127 AACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAAACTCTAGAATTTTAC 186

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||      |||||||||||||||   ||||||||
Db        247 GAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACT 306

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              |||   ||||||||||||||||||||||||   |||   ||||||||||||   |||
Db        307 TCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTG 366

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||:::|||||||||   ||||||
Db        367 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 426

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db        427 GCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 486

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        487 ATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 546

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606
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Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||||:::||||||||||||||||||||||||||||
Db        607 AGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 657

RESULT 13
AX154618
LOCUS       AX154618                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 22 from Patent WO0140257.
ACCESSION   AX154618
VERSION     AX154618.1  GI:14536193
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 22 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      189 a    173 c    136 g    162 t
ORIGIN

Alignment Scores:
Pred. No.:              2.57e-87        Length:         660
Score:                  883.00          Matches:        174
Percent Similarity:     91.88%          Conservative:   7
Best Local Similarity:  88.32%          Mismatches:     16
Query Match:            88.83%          Indels:         0
DB:                     6               Gaps:           0

US-09-917-265-50 (1-197) x AX154618 (1-660)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::|||||   |||:::|||   ||||||:::|||   ||||||:::|||||||||
Db         67 AGAAACCTCCCTGTGGCCACCCCAGGCCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||   |||
Db        127 AACCTGCTGAGGGCCGTCAGCAACATGCTGCAGAAGGCCAGACAAACTCTAGAATTTTAC 186

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||
Db        187 TCCTGCACTTCCGAAGAGACTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||      |||||||||||||||   ||||||||
Db        247 GAGGCCTGCTTACCACTGGAATTAATCAAGAATGAGAGTTGCCTAAATTCCAGAGAGACT 306

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              |||   ||||||||||||||||||||||||   |||   ||||||||||||   |||
Db        307 TCTTTCATAACTAATGGGAGTTGCCTAGCCTCCAGAAAGACCTCTTTTATGACAACCCTG 366

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||:::|||||||||   ||||||
Db        367 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGACCATGAAT 426

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||:::||||||||||||||||||||||||||||||||||||||||||
Db        427 GCAAAGCTTCTGATGAATCCTAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 486

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||   ||||||||||||||||||||||||
Db        487 ATTGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGAGACTGTGCCACAAAAATCCTCC 546

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606
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Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
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Db        607 AGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 657

RESULT 14
AX154620
LOCUS       AX154620                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 24 from Patent WO0140257.
ACCESSION   AX154620
VERSION     AX154620.1  GI:14536195
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 24 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      181 a    178 c    144 g    157 t
ORIGIN

Alignment Scores:
Pred. No.:              2.57e-87        Length:         660
Score:                  883.00          Matches:        174
Percent Similarity:     91.88%          Conservative:   7
Best Local Similarity:  88.32%          Mismatches:     16
Query Match:            88.83%          Indels:         0
DB:                     6               Gaps:           0

US-09-917-265-50 (1-197) x AX154620 (1-660)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::||||||   |||:::|||   ||||||:::|||   ||||||:::||||||||||
Db         67 AGAAACCTCCCCGTGGCCACTCCAGACCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||:::|||||||||||   |||
Db        127 AACCTGCTGAGGGCTGTCAGCAACACGCTCCAGAAGGCCAAACAAACCCTAGAATTTTAC 186

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||      ||||||||||||||||||||||   |||
Db        247 GAGGCCTGTTTACCACTGGAATTAGCCACGAATGAGAGTTGCCTGGCTTCCAGAGGGATC 306

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||   |||   |||||||||||   |||
Db        307 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 366

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
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Db        367 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 426

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        427 GCAAAGCTGTTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGGCAGCT 486

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              |||   ||||||:::||||||||||||   ||||||   |||   ||||||||||||||||
Db        487 ATTGCTGAGCTAATGCAGGCCCTGAATGTCAACAGTGAGACTGCGCCACAAAAATCCTCC 546

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTTGAAGAACCGGATTTTTATAAGACTAAAATCAAGCTCTGCATACTTCTTCATGCCTTC 606
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Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        607 AGAATTCGTGCAGTGACCATCGATAGAATGATGAGCTATCTGAATTCTTCC 657

RESULT 15
AX154619
LOCUS       AX154619                660 bp    DNA     linear   PAT 22-JUN-2001
DEFINITION  Sequence 23 from Patent WO0140257.
ACCESSION   AX154619
VERSION     AX154619.1  GI:14536194
KEYWORDS    .
SOURCE      synthetic construct.
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1  (bases 1 to 660)
  AUTHORS   Leong,S.R. and Punnonen,J.
  TITLE     Cytokine polypeptides and nucleic acids
  JOURNAL   Patent: WO 0140257-A 23 07-JUN-2001;
            Maxygen, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .660
                     /organism="synthetic construct"
                     /db_xref="taxon:32630"
                     /note="Synthetic Sequence"
BASE COUNT      182 a    180 c    144 g    154 t
ORIGIN

Alignment Scores:
Pred. No.:              9.04e-87        Length:         660
Score:                  878.00          Matches:        173
Percent Similarity:     91.88%          Conservative:   8
Best Local Similarity:  87.82%          Mismatches:     16
Query Match:            88.33%          Indels:         0
DB:                     6               Gaps:           0

US-09-917-265-50 (1-197) x AX154619 (1-660)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::||||||   |||:::|||   ||||||:::|||   ||||||:::||||||||||
Db         67 AGAAACCTCCCCGTGGCCACCCCAGGCCCAGGAATGTTCCCATGCCTTCACCACTCCCAA 126

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||:::|||||||||||   |||
Db        127 AACCTGCTGAGGGCTGTCAGCAACACGCTCCAGAAGGCCAAACAAACCCTAGAATTTTAC 186

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        187 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 246

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||      ||||||||||||||||||||||   |||
Db        247 GAGGCCTGTTTACCACTGGAATTAGCCACGAATGAGAGTTGCCTGGCTTCCAGAGGGATC 306

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||   |||   |||||||||||   |||
Db        307 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACAACCCTG 366

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||:::|||||||||||||||||||||||
Db        367 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 426

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||   |||
Db        427 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGGCAGCT 486

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              |||   ||||||:::||||||||||||   ||||||   |||   ||||||||||||||||
Db        487 ATTGCTGAGCTAATGCAGGCCCTGAATGTCAACAGTGAGACTGCGCCACAAAAATCCTCC 546

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        547 CTGGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 606
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Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||||:::||||||||||||||||||||||||||||
Db        607 AGAATTCGGGCAGTGACCATCAATAGAATGATGAGCTATCTGAATTCTTCC 657
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Search completed: July 17, 2003, 06:40:25
Job time : 1763.08 secs

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: July 16, 2003, 13:41:48 ; Search time 139.28 Seconds
(without alignments)
3185.273 Million cell updates/sec

Title: US-09-917-265-50
Perfect score: 994
Sequence: 1 RSLPTASPSPGIFQCLNHSQ.....HAFRIRAVTIDRMMSYLNSS 197

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Ygapop 10.0 , Ygapext 0.5
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Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-DB=N_Geneseq_101002 -QFMT=fastap -SUFFIX=p2n.rng -MINMATCH=0.1 -LOOPCL=0
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	994	100.0	591	20	AAX18179	Canine mature CLAF
2	994	100.0	669	19	AAV13819	Canine IL-12 P35 s
3	994	100.0	669	20	AAX35626	Nucleic acid encod
4	994	100.0	669	20	AAX03163	Nucleic acid encod
5	994	100.0	669	22	AAI64389	Canine coding sequ
6	994	100.0	1282	20	AAX18178	Canine full length
7	989	99.5	669	19	AAV13818	Canine IL-12 P35 s
8	989	99.5	669	20	AAX35616	Nucleic acid encod
9	989	99.5	669	20	AAX03153	Nucleic acid encod
10	989	99.5	669	22	AAI64379	Canine coding sequ
11	932	93.8	591	19	AAV56629	Feline FLAFp35 cDN
12	932	93.8	689	19	AAV56641	Feline FLAFp35 DNA
13	932	93.8	1441	19	AAV56628	Feline FLAFp35 cDN
14	920	92.6	669	22	AAF26083	Feline IL-12p35 en
15	920	92.6	669	22	AAF26086	Feline IL-12p35 en
16	920	92.6	4201	22	AAF26077	Feline IL-12p35 en
17	909	91.4	639	22	AAF26098	Plasmid pMOL-fIL12
18	909	91.4	679	22	AAF26097	Feline fil2p35a D
19	893	89.8	660	22	AAD15216	Modified human cyt
20	888	89.3	660	22	AAD15213	Modified human cyt
21	888	89.3	660	22	AAD15220	Modified human cyt
22	883	88.8	660	22	AAD15217	Modified human cyt
23	883	88.8	660	22	AAD15219	Modified human cyt
24	878	88.3	660	22	AAD15218	Modified human cyt
25	875	88.0	660	16	AAQ97485	Human interleukin-
26	875	88.0	660	19	AAV07218	DNA encoding human
27	875	88.0	762	20	AAV83207	Interleukin (IL)-1
28	875	88.0	762	21	AAF21323	Human low adenosin
29	875	88.0	762	21	AAA35201	Human adenosine re
30	875	88.0	1316	18	AAT63621	Interleukin-12 p35
31	875	88.0	1364	17	AAT48099	Human interleukin-
32	875	88.0	1364	19	AAV42536	Human interleukin-
33	875	88.0	1364	19	AAV15228	Heterodimeric huma
34	875	88.0	1364	21	AAZ28863	Human interleukin-
35	875	88.0	1364	22	AAF56281	IL-12 vaccine adju
36	875	88.0	4521	21	AAF21326	Human low adenosin
37	875	88.0	4521	21	AAA35204	Human adenosine re
38	875	88.0	5686	20	AAZ40415	Plasmid pIN1143 co
39	875	88.0	8578	24	AAD31545	pIRES-hB7-1-IL12.1
40	875	88.0	8578	24	AAD31546	pIRES-hB7-1-IL12.0
41	875	88.0	8608	24	AAD31548	pIRES-hB7-1-IL12.2
42	875	88.0	8623	24	AAD31547	pIRES-hB7-1-IL12.3
43	875	88.0	8629	24	AAD31552	pIRES-IL12.2-hb7-1
44	875	88.0	8638	24	AAD31549	pIRES-hB7-1-IL12.4
45	875	88.0	8644	24	AAD31551	pIRES-IL12.3-hb7-1

ALIGNMENTS

RESULT 1
AAX18179
ID AAX18179 standard; cDNA; 591 BP.
XX
AC AAX18179;
XX
DT 07-MAY-1999 (first entry)
XX
DE Canine mature CLAF p35 subunit coding sequence.
XX
KW CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW canine infectious hepatitis; ds.
XX
OS Canis sp.
XX
PN WO9855511-A1.
XX

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PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74325.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 34-35; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 591 BP; 173 A; 146 C; 127 G; 145 T; 0 other;

Alignment Scores:
Pred. No.:              6.16e-104       Length:         591
Score:                  994.00          Matches:        197
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     20              Gaps:           0

US-09-917-265-50 (1-197) x AAX18179 (1-591)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
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Db          1 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
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Db        241 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
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Db        361 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 591

RESULT 2
AAV13819
ID   AAV13819 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13819;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41793.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 11; Pages 11-12; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 669 BP; 185 A; 177 C; 144 G; 163 T; 0 other;

Alignment Scores:
Pred. No.:              7.32e-104       Length:         669
Score:                  994.00          Matches:        197
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     19              Gaps:           0

US-09-917-265-50 (1-197) x AAV13819 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135
```

```
Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
```

RESULT 3
AAX35626
ID AAX35626 standard; cDNA to mRNA; 669 BP.
XX
AC AAX35626;
XX
DT 09-JUL-1999 (first entry)
XX
DE Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS Canis sp.
XX
FH Key Location/Qualifiers
FT CDS 1..669
FT /*tag= a
XX
PN JP11106350-A.
XX
PD 20-APR-1999.
XX
PF 15-MAY-1998; 98JP-0133345.
XX
PR 07-AUG-1997; 97JP-0213755.
PR 16-MAY-1997; 97JP-0127690.
XX
PA (TORA) TORAY IND INC.
XX
DR WPI; 1999-308068/26.
DR P-PSDB; AAY02343.
XX
PT A prevention and treating agent containing interleukin 12 (CaIL12) -
PT for prevention and treatment of dog and cat immune diseases
XX
PS Claim 1; Page 15-16; 16pp; Japanese.
XX
CC The present sequence encodes canine interleukin-12 (IL-12). The
CC specification describes a method for the prevention and treatment
CC of dog and cat immune diseases. The treatment used an agent comprising
CC dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC useful for preventing and treating dog and cat immune diseases,
CC including tumours, skin diseases, infectious diseases and allergic
CC diseases.
XX
SQ Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

Alignment Scores:

Pred. No.:	7.32e-104	Length:	669
Score:	994.00	Matches:	197
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	20	Gaps:	0

US-09-917-265-50 (1-197) x AAX35626 (1-669)

```
Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666
```

RESULT 4
AAX03163
ID AAX03163 standard; cDNA to mRNA; 669 BP.
XX
AC AAX03163;
XX
DT 30-MAR-1999 (first entry)
XX
DE Nucleic acid encoding canine interleukin 12.
XX
KW Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW skin disease; viral infection; allergic disease; breast tumour;

```
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;   98WO-JP02031.
XX
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84374.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 33-34; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

Alignment Scores:
Pred. No.:              7.32e-104      Length:         669
Score:                  994.00         Matches:        197
Percent Similarity:     100.00%        Conservative:   0
Best Local Similarity:  100.00%        Mismatches:     0
Query Match:            100.00%        Indels:         0
DB:                     20             Gaps:           0

US-09-917-265-50 (1-197) x AAX03163 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666

RESULT 5
AAI64389
ID   AAI64389 standard; DNA; 669 BP.
XX
AC   AAI64389;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #4.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= "Canine protein #4"
FT   sig_peptide     1..75
FT                   /*tag= b
FT   mat_peptide     76..666
FT                   /*tag= c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66483.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian  -
XX
PS   Claim 6; Page 18; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
```

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CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 669 BP; 184 A; 177 C; 145 G; 163 T; 0 other;

Alignment Scores:
Pred. No.:              7.32e-104       Length:         669
Score:                  994.00          Matches:        197
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     22              Gaps:           0

US-09-917-265-50 (1-197) x AAI64389 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        616 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 666

RESULT 6
AAX18178
ID   AAX18178 standard; cDNA; 1282 BP.
XX
AC   AAX18178;
XX
DT   07-MAY-1999  (first entry)
XX
DE   Canine full length CLAF p35 subunit coding sequence.
XX
KW   CLAF; canine lymphocyte activation factor; p35 subunit; p40 subunit; dog;
KW   viral disease; canine distemper; canine parvovirus; autoimmune disease;
KW   canine infectious hepatitis; ds.
XX
OS   Canis sp.
XX
PN   WO9855511-A1.
XX
PD   10-DEC-1998.
XX
PF   26-MAY-1998;   98WO-JP02295.
XX
PR   03-JUN-1997;   97JP-0161936.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Eda Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1999-070260/06.
DR   P-PSDB; AAW74324.
XX
PT   Canine cytokine protein which activates canine cytotoxic T
PT   lymphocytes - is useful for treatment of viral and autoimmune
PT   diseases in dogs
XX
PS   Claim 8; Page 33-34; 51pp; Japanese.
XX
CC   This sequence encodes the canine lymphocyte activation factor (CLAF) of
CC   the invention. CLAF activates lymphocytes, especially canine cytotoxic
CC   T cells. The protein contains a p35 and a p40 subunit. CLAF or antibodies
CC   recognising it may be used in the treatment of viral diseases in dogs
CC   (such as canine distemper, canine parvovirus and canine infectious
CC   hepatitis). The antibodies may also be used in isolation of CLAF from
CC   culture of the transformant host cells by affinity chromatography. The
CC   p40 homodimer can be used for the treatment of autoimmune diseases in
CC   dogs.
XX
SQ   Sequence 1282 BP; 391 A; 279 C; 257 G; 355 T; 0 other;

Alignment Scores:
Pred. No.:              1.81e-103       Length:         1282
Score:                  994.00          Matches:        197
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            100.00%         Indels:         0
DB:                     20              Gaps:           0

US-09-917-265-50 (1-197) x AAX18178 (1-1282)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 AGGAGCCTCCCCACAGCCTCACCGAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 200

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 260

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 320

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 380

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 440

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        441 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 500

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        501 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 560

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        561 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 620
```

```
Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        621 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 680

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        681 AGAATTCGTGCGGTGACCATCGATAGAATGATGAGTTATCTGAATTCTTCC 731

RESULT 7
AAV13818
ID   AAV13818 standard; cDNA to mRNA; 669 BP.
XX
AC   AAV13818;
XX
DT   14-MAY-1998  (first entry)
XX
DE   Canine IL-12 P35 subunit cDNA.
XX
KW   Canine; interleukin-12 P35 subunit; IL-12 P35 subunit; antitumour;
KW   antiviral; vaccine adjuvant; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin-12_P35_subunit
XX
PN   JP10036397-A.
XX
PD   10-FEB-1998.
XX
PF   08-NOV-1996;   96JP-0296789.
XX
PR   23-MAY-1996;   96JP-0128104.
PR   08-NOV-1995;   95JP-0289729.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1998-174914/16.
DR   P-PSDB; AAW41792.
XX
PT   Canine interleukin 12 - comprises P40 and P35 subunits; useful in
PT   veterinary medicine, e.g. antitumour, antivirus and vaccine adjuvant
PT   activities are expected
XX
PS   Claim 9; Page 9; 12pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin-12 (IL-12) P35
CC   subunit. A canine IL-12 comprising a P40 and P35 subunit is capable
CC   of inducing an antiviral activating factor and the expression of
CC   class II MHC molecules in canine tumour cells, stimulating
CC   proliferation of canine blastogenic lymphocytes and activating
CC   canine leukocytes to inhibit canine tumour cells. The canine IL-12
CC   can be used in veterinary medicines, e.g. antitumour, antivirus and
CC   vaccine adjuvant activities are expected.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

Alignment Scores:
Pred. No.:              2.72e-103       Length:         669
Score:                  989.00          Matches:        196
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  99.49%          Mismatches:     0
Query Match:            99.50%          Indels:         0
DB:                     19              Gaps:           0

US-09-917-265-50 (1-197) x AAV13818 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||||||||:::||||||
Db        616 AGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 666

RESULT 8
AAX35616
ID   AAX35616 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX35616;
XX
DT   09-JUL-1999  (first entry)
XX
DE   Nucleic acid encoding canine Interleukin-12 (IL-12).
XX
KW   Interleukin-12; IL-12; dog; cat; immune disease; CaIL12; heterodimer;
KW   tumour; skin disease; infectious disease; allergic disease; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
XX
PN   JP11106350-A.
XX
PD   20-APR-1999.
XX
PF   15-MAY-1998;   98JP-0133345.
XX
PR   07-AUG-1997;   97JP-0213755.
PR   16-MAY-1997;   97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 1999-308068/26.
DR   P-PSDB; AAY02340.
XX
PT   A prevention and treating agent containing interleukin 12 (CaIL12) -
PT   for prevention and treatment of dog and cat immune diseases
XX
PS   Claim 1; Page 13; 16pp; Japanese.
```

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XX
CC   The present sequence encodes canine interleukin-12 (IL-12). The
CC   specification describes a method for the prevention and treatment
CC   of dog and cat immune diseases. The treatment used an agent comprising
CC   dog IL-12 (CaIL12) proteins to form a heterodimer. The agent is
CC   useful for preventing and treating dog and cat immune diseases,
CC   including tumours, skin diseases, infectious diseases and allergic
CC   diseases.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

Alignment Scores:
Pred. No.:              2.72e-103       Length:         669
Score:                  989.00          Matches:        196
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  99.49%          Mismatches:     0
Query Match:            99.50%          Indels:         0
DB:                     20              Gaps:           0

US-09-917-265-50 (1-197) x AAX35616 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||||||||||||||||||:::|||||||
Db        616 AGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 666

RESULT 9
AAX03153
ID   AAX03153 standard; cDNA to mRNA; 669 BP.
XX
AC   AAX03153;
XX
DT   30-MAR-1999  (first entry)
XX
DE   Nucleic acid encoding canine interleukin 12.
XX
KW   Canine; interleukin 12; IL-12; feline; immunological disease; tumour;
KW   skin disease; viral infection; allergic disease; breast tumour;
KW   oesinophilic granuloma; epidermoid tumour; skin tumour; lipoma;
KW   othematoma; pneumonoedema; skin soft pedicled soft tumour; anal tumour;
KW   otitis externa; dermatitis; eczema; fungal skin disease; pyoderma;
KW   allergic dermatitis; nettle rash; traumatic dermatitis; hair loss;
KW   dog Parvovirus infection; distemper virus; cat plaque virus infection;
KW   feline leukaemia; allergy; pollinosis; ds.
XX
OS   Canis sp.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag=  a
FT                   /product= interleukin_12
XX
PN   WO9851327-A1.
XX
PD   19-NOV-1998.
XX
PF   07-MAY-1998;    98WO-JP02031.
XX
PR   16-MAY-1997;    97JP-0127690.
XX
PA   (TORA ) TORAY IND INC.
XX
PI   Okano F,  Satoh M,  Yamada K;
XX
DR   WPI; 1999-070100/06.
DR   P-PSDB; AAW84372.
XX
PT   New therapeutic and prophylactic agents  - comprise
PT   genetically-engineered canine interleukin 12, used to treat, e.g.
PT   canine and feline immunological diseases
XX
PS   Claim 1; Page 26-27; 45pp; Japanese.
XX
CC   The present sequence encodes a canine interleukin 12 (IL-12) protein.
CC   The IL-12 protein can be used in therapeutic or prophylactic agents.
CC   The agents can be used to prevent and treat canine and feline
CC   immunological diseases including dog and cat tumours, skin diseases,
CC   viral infections and allergic diseases, especially tumours, breast
CC   tumour, oesinophilic granuloma, epidermoid tumour, skin tumour, lipoma,
CC   othematoma, pneumonoedema, skin soft pedicled soft tumour and anal
CC   tumour; skin diseases, otitis externa, dermatitis, eczema, fungal
CC   diseases of the skin, pyoderma, allergic dermatitis, nettle rash,
CC   traumatic dermatitis and hair loss; infections; dog Parvovirus infection
CC   and distemper virus, cat plaque virus infection and feline leukaemia, and
CC   allergic diseases, e.g. pollinosis.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

Alignment Scores:
Pred. No.:              2.72e-103       Length:         669
Score:                  989.00          Matches:        196
Percent Similarity:     100.00%         Conservative:   1
Best Local Similarity:  99.49%          Mismatches:     0
Query Match:            99.50%          Indels:         0
DB:                     20              Gaps:           0

US-09-917-265-50 (1-197) x AAX03153 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
                    ||||||||||||||||||||||||||||||||||||||:::||||||
Db        616 AGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 666

RESULT 10
AAI64379
ID   AAI64379 standard; DNA; 669 BP.
XX
AC   AAI64379;
XX
DT   23-NOV-2001  (first entry)
XX
DE   Canine coding sequence #2.
XX
KW   Canine; dog; immunostimulant; interleukin 12; IL12; immunopathy; ds.
XX
OS   Canis familiaris.
XX
FH   Key             Location/Qualifiers
FT   CDS             1..669
FT                   /*tag= a
FT                   /product= "Canine protein #2"
FT   sig_peptide     1..75
FT                   /*tag= b
FT   mat_peptide     76..666
FT                   /*tag= c
XX
PN   JP2001161378-A.
XX
PD   19-JUN-2001.
XX
PF   26-SEP-2000; 2000JP-0292946.
XX
PR   01-OCT-1999;   99JP-0281234.
XX
PA   (TORA ) TORAY IND INC.
XX
DR   WPI; 2001-592466/67.
DR   P-PSDB; AAG66481.
XX
PT   Preparation of a highly pure protein, interleukin 12, a protein
PT   inhibiting the activity of interleukin 12, and a treating agent and a
PT   treating method for immunopathy of mammalian -
XX
PS   Claim 6; Page 15; 21pp; Japanese.
XX
CC   The present invention relates to a method for the preparation of a highly
CC   pure protein in which interleukin 12 (IL12) and/or a protein inhibiting
CC   the activity of IL12 is contacted to an ion exchanging carrier and/or a
CC   pigment carrier to get IL12 and/or a protein inhibiting the activity of
CC   IL12. The protein is used as a preventive agent for dog immunopathy. The
CC   present sequence was used in the method of the present invention.
XX
SQ   Sequence 669 BP; 183 A; 178 C; 146 G; 162 T; 0 other;

Alignment Scores:
Pred. No.:              2.72e-103      Length:          669
Score:                  989.00         Matches:         196
Percent Similarity:     100.00%        Conservative:    1
Best Local Similarity:  99.49%         Mismatches:      0
Query Match:            99.50%         Indels:          0
DB:                     22             Gaps:            0

US-09-917-265-50 (1-197) x AAI64379 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         76 AGGAGCCTCCCCACAGCCTCACCAAGCCCAGGAATATTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        136 AACCTGCTGAGAGCCGTCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTATAT 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAGGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        316 TCTTTGATAACTAACGGGAGTTGCCTGGCCTCTGGAAAGGCCTCTTTTATGACGGTCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        376 TGCCTTAGCAGCATCTATGAGGACTTGAAGATGTACCAGATGGAATTCAAGGCCATGAAC 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTTTTAATGGATCCCAAGAGGCAGATCTTTCTGGATCAAAACATGCTGACGGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        496 ATCGATGAGCTGTTACAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAAATCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAGCCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||||||||||||||||||||||:::||||||
Db        616 AGAATTCGTGCGGTGACCATCGACAGAATGATGAGCTATCTGAGTTCTTCC 666

RESULT 11
AAV56629
ID   AAV56629 standard; cDNA; 591 BP.
XX
AC   AAV56629;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA mature transcript.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
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XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76176.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 23; Page 59; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine mature protein, FLAFp35.
CC   This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus.
XX
SQ   Sequence 591 BP; 179 A; 151 C; 120 G; 141 T; 0 other;

Alignment Scores:
Pred. No.:              7.2e-97       Length:        591
Score:                  932.00        Matches:       183
Percent Similarity:     95.94%        Conservative:  6
Best Local Similarity:  92.89%        Mismatches:    8
Query Match:            93.76%        Indels:        0
DB:                     19            Gaps:          0

US-09-917-265-50 (1-197) x AAV56629 (1-591)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::|||||||||   :::|||||||||||||:::|||||||||||||||||||||||
Db          1 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 60

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
                 ||||||||||||:::|||||||||||||||||||||||||||||||||||   |||
Db         61 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 120

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 180

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 240

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              |||||||||||||||||||||||||||||||   |||   ||||||||||||   |||
Db        241 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 300

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        301 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 360

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 420

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              |||||||||||||||||||||||||   ||||||||||||||||||||   ||||||
Db        421 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 480

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 540

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              |||||||||||||||||||||:::|||||||||||||||||||||||||
Db        541 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 591

RESULT 12
AAV56641
ID   AAV56641 standard; DNA; 689 BP.
XX
AC   AAV56641;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 DNA fragment.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ss.
XX
OS   Felis catus.
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 24; Page 67; 94pp; Japanese.
XX
CC   This sequence encodes a fragment of a novel feline cytokine protein,
CC   FLAFp35. This protein can be used in the production of a FLAFp35/FLAFp40
CC   heterodimer which can potentiate the cytotoxic activity of feline
CC   cytotoxic T lymphocyte cells. Such proteins are used for treatment of
CC   feline autoimmune diseases e.g. as caused by feline herpes virus or
CC   feline calcivirus.
XX
SQ   Sequence 689 BP; 192 A; 193 C; 145 G; 159 T; 0 other;

Alignment Scores:
Pred. No.:              8.92e-97      Length:        689
Score:                  932.00        Matches:       183
Percent Similarity:     95.94%        Conservative:  6
Best Local Similarity:  92.89%        Mismatches:    8
Query Match:            93.76%        Indels:        0
DB:                     19            Gaps:          0

US-09-917-265-50 (1-197) x AAV56641 (1-689)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::|||||||||   :::|||||||||||||:::|||||||||||||||||||||||
Db         82 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 141

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
                 ||||||||||||:::|||||||||||||||||||||||||||||||||||   |||
Db        142 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 201

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        202 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 261

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GAGGCCTGCCTGCCACTGGAACTGACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 321
```

```
Qy          81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
               ||||||||||||||||||||||||||||||||   |||   ||||||||||||   |||
Db         322 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 381

Qy         101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
               ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db         382 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 441

Qy         121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         442 GCAAAGCTGCTGATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 501

Qy         141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
               ||||||||||||||||||||||||||   ||||||||||||||||||||   ||||||
Db         502 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 561

Qy         161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         562 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 621

Qy         181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
               ||||||||||||||||||||:::||||||||||||||||||||||||||
Db         622 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 672

RESULT 13
AAV56628
ID   AAV56628 standard; cDNA; 1441 BP.
XX
AC   AAV56628;
XX
DT   23-NOV-1998  (first entry)
XX
DE   Feline FLAFp35 cDNA.
XX
KW   Cytokine; feline; FLAFp40; FLAFp35; heterodimer; cytotoxic; treatment;
KW   T lymphocyte cell; autoimmune disease; ds.
XX
OS   Felis catus.
XX
FH   Key             Location/Qualifiers
FT   CDS             133..811
FT                   /*tag= a
FT   sig_peptide     133..217
FT                   /*tag= b
FT   mat_peptide     218..808
FT                   /*tag= c
FT                   /product= "FLAFp35"
FT                   /note= "feline cytokine"
XX
PN   WO9746583-A1.
XX
PD   11-DEC-1997.
XX
PF   29-MAY-1997;   97WO-JP01824.
XX
PR   04-JUN-1996;   96JP-0165249.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Fujiyasu T,  Imagawa Y,  Imamura T,  Maeda H,  Tokiyoshi S;
XX
DR   WPI; 1998-042118/04.
DR   P-PSDB; AAW76175.
XX
PT   Novel feline cytokine protein - useful for treating feline
PT   auto:immune diseases, e.g. those caused by feline herpes virus or
PT   feline calcivirus
XX
PS   Claim 22; Page 57-58; 94pp; Japanese.
XX
CC   This sequence encodes a novel feline cytokine protein, FLAFp35. This
CC   protein can be used in the production of a FLAFp35/FLAFp40 heterodimer
CC   which can potentiate the cytotoxic activity of feline cytotoxic T
CC   lymphocyte cells. Such proteins are used for treatment of feline
CC   autoimmune diseases e.g. as caused by feline herpes virus or feline
CC   calcivirus.
XX
SQ   Sequence 1441 BP; 451 A; 325 C; 258 G; 407 T; 0 other;

Alignment Scores:
Pred. No.:              2.49e-96        Length:         1441
Score:                  932.00          Matches:        183
Percent Similarity:     95.94%          Conservative:   6
Best Local Similarity:  92.89%          Mismatches:     8
Query Match:            93.76%          Indels:         0
DB:                     19              Gaps:           0

US-09-917-265-50 (1-197) x AAV56628 (1-1441)

Qy           1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
               |||:::|||||||||   :::||||||||||||:::||||||||||||||||||||||
Db         218 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 277

Qy          21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
                 ||||||||||||:::||||||||||||||||||||||||||||||||||   |||
Db         278 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 337

Qy          41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         338 TCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 397

Qy          61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         398 GAGGCCTGCTTACCACTGGAATTAACCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 457

Qy          81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
               ||||||||||||||||||||||||||||||||   |||   ||||||||||||   |||
Db         458 TCTCTGATAACTAATGGGAGTTGCCTGGCCTCCAGAAAGACCTCTTTTATGACGACCCTG 517

Qy         101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
               ||||||||||||||||||||||||||||||||||||||:::||||||||||||||||||
Db         518 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 577

Qy         121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         578 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 637

Qy         141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
               ||||||||||||||||||||||||||   ||||||||||||||||||||   ||||||
Db         638 ATTGATGAGCTGTTACAGGCCCTGAATGTCAACAGTGTGACTGTGCCACAGAACTCCTCC 697

Qy         161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         698 CTGGAAGAACCAGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 757

Qy         181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
               ||||||||||||||||||||:::||||||||||||||||||||||||||
Db         758 AGAATTCGTGCAGTGACCATCAATAGAATGATGAGCTACCTGAATTCTTCC 808

RESULT 14
AAF26083
ID   AAF26083 standard; DNA; 669 BP.
XX
AC   AAF26083;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA SEQ ID 4.
XX
KW   Feline; cat; vaccine; gp140; IL-12; IL-16; lentivirus infection;
KW   interleukin; antiviral; cytotoxic immune response; Th1 response; ds.
XX
OS   Felis sp.
XX
PN   WO200104280-A2.
```

```
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02262.
XX
PR   08-JUL-1999;   99CH-0001258.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
XX
PI   Leutenegger C,  Schroff M,  Wittig B,  Lutz H;
XX
DR   WPI; 2001-147190/15.
XX
PT   Vaccine for treating or preventing lentivirus infection in cats,
PT   contains nucleic acid sequence encoding viral protein under control of
PT   eukaryotic promoter  -
XX
PS   Claim 14; Page 37; 37pp; German.
XX
CC   This invention describes a novel vaccine (A) for prevention or treatment
CC   of lentivirus infection in felines which comprises an immunizing nucleic
CC   acid sequence (I) that contains, or comprises, at least part of a gene
CC   encoding a protein (II) of the virus, under control of a eukaryotic
CC   promoter functional in the relevant animal. (II) is especially the
CC   envelope (env) protein. The invention also describes (1) vaccine (A)
CC   containing an immunizing protein, or fragment, from a lentivirus plus at
CC   least one of interleukin (IL)-12 and/or -16; and (2) preparation of a
CC   lentivirus protein, or fragment, especially derived from feline immune
CC   deficiency virus (FIV), by expressing the corresponding nucleic acid
CC   sequence in a host cell. The products of the invention have antiviral
CC   activity. The vaccine (A) and related protein-based vaccines, are
CC   particularly used to treat or prevent lentivirus infections in domestic
CC   cats, especially feline immune deficiency virus (FIV). Vaccination with
CC   (A) allows differentiation between vaccinated and infected animals, from
CC   the antibody status. The vaccines may be formulated with an adjuvant
CC   (particularly interleukin-12 and/or IL-16) that elicits a cytotoxic
CC   immune response, particularly a Th1 response.
XX
SQ   Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 other;

Alignment Scores:
Pred. No.:              2e-95          Length:         669
Score:                  920.00         Matches:        179
Percent Similarity:     94.92%         Conservative:   8
Best Local Similarity:  90.86%         Mismatches:     10
Query Match:            92.56%         Indels:         0
DB:                     22             Gaps:           0

US-09-917-265-50 (1-197) x AAF26083 (1-669)

Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::|||||||||   :::|||||||||||:::|||||||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
                 ||||||||||||:::|||||||||||||||||||||||||||||||||   |||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||   ||||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              |||||||||||||||||||||||||   |||   |||   ||||||||||||   |||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              ||||||||||||||||||||||||||||||||||||:::||||||||||||||||||||

Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||:::|||||||||||||||||||||||||||||||||   ||||||
Db        496 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||||:::||||||||||||||||||||:::|||
Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666

RESULT 15
AAF26086
ID   AAF26086 standard; DNA; 669 BP.
XX
AC   AAF26086;
XX
DT   24-APR-2001  (first entry)
XX
DE   Feline IL-12p35 encoding DNA.
XX
KW   Feline; cat; vaccine; IL-12; interleukin; immunizing antigen; infection;
KW   immunostimulant; tumor; antiviral; antitumor; interferon-gamma;
KW   Th1 defect; autoimmune disease; IL-12p40; IL-12p35; ds.
XX
OS   Felis sp.
XX
PN   WO200104155-A2.
XX
PD   18-JAN-2001.
XX
PF   08-JUL-2000; 2000WO-DE02263.
XX
PR   08-JUL-1999;   99CH-0001259.
XX
PA   (MOLO-) MOLOGEN FORSCH ENTWICKLUNGS & VERTRIEBS.
PA   (UYZU-) UNIV ZUERICH.
PA   (REGC ) UNIV CALIFORNIA.
XX
PI   Lutz H,  Leutenegger C,  Pedersen N,  Schroff M,  Wittig B;
XX
DR   WPI; 2001-147178/15.
XX
PT   Recombinant feline interleukin-12, useful as immunostimulant and for
PT   treating e.g. viral infections in cats, and related nucleic acid
PT   constructs  -
XX
PS   Claim 3; Page 31; 35pp; German.
XX
CC   This invention describes a novel feline interleukin-12 (fIL-12)
CC   polypeptide (I) that is expressed, by recombinant gene expression in
CC   eukaryotic or prokaryotic cells, in the form of both polypeptide chains
CC   of subunits p35 and p40. These proteins are formed so that, in equimolar
CC   concentrations and in presence of an immunizing antigen, they can be
CC   administered to carnivores, particularly domestic cats. The invention
CC   also describes a nucleic acid construct (II) encoding fIL-12 containing
CC   sequences at least 95% identical with the p40- and p35-encoding sequences
CC   (A, 990 bp and B, 669 bp respectively), reproduced in the specification,
CC   as immunostimulants for immunization against infectious diseases and/or
CC   for treating infections or tumors in felines, especially domestic cats.
CC   The products of the invention have immunostimulatory, antiviral and
CC   antitumor activity. Nucleic acid constructs that encode (II) are useful
CC   as adjuvants for prophylactic immunization against viral diseases and for
CC   treating diseases associated with a Th1 defect. IL-12 induces synthesis
CC   of interferon gamma (Th1 response). The feline interleukin-12 polypeptide
CC   is useful for carnivores, and particularly domestic cats in the
```

CC following: (i) as immunostimulant, for preventative or therapeutic use;
CC and (ii) treating tumors and autoimmune diseases, or diseases associated
CC with a Th1 defect, especially pre-existing infections by feline immune
CC deficiency virus (FIV), feline leukemia virus and corona virus.
XX
SQ Sequence 669 BP; 189 A; 179 C; 140 G; 161 T; 0 other;

Alignment Scores:

Pred. No.:	2e-95	Length:	669
Score:	920.00	Matches:	179
Percent Similarity:	94.92%	Conservative:	8
Best Local Similarity:	90.86%	Mismatches:	10
Query Match:	92.56%	Indels:	0
DB:	22	Gaps:	0

US-09-917-265-50 (1-197) x AAF26086 (1-669)

```
Qy          1 ArgSerLeuProThrAlaSerProSerProGlyIlePheGlnCysLeuAsnHisSerGln 20
              |||:::|||||||||   :::|||||||||||||:::|||||||||||||||||||||
Db         76 AGGAACCTCCCCACACCCACACCAAGCCCAGGAATGTTCCAGTGCCTCAACCACTCCCAA 135

Qy         21 AsnLeuLeuArgAlaValSerAsnThrLeuGlnLysAlaArgGlnThrLeuGluLeuTyr 40
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||   |||
Db        136 ACCCTGCTGCGAGCCATCAGCAACACGCTTCAGAAGGCCAGACAAACTCTAGAATTTTAC 195

Qy         41 SerCysThrSerGluGluIleAspHisGluAspIleThrLysAspLysThrSerThrVal 60
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        196 CCCTGCACTTCCGAAGAGATTGATCATGAAGATATCACAAAAGATAAAACCAGCACAGTG 255

Qy         61 GluAlaCysLeuProLeuGluLeuThrMetAsnGluSerCysLeuAlaSerArgGluIle 80
              ||||||||||||||||||||||   |||||||||||||||||||||||||||||||||
Db        256 GAGGCCTGCTTACCACTGGAATTAGCCATGAATGAGAGTTGCCTGGCTTCCAGAGAGATC 315

Qy         81 SerLeuIleThrAsnGlySerCysLeuAlaSerGlyLysAlaSerPheMetThrValLeu 100
              |||||||||||||||||||||||||   |||   |||   ||||||||||||   |||
Db        316 TCTCTGATAACTAATGGGAGTTGCCTGGTGTCCAGAAAGACCTCTTTTATGACGACCCTG 375

Qy        101 CysLeuSerSerIleTyrGluAspLeuLysMetTyrGlnMetGluPheLysAlaMetAsn 120
              |||||||||||||||||||||||||||||||||||:::|||||||||||||||||||
Db        376 TGCCTTAGCAGTATCTATGAGGACTTGAAGATGTACCAGGTGGAGTTCAAGGCCATGAAT 435

Qy        121 AlaLysLeuLeuMetAspProLysArgGlnIlePheLeuAspGlnAsnMetLeuThrAla 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        436 GCAAAGCTGTTAATGGATCCTAAAAGGCAGATCTTTCTGGATCAAAACATGCTGACAGCT 495

Qy        141 IleAspGluLeuLeuGlnAlaLeuAsnPheAsnSerValThrValProGlnLysSerSer 160
              ||||||||||||:::|||||||||||||||||||||||||||||||||   ||||||
Db        496 ATTGATGAGCTGATGCAGGCCCTGAATTTCAACAGTGTGACTGTGCCACAGAACTCCTCC 555

Qy        161 LeuGluGluProAspPheTyrLysThrLysIleLysLeuCysIleLeuLeuHisAlaPhe 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        556 CTTGAAGAACCGGATTTTTATAAAACTAAAATCAAGCTCTGCATACTTCTTCATGCTTTC 615

Qy        181 ArgIleArgAlaValThrIleAspArgMetMetSerTyrLeuAsnSerSer 197
              ||||||||||||||||||:::|||||||||||||||||||:::|||
Db        616 AGAATCCGTGCAGTGACCATCAATAGAATGATGAGCTATCTGAATGCTTCC 666
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Search completed: July 16, 2003, 20:23:58
Job time : 141.28 secs